

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:40:10 : Search time 72.79 Seconds
(without alignments)
73.255 Million cell updates/sec

Title: US-09-289-346a-7
Perfect score: 359
Sequence: 1 TLVGFPOVGRSGARSGCQT.....FQFHNLSALALAFDKTRFP 70

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Bred. No. is the number of results predicted by chance to have a
score equal to or higher than the observed score. This number is printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB	ID	Description
1	342	95.3	352	1	OOCCVLT
2	242	67.4	361	1	AAI protein - toma
3	229	63.8	358	2	AAI protein - toma
4	222	61.8	362	1	Hypothetical prote
5	216	60.2	349	2	AAI protein - toma
6	215	60.2	349	2	replicase - pepper
7	215	59.9	359	2	gene C1 protein -
8	215	59.9	359	2	AAI protein - beet
9	211	58.1	355	2	AAI protein - toma
10	210	58.5	355	1	AAI protein - toma
11	207	57.7	358	1	AAI protein - toma
12	205	57.1	351	2	AAI protein - toma
13	205	57.1	359	2	AAI protein - toma
14	195	54.3	352	2	replication-associ
15	193	53.8	357	2	AAI protein - toma
16	193	53.8	357	2	AAI protein - toma
17	193	53.8	357	2	AAI protein - toma
18	170	45.1	361	1	AAI protein - toma
19	168	44.7	361	1	AAI protein - toma
20	168	44.7	361	1	AAI protein - toma
21	168	44.7	361	1	AAI protein - toma
22	168	44.7	361	1	AAI protein - toma
23	168	44.7	361	1	AAI protein - toma
24	168	44.7	361	1	AAI protein - toma
25	168	44.7	361	1	AAI protein - toma
26	168	44.7	361	1	AAI protein - toma
27	168	44.7	361	1	AAI protein - toma
28	168	44.7	361	1	AAI protein - toma
29	168	44.7	361	1	AAI protein - toma

30	59.5	16.6	224	2	140474	pro-sigma-E proces
31	59.5	16.6	4466	1	517653	dynem beta heavy
32	59	16.4	370	2	734050	hypothetical prote
33	59	16.4	370	2	734050	hypothetical prote
34	59	16.4	370	2	734050	hypothetical prote
35	58.5	16.3	289	2	871667	hypothetical prote
36	58.5	16.3	354	2	A75087	hypothetical prote
37	58.5	16.3	1402	2	F84062	hypothetical prote
38	58	16.2	390	2	730020	hypothetical prote
39	57.5	16.0	230	2	S46332	hypothetical prote
40	57.5	16.0	234	2	D84075	hypothetical prote
41	57.5	16.0	234	2	D83718	hypothetical prote
42	57.5	16.0	234	2	D83718	hypothetical prote
43	57.5	16.0	234	2	D83718	hypothetical prote
44	57.5	16.0	234	2	D83718	hypothetical prote
45	57.5	16.0	234	2	D83718	hypothetical prote

ALIGNMENTS

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RESULT 1
OOCCVLT
AAI protein - toma
Species: toma golden mosaic virus
A:Note: host Nicotiana sp. (tobacco)
C:Date: 28-Aug-1985 #sequence-revision 28-Aug-1985 #taxL-change 08-Apr-1994
E:Accession: A04170
E:Hamilton, 1977-2000, Steila V.E.; Coutts, R.H.A.; Buck, K.W.
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of toma
A:Reference number: A04163
A:Molecule type: DNA
A:Accession: A04170
A:Residues: 1,352 <184>
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A
C:Genetics:
A:Map position: segment A
C:Superfamily: toma golden mosaic virus AAI protein

Query Match 95.3%; Score 342; DB 1; Length 352;
Best Local Similarity 95.7%; Pred. No. 2,3e-31;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 1 TLVGFPOVGRSGARSGCQTNNMAAALNASKREKALOTIRKIPKYLQFHNLSNL 60
DB 111 TLVGFPOVGRSGARSGCQTNNMAAALNASKREKALOTIRKIPKYLQFHNLSNL 170

Cy 61 AAIKDKTRFP 70
DB 171 DAIKDKTRFP 180

RESULT 2
OOCCVLT
AAI protein - potato yellow mosaic virus (Isolate Venezuela)
Species: potato yellow mosaic virus
C:Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #taxL-change 16-Jun-2000
E:Accession: U00364
E:Coutts, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato ye
A:Reference number: J00362; M01D:91311403
A:Accession: J00364
A:Status: translation not shown
A:Genetics:
A:Residues: 1,361 <CON>
A:Cross-references: GB:D00940; NID:9222458; PIDN:BA00782.1; PID:9222459
A:Map position: segment A
C:Superfamily: toma golden mosaic virus AAI protein

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Query Match
Best Local Similarity 67.4%; Score 242; DB 1; Length 361;
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

OY 1 TLWNGEFOVDRSARGCCTSDNDAAEALNASSKEAALQIIRKIPKYLQFPHNLNSAL 60
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TLWNGEFOVDRSARGCCTSDNDAAEALNASSKEAALQIIRKIPKYLQFPHNLNSAL 169
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 AATFDKTPP 69
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 170 DRIETPPLETVYSPFLSSSFDRVPE 179
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
Hypothetical protein, 40.4K - cassava latent virus (Nigerian isolate)
C:Species: cassava latent virus
C:Accession: S07594
C:Description: #sequence-revision 07-Sep-1990 #textL-change 20-Sep-1999
R:Morris, B.; Coates, L.; Lowe, S.; Richardson, K.; Eddy, P.
Nucleic Acids Res. 18, 197-198, 1990
A:Title: Nucleotide sequence of the infectious cloned DNA components of African cassava
A:Reference number: S07590; MUID:90174930
A:Accession: S07594
A:Status: translation not shown
A:Molecule type: DNA
A:Cross-references: EMBL:X17095; NID:959371; PTDN:CAA34953.1; PID:959376
A:Map position: segment DNA1
C:Superfamily: tomato golden mosaic virus A11 protein

Query Match
Best Local Similarity 63.8%; Score 229; DB 2; Length 358;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

OY 1 TLWNGEFOVDRSARGCCTSDNDAAEALNASSKEAALQIIRKIPKYLQFPHNLNSAL 60
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 109 TLWNGEFOVDRSARGCCTSDNDAAEALNASSKEAALNIVRELVPDVLQFPHNLNSAL 168
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 AATFDKTPP 70
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 169 DRIFQPPPP 178
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
A11 protein - tomato yellow leaf curl virus (strain Australia)
M:Alternate names: CI protein
C:Species: tomato yellow leaf curl virus
C:Date: 17-Feb-1994 #sequence-revision 17-Feb-1994 #textL-change 07-May-1999
C:Accession: J01887
R:Dev. Virol. 74, 147-151, 1993
J. Gen. Virol. 74, 147-151, 1993
A:Title: Nucleotide sequence and genome organization of tomato leaf curl geminivirus.
A:Accession: J01887; MUID:9153778
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-362 <DRY>
A:Cross-references: GB:S53251
C:Superfamily: tomato golden mosaic virus A11 protein

Query Match
Best Local Similarity 61.8%; Score 222; DB 1; Length 362;
Matches 45; Conservative 9; Mismatches 15; Indels 16; Gaps 1;

OY 1 TLWNGEFOVDRSARGCCTSDNDAAEALNASSKEAALQIIRKIPKYLQFPHNLNSAL 60
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 110 TLWNGEFOVDRSARGCCTSDNDAAEALNASSKEAALNIVRELVPDVLQFPHNLNSAL 169
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 AATFDKTPP 69
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 170 DRIETPPLETVYSPFLSSSFDRVPE 194
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
J02300
replicase - pepper huasteco virus (component A)
M:Alternate names: ORF A11 protein
C:Species: pepper huasteco virus
C:Accession: J02300
C:Description: #sequence-revision 14-Jul-1994 #textL-change 20-Sep-1999
R:Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Herrera-Estrella, L.; Rivera-Bustamante,
J. Gen. Virol. 74, 2225-2231, 1993
A:Title: Complete nucleotide of pepper huasteco virus: Analysis and comparison with b
A:Reference number: J02299; MUID:94015007
A:Accession: J02300
A:Status: type DNA
A:Molecule type: DNA
A:Residues: 1-349 <DRY>
A:Cross-references: GB:X70418; NID:961023; PTDN:CAA9856.1; PID:961025
C:Superfamily: tomato golden mosaic virus A11 protein

Query Match
Best Local Similarity 60.2%; Score 216; DB 2; Length 349;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

OY 1 TLWNGEFOVDRSARGCCTSDNDAAEALNASSKEAALQIIRKIPKYLQFPHNLNSAL 60
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TLWNGEFOVDRSARGCCTSDNDAAEALNASSKEAALQIIRKIPKYLQFPHNLNSAL 169
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 AATFDKTPP 70
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 170 NRITQPPPP 179
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
S31875
A11 protein - pepper rizado amarillo virus
C:Species: pepper rizado amarillo virus
C:Accession: S31875
C:Description: #sequence-revision 26-May-1995 #textL-change 20-Sep-1999
R:Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Jimenez, B.; Herrera-Estrella, L.; Rivera
submitted to the EMBL Data Library, February 1993
A:Description: Complete nucleotide sequence of pepper huasteco virus: analysis and co
A:Reference number: S31872
A:Accession: S31875
A:Status: preliminary
A:Molecule type: type DNA
A:Residues: 1-349 <DRY>
A:Cross-references: EMBL:X70418; NID:961023; PTDN:CAA9856.1; PID:961025
A:Note: the source is designated as pepper huasteco virus
C:Superfamily: tomato golden mosaic virus A11 protein

Query Match
Best Local Similarity 60.2%; Score 216; DB 2; Length 349;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

OY 1 TLWNGEFOVDRSARGCCTSDNDAAEALNASSKEAALQIIRKIPKYLQFPHNLNSAL 60
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TLWNGEFOVDRSARGCCTSDNDAAEALNASSKEAALQIIRKIPKYLQFPHNLNSAL 169
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 AATFDKTPP 70
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 170 NRITQPPPP 179
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
S39211
gene CI protein - tomato yellow leaf curl virus

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C:Species: tomato yellow leaf curl virus
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #excl_change 20-Sep-1999
 C:Accession: S39211
 A:Notes: The nucleotide sequence was submitted to the EMBL Data Library, August 1991
 A:Description: High similarity among the tomato yellow leaf curl virus isolates from the
 A:Reference number: S39209
 A:Accession: S39211
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-359 <NR>
 A:Cross-references: EMBL:J25751; NID:9433655; PIDN:CA61026.1; PID:9433658
 C:Superfamily: tomato golden mosaic virus A11 protein

Query Match 59.9%; Score 215; DB 2; Length 359;
 Best Local Similarity 58.0%; Pred. No. 7,1e-17;
 Matches 40; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

OY 2 LVMGEVDGNSARGCQTSNDAAAEALVANSKEEALQIIRKIPKYLFPFHNLNSAL 61
 DB 111 LEMKPTQIDGNSARGCQTSNDAAAEALVANSKEEALQIIRKIPKYLFPFHNLNSAL 170
 OY 62 AIFDKTPEP 70
 DB 171 RVFQVPPAP 179

RESULT 8
 S28360
 A11 protein - beet curly top virus
 C:Species: beet curly top virus
 C:Date: 07-May-1993 #sequence_revision 07-May-1993 #excl_change 20-Sep-1999
 C:Accession: S28360
 R:Stanley, J., Makham, P.G., Callis, R.J., Pinner, M.S.
 A:Title: The nucleotide sequence of an infectious clone of the geminivirus beet curly to
 A:Reference number: S28360
 A:Accession: S28360
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-385 <STA>
 A:Cross-references: DB:W4597; EMBL:X04144; NID:9210678; PIDN:AAA2751.1; PID:9210679
 C:Superfamily: tomato golden mosaic virus A11 protein

Query Match 59.1%; Score 212; DB 2; Length 385;
 Best Local Similarity 55.7%; Pred. No. 1.7e-16;
 Matches 39; Conservative 15; Mismatches 16; Gaps 0;

OY 1 TLWGEVDGNSARGCQTSNDAAAEALVANSKEEALQIIRKIPKYLFPFHNLNSAL 60
 DB 137 TLWGEVDGNSARGCQTSNDAAAEALVANSKEEALQIIRKIPKYLFPFHNLNSAL 196
 OY 61 AIFDKTPEP 70
 DB 197 OKTFORPEP 206

RESULT 9
 S22593
 hypothetical protein C4 - tomato yellow leaf curl virus
 C:Species: tomato yellow leaf curl virus
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #excl_change 20-Sep-1999
 C:Accession: S22593
 A:Notes: The nucleotide sequence was submitted to the EMBL Data Library, August 1991
 A:Description: High similarity among the tomato yellow leaf curl virus isolates from the
 A:Reference number: S22588; MUID:92107650
 A:Accession: S22593
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-359 <KHE>

A:Cross-references: EMBL:X61153; NID:962211; PIDN:CA43466.1; PID:962217
 A:Notes: The nucleotide sequence was submitted to the EMBL Data Library, August 1991
 C:Superfamily: tomato golden mosaic virus A11 protein

Query Match 58.8%; Score 211; DB 2; Length 359;
 Best Local Similarity 56.5%; Pred. No. 2e-16;
 Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

OY 2 LVMGEVDGNSARGCQTSNDAAAEALVANSKEEALQIIRKIPKYLFPFHNLNSAL 61
 DB 111 LEMKPTQIDGNSARGCQTSNDAAAEALVANSKEEALQIIRKIPKYLFPFHNLNSAL 170
 OY 62 AIFDKTPEP 70
 DB 171 RVFQVPPAP 179

RESULT 10
 G0CWM1
 A11 protein - abutilon mosaic virus (isolate west india)
 C:Species: abutilon mosaic virus
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #excl_change 08-Apr-1994
 C:Accession: A36214
 R:Friessmuth, T.; Zimmat, G.; Jaske, H.
 A:Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as
 A:Reference number: A36214; MUID:91020964
 A:Accession: A36214
 A:Molecule type: DNA
 A:Residues: 1-355 <PR1>
 A:Cross-references: EMBL:X15983
 C:Genetics:
 A:Map position: segment A
 C:Superfamily: tomato golden mosaic virus A11 protein

Query Match 58.5%; Score 210; DB 1; Length 355;
 Best Local Similarity 57.1%; Pred. No. 2.6e-16;
 Matches 40; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

OY 1 TLWGEVDGNSARGCQTSNDAAAEALVANSKEEALQIIRKIPKYLFPFHNLNSAL 60
 DB 111 TLWGEVDGNSARGCQTSNDAAAEALVANSKEEALQIIRKIPKYLFPFHNLNSAL 169
 OY 61 AIFDKTPEP 70
 DB 170 ERTFNKPEP 179

RESULT 11
 A11 protein - tomato mottle virus (isolate Florida)
 C:Species: tomato mottle virus
 C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #excl_change 07-May-1999
 C:Accession: J01870
 R:Abouzaid, A.M.; Polston, J.E.; Hiebert, E.
 A:Title: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated f
 A:Reference number: J01870
 A:Accession: J01870
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-358 <ABO>
 A:Cross-references: GB:L14460
 C:Genetics:
 A:Map position: segment A
 C:Superfamily: tomato golden mosaic virus A11 protein

Query Match 57.7%; Score 207; DB 1; Length 358;
 Best Local Similarity 54.3%; Pred. No. 5.8e-16;
 Matches 38; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

OY 1 TLWGEFQVDSNRAGCGQTSNDAAEAALNASKSEALQITREKIPKYLQFQFNLSALAI 60
 DB 107 TLEMDQFQDSNRAGCGQTSNDAAEAALNASKSEALQITREKIPKYLQFQFNLSALAI 166
 OY 61 AATFQKPEP 70
 DB 167 ERTFAKPEP 176

RESULT 12

Query Match
 Best Local Similarity 57.1%; Score 205; DB 2; Length 351;
 Matches 40; Conservative 5; Mismatches 18; Indels 0; Gaps 0;
 A:Reference: 502327; MUID:94065670
 A:Accession: 502327
 A:Molecule type: DNA
 A:Residues: 1-351 <HON>
 A:Cross-references: EMBL:224758; NID:9395351; PIDN:CAAB0891.1; PID:9584046
 C:Superfamily: tomato golden mosaic virus A1 protein

OY 4 WGEFQVDSNRAGCGQTSNDAAEAALNASKSEALQITREKIPKYLQFQFNLSALAI 63
 DB 113 WGFQFQDSNRAGCGQTSNDAAEAALNASKSEALQITREKIPKYLQFQFNLSALAI 172
 OY 64 FQKPEP 70
 DB 173 FTKPEP 179

RESULT 13

Query Match
 Best Local Similarity 57.1%; Score 205; DB 2; Length 351;
 Matches 38; Conservative 11; Mismatches 20; Indels 0; Gaps 0;
 A:Reference: 502327; MUID:94065670
 A:Accession: 502327
 A:Molecule type: DNA
 A:Residues: 1-351 <HON>
 A:Cross-references: EMBL:2248390; NID:91041671; PID:91334964
 C:Superfamily: tomato golden mosaic virus A1 protein

OY 2 LWGEFQVDSNRAGCGQTSNDAAEAALNASKSEALQITREKIPKYLQFQFNLSALAI 61
 DB 111 LEMQFQDSNRAGCGQTSNDAAEAALNASKSEALQITREKIPKYLQFQFNLSALAI 170
 OY 62 AATFQKPEP 70
 DB 171 KVFQVPEP 179

RESULT 14

S59885

replication-associated protein C1 - tomato yellow leaf curl virus
 C:Species: tomato yellow leaf curl virus
 C:Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 20-Sep-1999
 C:Accession: S59885
 C:Description: S59885, B. D. submitted to the EMBL Data Library, February 1995
 A:Description: Nucleotide sequences from tomato leaf curl viruses from different countries
 A:Reference number: S59346
 A:Accession: S59885
 A:Status: preliminary
 A:Residues: 1-1360 <HON>
 A:Cross-references: EMBL:248182; NID:9944838; PIDN:CAAB8229.1; PID:9974211
 C:Superfamily: tomato golden mosaic virus A1 protein

Query Match
 Best Local Similarity 54.3%; Score 195; DB 2; Length 360;
 Matches 38; Conservative 12; Mismatches 16; Indels 0; Gaps 0;
 OY 4 WGEFQVDSNRAGCGQTSNDAAEAALNASKSEALQITREKIPKYLQFQFNLSALAI 63
 DB 113 FQVQFQDSNRAGCGQTSNDAAEAALNASKSEALQITREKIPKYLQFQFNLSALAI 172
 OY 64 FQKPEP 65
 DB 173 FTKPEP 178

RESULT 15

Query Match
 Best Local Similarity 53.8%; Score 193; DB 1; Length 357;
 Matches 38; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
 A:Reference: 502327; MUID:94065670
 A:Accession: 502327
 A:Molecule type: DNA
 A:Residues: 1-351 <HON>
 A:Cross-references: GB:X15656; NID:962204; PIDN:CAAB3688.1; PID:962207
 C:Superfamily: tomato golden mosaic virus A1 protein

OY 4 WGEFQVDSNRAGCGQTSNDAAEAALNASKSEALQITREKIPKYLQFQFNLSALAI 63
 DB 111 FQVQFQDSNRAGCGQTSNDAAEAALNASKSEALQITREKIPKYLQFQFNLSALAI 170
 OY 64 F 64
 DB 171 F 171

Search completed: January 3, 2002, 15:40:11
 Job time: 307 sec

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GenCore version 4.5
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OM protein - protein search, using SW model

Run on: January 3, 2002, 15:57:17 ; Search time 43.68 seconds
(without alignments)

58.758 Million cell updates/sec

Title: us-09-289-346a-7

Accession: 1 TLWGEFQVDSRARGSCOT.....POPHNLSALAEFKTPPEP 70

Sequence: BLOSUM62

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100055

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Lasting first 45 summaries

Database: SWISSProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	342	95.3	352	VAL1_TGMY	P03567 tomato gold
2	242	67.4	361	VAL1_PMYV	P27298 potato yell
3	229	63.8	356	VAL1_CVVK	P14582 cassava lat
4	229	63.8	356	VAL1_CVVK	P14582 cassava lat
5	229	63.8	356	VAL1_CVVK	P14582 cassava lat
6	216	60.2	345	VAL1_PMYV	P27260 tomato yell
7	215	59.9	359	VAL1_TYCU	P38609 tomato yell
8	212	59.1	358	VAL1_TYCU	P14991 beet curly
9	211	58.8	353	VAL1_TYCU	P05175 bean golden
10	211	58.8	359	VAL1_TYCU	P27260 tomato yell
11	210	58.5	355	VAL1_TYCU	P21947 beet curly
12	210	58.5	355	VAL1_TYCU	P21947 beet curly
13	197	53.8	353	VAL1_TYCU	P06657 tomato mott
14	197	53.8	353	VAL1_TYCU	P06657 tomato mott
15	189	48.9	347	VAL1_TYCU	P29408 squash leaf
16	189	48.9	347	VAL1_TYCU	P29408 squash leaf
17	163	44.7	347	VAL1_TYCU	O94924 homo sapien
18	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
19	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
20	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
21	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
22	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
23	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
24	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
25	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
26	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
27	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
28	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
29	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
30	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
31	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
32	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
33	163	44.7	347	VAL1_TYCU	O94924 mesocricetu

Result No.	Score	Query Match	Length	ID	Description
1	342	95.3	352	VAL1_TGMY	P03567 tomato gold
2	242	67.4	361	VAL1_PMYV	P27298 potato yell
3	229	63.8	356	VAL1_CVVK	P14582 cassava lat
4	229	63.8	356	VAL1_CVVK	P14582 cassava lat
5	229	63.8	356	VAL1_CVVK	P14582 cassava lat
6	216	60.2	345	VAL1_PMYV	P27260 tomato yell
7	215	59.9	359	VAL1_TYCU	P38609 tomato yell
8	212	59.1	358	VAL1_TYCU	P14991 beet curly
9	211	58.8	353	VAL1_TYCU	P05175 bean golden
10	211	58.8	359	VAL1_TYCU	P27260 tomato yell
11	210	58.5	355	VAL1_TYCU	P21947 beet curly
12	210	58.5	355	VAL1_TYCU	P21947 beet curly
13	197	53.8	353	VAL1_TYCU	P06657 tomato mott
14	197	53.8	353	VAL1_TYCU	P06657 tomato mott
15	189	48.9	347	VAL1_TYCU	P29408 squash leaf
16	189	48.9	347	VAL1_TYCU	P29408 squash leaf
17	163	44.7	347	VAL1_TYCU	O94924 homo sapien
18	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
19	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
20	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
21	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
22	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
23	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
24	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
25	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
26	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
27	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
28	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
29	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
30	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
31	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
32	163	44.7	347	VAL1_TYCU	O94924 mesocricetu
33	163	44.7	347	VAL1_TYCU	O94924 mesocricetu

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ID VAL1.PYVWV STANDARD: PRT: 361 AA.
AC P27258:
DT 01-APR-1992 (Rel. 23, Created)
DT 01-APR-1992 (Rel. 23, Last sequence update)
DT 01-APR-1992 (Rel. 23, Last annotation update)
DE ALL PROTEIN
OS Forcav yellow mosaic virus (isolate Venezuela).
OC Viruses: ssDNA viruses: Geminitoviridae; Begomovirus.
NCBI_TaxID=10828:
X1
RM SOURCE FROM N.A.
RA PubMed:1856630.
RA EMBL:U00001.
RA "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus."
RL J. Gen. Virol. 72:1515-1520(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
CC
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CC -----
CC EMBL:U00001.
CC PIR:J00364; BM000782.1; -.
CC Interpro: IPR001191; Gemin1.AL1.
CC Pfam: PF00799; Gemin1.AL1; 1.
CC PRINTS: PR00227; GEMCONCAT1.
CC DR PRINTS: PR00228; GEMCONCAT1.
CC PRODOM: PD000736; Gemin1.AL1; 1.
CC NP-binding: 220
CC SEQUENCE 361 AA: 40850 MW: 5622A33BF1261383 CRC64:
SO
Query Match 67.4%; Score 242; DB 1; Length 361;
Best Local Similarity: 66.7%; Pred. No. 3.7e-20;
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0:
OY 1 TLVNGEFOVGRSARGCGTSDNAAEALNANSKEEDLQIRKIPKRYIQPHNNSAL 60
DB 110 TLVNGEFOVGRSARGCGTSDNAAEALNANSKEEDLQIRKIPKRYIQPHNNSAL 169
OY 61 AAIETKPTPE 69
DB 110 AAIETKPTPE 178
DB 170 DRIFKPEPAP 178
RESULT 3
VAL1.CLVK STANDARD: PRT: 358 AA.
AC P14982:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE ALL PROTEIN
OS Cassava latent virus (strain Most Keayan 844).
OC Viruses: ssDNA viruses: Geminitoviridae; Begomovirus.
NCBI_TaxID=10818:
X1
RM SOURCE FROM N.A.
RA PubMed:1856630.
RA EMBL:U00001.
RA "Nucleotide sequence of cassava latent virus DNA."
RT Stanley J., Gay M.R.
RL Nature 301:260-262(1983).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
CC
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CC -----
CC EMBL:U00001.
CC PIR:J00364; BM000782.1; -.
CC Interpro: IPR001191; Gemin1.AL1.
CC Pfam: PF00799; Gemin1.AL1; 1.
CC PRINTS: PR00227; GEMCONCAT1.
CC DR PRINTS: PR00228; GEMCONCAT1.
CC PRODOM: PD000736; Gemin1.AL1; 1.
CC NP-binding: 220
CC SEQUENCE 358 AA: 40346 MW: 5013E753E591D069 CRC64:
SO
Query Match 63.8%; Score 229; DB 1; Length 358;
Best Local Similarity: 60.0%; Pred. No. 1.1e-18;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0:
OY 1 TLVNGEFOVGRSARGCGTSDNAAEALNANSKEEDLQIRKIPKRYIQPHNNSAL 60
DB 109 TLVNGEFOVGRSARGCGTSDNAAEALNANSKEEDLQIRKIPKRYIQPHNNSAL 168
OY 61 AAIETKPTPE 70
DB 169 DRIFKPEPAP 178
DB 169 DRIFKPEPAP 178
RESULT 4
VAL1.CLVK STANDARD: PRT: 358 AA.
AC P14972:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE ALL PROTEIN
OS Cassava latent virus (strain Nigerian).
OC Viruses: ssDNA viruses: Geminitoviridae; Begomovirus.
NCBI_TaxID=10819:
X1
RM SOURCE FROM N.A.
RA PubMed:2308831.
RA MEDLINE:90174930.
RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.
RA "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain)."
RL Nucleic Acids Res. 18:197-198(1990).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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CC -----
CC EMBL:U00001.
CC PIR:J00364; BM000782.1; -.
CC Interpro: IPR001191; Gemin1.AL1.
CC Pfam: PF00799; Gemin1.AL1; 1.
CC PRINTS: PR00227; GEMCONCAT1.
CC DR PRINTS: PR00228; GEMCONCAT1.
CC PRODOM: PD000736; Gemin1.AL1; 1.
CC NP-binding: 220
CC SEQUENCE 358 AA: 40033 MW: 10B16BB0CBDB5E2C CRC64:
SO

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OY 1 TLWGEFVDGRSANGCCTSDNDAEAALMASSKEPAALQIREKIPKTYLQFPHNINSAL 60
   1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 109 TYWGEFQIDGRSANGCQSDNDAEYAKALNSGSEALINVIREFADPVLQFPHNINSAL 168
OY 61 AAIPKTRPP 70
   ||:|:|
DB 169 DRIFORPEPAP 178

RESULT 5
VAL1.TYLCV STANDARD: PRT: 362 AA.
AC P36279:
DR 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE AL1 PROTEIN (C1 PROTEIN).
OS C1.
SN Tomato yellow leaf curl virus (strain Australia) (TYLCV).
SC Virus: ssDNA viruses; Geminiviridae; Begomovirus.
NCB_LocusID=58447;
RX SEQUENCE FROM N.A.
RP MEDLINE=93339778; PubMed=8423446;
RA Dry I. B., Ridgen J. E., Krake L. R., Mullineaux P. M., Rezaian M. A.;
R "Nucleotide sequence and genome organization of tomato leaf curl
R geminivirus"; 74:147-151(1993).
CC 1 - SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
DR InterPro: IPR001191; Gemin1.AL1.
DR Pfam: PF00799; Gemin1.AL1.
DR PRINTS: PR00227; GEMCOATC.VL1.
DR PRODOM: PD000736; GEMCOATC.VL1.
DR NCBI_TaxID=37139;
FT NP_BIND 221 228 ATP (POTENTIAL).
SO SEQUENCE 362 AA; 41197 MW; 3436784BA704098 CRC64;

Query Match 61.8%; Score 222; DB 1; Length 362;
Best Local Similarity 52.9%; Pred. No. 7e-18;
Matches 45: Conservative 9; Mismatches 15; Indels 16; Gaps 1;
OY 1 TLWGEFVDGRSANGCCTSDNDAEAALMASSKEPAALQIREKIPKTYLQFPHNINSAL 60
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 110 TLENGEFOIDGRSANGCQSDNDAEYAKALNSGSEALINVIREFADPVLQFPHNINSAL 169
OY 61 AAT-----FDRPE 69
   ||:|:|
DB 170 DRIFPEPELVYSPYSSSPDRPE 194

RESULT 6
VAL1.PHV STANDARD: PRT: 349 AA.
AC Q06923:
DR 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN.
OS Pepper huasteco virus (PHV).
SC Virus: ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=28349;
RX SEQUENCE FROM N.A.
RP MEDLINE=94015007; PubMed=8409944;
RA Torres-Pacheco I., Garzon-Tiznado J. A., Herrera-Estrella L.,
RA Rivera-Bustamante R. F.;
R "Complete nucleotide sequence of pepper huasteco virus: analysis and
R comparison with bipartite geminiviruses";

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RL J. Gen. Virol. 74:2225-2231(1993).
CC 1 - SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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CC or send an email to license@isb-slb.ch).
CC -----
CC EMBL: X70419; GMA49856.1;
CC S18211; S19211; S20300.
CC InterPro: IPR001191; Gemin1.AL1.
CC Pfam: PF00799; Gemin1.AL1.
CC PRINTS: PR00227; GEMCOATC.VL1.
CC PRODOM: PD000736; GEMCOATC.VL1.
CC NCBI_TaxID=37139;
CC ATP-BINDING 221 228
CC NP_BIND 221 228
CC SEQUENCE 349 AA; 39722 MW; D5F8E76CDB5970F84 CRC64;

Query Match 60.2%; Score 216; DB 1; Length 349;
Best Local Similarity 58.6%; Pred. No. 3.2e-17;
Matches 41: Conservative 12; Mismatches 17; Indels 0; Gaps 0;
OY 1 TLWGEFVDGRSANGCCTSDNDAEAALMASSKEPAALQIREKIPKTYLQFPHNINSAL 60
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 110 TYWGEFQIDGRSANGCQSDNDAEYAKALNSGSEALINVIREFADPVLQFPHNINSAL 169
OY 61 AAIPKTRPP 70
   ||:|:|
DB 170 NRIFORPEP 179

RESULT 7
VAL1.TYLCV STANDARD: PRT: 359 AA.
AC P36209:
DR 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE AL1 PROTEIN (C1 PROTEIN).
OS C1.
SN Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
SC Virus: ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=37139;
RX SEQUENCE FROM N.A.
RP MEDLINE=9425616; PubMed=8198442;
RA Hughes E., Hughes E., Ascorbo G.;
R "Nucleotide sequence and genome organization of tomato leaf curl virus isolates
R from the west Mediterranean basin: the nucleotide sequence of an
R infectious clone from Spain";
R Arch. Virol. 135:165-170(1994).
CC 1 - SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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CC or send an email to license@isb-slb.ch).
CC -----
CC EMBL: X70419; GMA49856.1;
CC S18211; S19211; S20300.
CC InterPro: IPR001191; Gemin1.AL1.
CC Pfam: PF00799; Gemin1.AL1.
CC PRINTS: PR00227; GEMCOATC.VL1.

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DR PRODOM: PD000736; GemInL_All: 1.
KW ATP-Binding: 228
NP_BIND 228
SEQUENCE 359 AA; 41065 MW; 20170AS1E780A3C CRC64:
50

Query Match
Best Local Similarity 59.9%; Score 215; DB 1; Length 359;
Matches 40; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

OY 2 TWMEGEFVDGRSANGCCTSDNAAEALMASSKEPALQIIREKIPKYLQFPHNLSAL 61
DB 111 LEMKQFVDRSANGCCTSDNAAEALMASSKEPALQIIREKIPKYLQFPHNLSAL 170
OY 62 AIFKXPPEP 70
DB 171 RVFQVPPAP 179

RESULT 8
VALL_BCMV ID VALL_BCMV STANDARD: PRT: 358 AA.
AC p1491:
DR 01-APR-1990 (rel. 14, Created)
DM 01-APR-1992 (rel. 14, Last sequence update)
DT 01-AUG-1992 (rel. 12, Last annotation update)
OS Best curly top virus (BCTV).
CC Viruses: aspdn viruses; GemInVIRidae; Currovirus.
CC Entitles requires a license agreement (See http://www.1ab-slb.ch/announce/
or send an email to license@slb-slb.ch).
CC EMBL: X04144; -; NOT_ANNOTATED.CDS.
DR InterPro: IPR001191; GemInL_All: 1.
DR Pfam: PF00799; GemInL_All: 1.
DR PRINTS: PR00227; GEMCOATV.L1.
DR PRINTS: PR00228; GEMCOATV.L1.
DR PRODOM: PD000736; GemInL_All: 1.
KW ATP-Binding: 222
NP_BIND 222
SEQUENCE 358 AA; 40889 MW; 39A45FE3CDB9C333 CRC64:
50

Query Match
Best Local Similarity 59.1%; Score 212; DB 1; Length 358;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

OY 1 TWMEGEFVDGRSANGCCTSDNAAEALMASSKEPALQIIREKIPKYLQFPHNLSAL 60
DB 110 TWMEGEFVDGRSANGCCTSDNAAEALMASSKEPALQIIREKIPKYLQFPHNLSAL 169
OY 61 AAIKXPPEP 70
DB 170 OKTQRRPDP 179

RESULT 9
VALL_BCMV ID VALL_BCMV STANDARD: PRT: 353 AA.

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AC P05175;
DR 13-AUG-1987 (rel. 05, Created)
DM 13-AUG-1987 (rel. 05, Last sequence update)
DT 01-OCT-1996 (rel. 34, Last annotation update)
OS A1 PROTEIN (40.2 KDa PROTEIN).
CC A1 PROTEIN (40.2 KDa PROTEIN).
OS Bean golden mosaic virus.
CC Viruses: aspdn viruses; Begomovirus.
CC NCBI_TaxID=10839;
RN SEQUENCE FROM N.A.
RA Howerth A.J., Gallon J., Bossert M., Goodhan R.M.;
RT Regulation in geminiviruses: a golden mosaic virus and a model for gene
PR Proc. Natl. Acad. Sci. U.S.A. 82:3572-3576(1985).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUS ALI PROTEIN FAMILY.
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CC EMBL: M10070; AAA6318.1; -
DR Pfam: PF00799; GemInL_All: 1.
DR PRINTS: PR00227; GEMCOATV.L1.
DR PRINTS: PR00228; GEMCOATV.L1.
DR PRODOM: PD000736; GemInL_All: 1.
KW ATP-Binding: 222
NP_BIND 222
SEQUENCE 353 AA; 40190 MW; 80FA7F9DF6029A34 CRC64:
50

Query Match
Best Local Similarity 58.8%; Score 211; DB 1; Length 353;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

OY 1 TWMEGEFVDGRSANGCCTSDNAAEALMASSKEPALQIIREKIPKYLQFPHNLSAL 60
DB 110 TWMEGEFVDGRSANGCCTSDNAAEALMASSKEPALQIIREKIPKYLQFPHNLSAL 169
OY 61 AAIKXPPEP 70
DB 170 ERIFKXPPEP 179

RESULT 10
VALL_BCMV ID VALL_BCMV STANDARD: PRT: 359 AA.
AC p27260:
DR 01-AUG-1992 (rel. 23, Created)
DM 01-AUG-1992 (rel. 23, Last sequence update)
DT 01-JUN-1994 (rel. 29, Last annotation update)
OS A1 PROTEIN (CI PROTEIN).
CC A1 PROTEIN (CI PROTEIN).
OS Tomato yellow leaf curl virus (strain Harmand) (TYLCV).
CC Viruses: aspdn viruses; GemInVIRidae; Begomovirus.
CC NCBI_TaxID=10833;
RN SEQUENCE FROM N.A.
RA MEDLINE:9210760; Pubmed-1840676;
RA Knochel-Haas B.; Bendallman M., Metzelt V., Accotto G.P., Crespi S.;
RT Whitefly-transmitted nonpersistent geminivirus.
CC Nucleic Acids Res. 19:6763-6769(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUS ALI PROTEIN FAMILY.
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DR EMBL: AF097484: AAF06823.1: -
 DR EMBL: AF097485: AAF06824.1: -
 DR EMBL: AL080162: CAB45751.1: -
 DR EMBL: AF056183: AAD28083.1: ALT_INTT.
 DR EMBL: AF001680: MD40.
 DR EMBL: AF004890: MD40.
 DR SMART: SMO0320: GPROTEINRPT.
 DR SMART: SMO0320: MD40: 5.
 DR PROSITE: PS00678: WD_REPEATS.1: 1.
 DR PROSITE: PS00682: WD_REPEATS.2: 3.
 DR PROSITE: PS50294: WD_REPEATS_REGION: 1.
 Repeat: WD Repeat: 127
 FT REPEAT 138 MD 1.
 FT REPEAT 174 MD 2.
 FT REPEAT 186 MD 3.
 FT REPEAT 228 MD 4.
 FT REPEAT 277 MD 5.
 FT REPEAT 329 MD 6.
 FT REPEAT 371 MD 7.
 SQ SEQUENCE 447 AA: 49797 MW: 8260087E1A71D3P9 CRC64:

Query Match 18.9%; Score 68; DB 1; Length 447;
 Best Local Similarity 32.7%; Pred. No. 2.6;

Matches 16; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

07 12 RSARGGCGTSMDAAEALNASKKEALQITREKIPERTLQFHNLSAL 60
 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
 38 KSRKRFQMGANGPFDDSSGSKRQKQYQRIKREKFOQHNFTHLNALL 86

Search completed: January 3, 2002, 15:57:17
 Job time: 1103 sec

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009727 ID 009727 PRELIMINARY: PRT: 226 AA.
AC 009727:
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE REP PROTEIN (FRAGMENT).
GN REP.
OS Leonurus mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=58177;
RM SOURCE FROM N.A.
RC STRAIN=HEW. BRAZIL. 1;
RL Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: U92532; AM5157.1;
DR Interpro: IPR001191; GeminI.AL1.
DR Pfam: PF00799; GEMCOV.AL1.
DR PRINTS: PR000736; GEMCOV.AL1.
DR PRODOM: PD000736; GeminI.AL1. 1.
FT NON_TER 226
SO SEQUENCE 226 AA: 25617 MW: 730DBE676083FC5 CRC64:

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Query Match 76.3%; Score 274; DB 12; Length 226;
Best Local Similarity 77.1%; Pred. No. 2,3e-23;
Matches 54; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

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OY 1 TLVGEFVDGSRAGCCGTSNDAAALAAVLAASSKEEAMIIKREKLPKRYLQFQHNLSALAI 60
DB 111 TLVGEFVDGSRAGCCGTSNDAAALAAVLAASSKEEAMIIKREKLPKRYLQFQHNLSNL 170
OY 61 AATFDKTPP 70
DB 171 DRIFAKAPP 180

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RESULT 3
OQHMF6 PRELIMINARY: PRT: 226 AA.
ID 090H6:
AC 090H6:
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE REPLICATION-ASSOCIATED PROTEIN (FRAGMENT).
GN REP.
OS Comato mild mottle geminivirus.
OC Viruses; ssDNA viruses; Geminiviridae; Unclassified Geminiviridae.
NCBI_TaxID=92943;
RM SOURCE FROM N.A.
RC STRAIN=HN6-HSN;
RA Nakhla M.K., Mejia L., Ramirez P., Korkashen J.P., Doyle M.M., Maxwell D.P.;
RT Molecular characterization and DNA-based detection methods for
RT vegetable-infecting geminiviruses in Central America.
RT Plant Dis. 83(1999):109-113.
DR EMBL: A011071; A003447.1; EMBL/Gemshark/DBD databases.
DR Interpro: IPR001192; GeminI.AL1.
DR Pfam: PF00799; GeminI.AL1.
DR PRINTS: PR00227; GEMCOV.AL1.
DR PRODOM: PD000736; GeminI.AL1. 1.
FT NON_TER 226
SO SEQUENCE 226 AA: 25941 MW: 22A116712871A23 CRC64:

```

```

Query Match 76.3%; Score 274; DB 12; Length 226;
Best Local Similarity 72.9%; Pred. No. 2,3e-23;
Matches 51; Conservative 12; Mismatches 7; Indels 0; Gaps 0;
OY 1 TLVGEFVDGSRAGCCGTSNDAAALAAVLAASSKEEAMIIKREKLPKRYLQFQHNLSALAI 60
I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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DB 111 TLVGEFVDGSRAGCCGTSNDAAALAAVLAASSKEEAMIIKREKLPKRYLQFQHNLSNL 170
OY 61 AATFDKTPP 70
DB 171 DRIFAKAPP 180
RESULT 4
O67574 PRELIMINARY: PRT: 361 AA.
ID 067574:
AC 067574:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2000 (TREMblrel. 17, Last annotation update)
DE PUTATIVE REPLICATIVE PROTEIN.
GN ALL.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=10839;
RM SOURCE FROM N.A.
RC STRAIN=H. FARIA J.C.;
RA Gilberston R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G., Maxwell D.P., Russell D.R.;
RL Phytopathology 81:980-985(1991).
RM
RN
RP SEQUENCE FROM N.A.
RA Gilberston R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C., Morales F.J., Maxwell D.P.;
RA Plant Dis. 75:536-542(1991).
RM
RN
RP SEQUENCE FROM N.A.
RA Faria J.C., Ahlquist P.G., Ahlquist P.G., Maxwell D.P.;
RL Submitted (MAY-1992) to the EMBL/Genbank/DBJ databases.
DR EMBL: M86868; AAA46312.1;
DR Interpro: IPR001191; GeminI.AL1.
DR Pfam: PF00799; GEMCOV.AL1.
DR PRINTS: PR00227; GEMCOV.AL1.
DR PRODOM: PD000736; GeminI.AL1. 1.
SO SEQUENCE 361 AA: 41041 MW: 0094C7ACAF06B788 CRC64:

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Query Match 75.8%; Score 272; DB 12; Length 361;
Best Local Similarity 72.9%; Pred. No. 6,2e-27;
Matches 51; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
OY 4 WSEFVDGSRAGCCGTSNDAAALAAVLAASSKEEAMIIKREKLPKRYLQFQHNLSALAI 63
DB 113 WGEFVDGSRAGCCGTSNDAAALAAVLAASSKEEAMIIKREKLPKRYLQFQHNLSMDRI 172
OY 64 FDKTPP 70
DB 173 FTKAPP 179

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RESULT 5
O90DH1 PRELIMINARY: PRT: 225 AA.
ID 090DH1:
AC 090DH1:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
GN REP.
OS Cowpea golden mosaic geminivirus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=69263;
RM SOURCE FROM N.A.
RC STRAIN=CGW-BR;
RA Faria J.C.;
RL Partial nucleotide sequence of cowpea golden mosaic geminivirus from Brazil. (SEP-1999) to the EMBL/Genbank/DBJ databases.

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DR EMBL: AF188708; AAF06318.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1.1.
DR PRINTS: PR00227; GEMCONVAL1.
DR PROSITE: PS00227; GEMCONVAL1.
DR NCBI_TaxID: 60606; Gemini_AL1.1.
PT NON TER P000225; 225
SEQUENCE 225 AA; 25766 MW; 1089C6BD8D1595D CMC64;

Query Match
Best Local Similarity 75.2%; Score 270; DB 12; Length 225;
Matches 51; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

OY 4 TITWGEFQVDRSARGGQTSNDAAAEALAAASKEPAALQITREKIPKYLQFPHNLSAL 63
DB 113 TMTWGEFQVDRSARGGQTSNDAAAEALAAASKEPAALQITREKIPKYLQFPHNLSNLR 172

OY 64 FDKTPEP 70
DB 173 FKPKPEP 179

RESULT 6
O98618 PRELIMINARY: PRT; 314 AA.
AC O98178;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAY-2000 (TREMblrel. 16, Last sequence update)
DR InterPro: IPR001191; Gemini_AL1.1.
DR REPLICATION ASSOCIATION PROTEIN.
GN ACL.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
ID 11
RA SEQUENCE FROM N.A.
RN LORREKUL P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RP "Detection of a geminivirus infecting sweet potato in the United
States.";
RL Plant Dis. 82:1253-1257(1998).
(2)
RN SEQUENCE FROM N.A.
RA LORREKUL P., Valverde R.A.;
RL Submitted (02-2000) to the EMBL/Genbank/DBJ databases.
RN LORREKUL P., Valverde R.A.;
RP InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1.1.
DR PRINTS: PR00227; GEMCONVAL1.
DR PROSITE: PS00227; GEMCONVAL1.
DR PRODOM: P0000736; Gemini_AL1.1.
SO SEQUENCE 314 AA; 35153 MW; 686220613046943F CMC64;

Query Match
Best Local Similarity 75.2%; Score 270; DB 12; Length 314;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

OY 1 TITWGEFQVDRSARGGQTSNDAAAEALAAASKEPAALQITREKIPKYLQFPHNLSAL 60
DB 110 TITWGEFQVDRSARGGQTSNDAAAEALAAASKEPAALQITREKIPKYLQFPHNLSNL 169

OY 61 AATPKTP 68
DB 170 DRFSKPP 177

RESULT 7
O98635 PRELIMINARY: PRT; 364 AA.
AC O98555;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DR REPLICATION INITIATION PROTEIN ACL.

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GN ACL.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=100755;
ID 11
RA SEQUENCE FROM N.A.
RN LORREKUL P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
RP "Detection of a geminivirus infecting sweet potato in the United
States.";
RL Plant Dis. 82:1253-1257(1998).
DR EMBL: AF104036; AAD47173.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR PRINTS: PR00227; GEMCONVAL1.
DR PROSITE: PS00227; GEMCONVAL1.
DR PRODOM: P0000736; Gemini_AL1.1.
SO SEQUENCE 364 AA; 40680 MW; 5F79752431A09DE CMC64;

Query Match
Best Local Similarity 75.2%; Score 270; DB 12; Length 364;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

OY 1 TITWGEFQVDRSARGGQTSNDAAAEALAAASKEPAALQITREKIPKYLQFPHNLSAL 60
DB 110 TITWGEFQVDRSARGGQTSNDAAAEALAAASKEPAALQITREKIPKYLQFPHNLSNL 169

OY 61 AATPKTP 68
DB 170 DRFSKPP 177

RESULT 8
O98633 PRELIMINARY: PRT; 185 AA.
AC O98693;
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-MAY-2000 (TREMblrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DR REP PROTEIN (FRAGMENT).
GN ACL.
OS sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=51034;
ID 11
RA SEQUENCE FROM N.A.
RN STRAIN=JMA034;
RA ROYE M.E., McLaughlin W.A., Nakhla N.K., Maxwell D.P.;
RL Plant Dis. 81:1251-1258(1997).
DR EMBL: U67926; ABB97865.1; -.
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1.1.
DR PRINTS: PR00227; GEMCONVAL1.
DR PROSITE: PS000736; Gemini_AL1.1.
DR PRODOM: P0000736; Gemini_AL1.1.
PT NON TER P000736; 1
SO SEQUENCE 185 AA; 20975 MW; 3913850A025A5EE1 CMC64;

Query Match
Best Local Similarity 74.4%; Score 267; DB 12; Length 185;
Matches 49; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

OY 1 TITWGEFQVDRSARGGQTSNDAAAEALAAASKEPAALQITREKIPKYLQFPHNLSAL 60
DB 89 TITWGEFQVDRSARGGQTSNDAAAEALAAASKEPAALQITREKIPKYLQFPHNLSNI 148

OY 61 AATPKTP 70
DB 149 DRFSKPP 158

RESULT 9
PB8975

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Ox NCBI_FaxID=6762;
Rn [1]
Sf SEQUENCE FROM N.A.
Pc STRAIN-CORAL;
Dr COLONY-0819; S. Ishii I., Yahara T.;
Rt "Molecular phylogeny of geminiviruses infecting wild plants in Japan.";
Lr J. Plant Res.: 110(247-257(1997)).
DR EMBL: AB001303; BA34010.1; -.
Dd InterPro: IPRO01191; Gemint_AL1.
DR Pfam: PF00799; Gemint_AL1; 1.
Dd PRINTS: PR00227; GEMCONT.M1.
DR PRODOM: PD00736; Gemint_AL1; 1.
Dd NON_TER 160 190
FT FT
SQ SEQUENCE 190 AA: 21444 MW: 93C374ZAEERDR7BE CRC64;

Query Match 69.4%; Score 249; DB 12; Length 190;
Best Local Similarity 58.8%; Pred.No.1.3e-20;
Matches 50; Conservative 6; Mismatches 11; Indels 16; Gaps 1;

Qy 1 TLWGEEDVGNRSARCGGCSNDMAAEMALNSKEEALOITREKIPERYLPFOPNINSL 60
Db ||| | | | | | | | | | | | | | | | | | | | : | : | | | | |
85 TLWGTFVDVGSRAGCCGANADACBAENALNAASKAFALSTIREKLDPFOYNINSLT 144

Oy 61 AAI-----FDKTEPE 69
Db 145 DRIEAPLEVPYCFPSNSSDOVE 169

RESULT 15
ID ID Q92OC4 PRELIMINARY; PRT: 208 AA.
AC Q92OC4;
DT 01-MAY-1999 (TRMBREL_10; Created)
DD 01-MAY-1999 (TRMBREL_10; Last sequence update)
OS 208 AA: 21444 MW: 93C374ZAEERDR7BE CRC64;
NC C1 AND C4 GENES, CHLORE ARBUS-T, PHOTOL AND COMPLETE CDS (FRAGMENT).
DN GN CI.
Os tobacco leaf cuti virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_FaxID=6762;
Rn [1]
Sf SEQUENCE FROM N.A.
Pc STRAIN-CORAL;
Dr COLONY-0819; S. Ishii I., Yahara T.;
Rt "Molecular phylogeny of geminiviruses infecting wild plants in Japan.";
Lr J. Plant Res.: 110(247-257(1997)).
DR EMBL: AB001294; BA33992.1; -.
Dd InterPro: IPRO01191; Gemint_AL1.
DR Pfam: PF00799; Gemint_AL1; 1.
Dd PRINTS: PR00227; GEMCONT.M1.
DR PRODOM: PD00736; Gemint_AL1; 1.
Dd NON_TER 160 190
FT FT
SQ SEQUENCE 208 AA: 23526 MW: 249CC31DE8DR79C72D CRC64;

Query Match 69.4%; Score 249; DB 12; Length 208;
Best Local Similarity 58.8%; Pred.No.1.3e-20;
Matches 50; Conservative 6; Mismatches 11; Indels 16; Gaps 1;

Qy 1 TLWGEEDVGNRSARCGGCSNDMAAEMALNSKEEALOITREKIPERYLPFOPNINSL 60
Db ||| | | | | | | | | | | | | | | | | | | | : | : | | | | |
107 TLWGTFVDVGSRAGCCGANADACBAENALNAASKAFALSTIREKLDPFOYNINSLT 161

Oy 61 AAI-----FDKTEPE 69
Db 162 DRIEAPLEVPYCFPSNSSDOVE 186

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Search completed: January 3, 2002, 15:56:25

Job time: 1121 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM protein - protein search, using sw model

Run on: January 3, 2002, 15:38:50 ; Search time 65.28 seconds
(without alignments)
24.130 Million cell updates/sec

Title: US-09-289-346a-7

Product score: 1 T1WGEFVDYRSGRCQCTNSDAAEMLASSEEALITREKIPKYLFPFHINLSAL

Scoring table: BLAST/BLAST2

Gapop 10.0 , deapex 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Databases: 1: /cgn2.6/p10data/2/1aa/5A.COMB.pep.*
2: /cgn2.6/p10data/2/1aa/5B.COMB.pep.*
3: /cgn2.6/p10data/2/1aa/6A.COMB.pep.*
4: /cgn2.6/p10data/2/1aa/6B.COMB.pep.*
5: /cgn2.6/p10data/2/1aa/PCOTUS.COMB.pep.*
6: /cgn2.6/p10data/2/1aa/backflist1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	ID	Description
1	213	59.3	353	4	US-08-838-151A-44
2	213	59.3	353	4	US-08-838-151A-46
3	213	59.3	353	4	US-08-838-151A-49
4	213	59.3	353	4	US-08-838-151A-52
5	213	59.3	353	4	US-08-838-151A-55
6	211	58.8	359	4	US-08-800-103B-4
7	211	58.8	359	4	US-08-800-103B-6
8	211	58.8	359	4	US-08-800-103B-8
9	211	58.8	359	4	US-08-838-151A-2
10	211	58.8	361	4	US-08-838-151A-4
11	211	58.8	361	4	US-08-838-151A-6
12	211	58.8	361	4	US-08-838-151A-8
13	211	58.8	361	4	US-08-838-151A-10
14	211	58.8	361	4	US-08-838-151A-12
15	193	53.8	357	4	US-08-838-151A-20
16	193	53.8	357	4	US-08-838-151A-30
17	185	51.5	357	4	US-08-838-151A-40
18	63.5	17.7	2161	1	US-07-745-206A-2
19	63.5	17.7	2161	1	US-08-455-543A-49
20	63.5	17.7	2161	1	US-08-455-543A-51
21	63.5	17.7	2161	2	US-08-723-100C-41
22	63.5	17.7	2161	2	US-08-723-100C-49
23	63.5	17.7	2161	2	US-08-311-363-2
24	60.5	16.9	131	4	US-08-828-592A-14
25	58	15.9	374	2	US-08-828-592A-51
26	57	15.9	454	3	US-08-446-100-26
27	57	15.9	454	3	US-08-446-100-27

28	57	15.9	454	3	US-08-446-100-28	Sequence 28, Appl
29	57	15.9	454	3	US-08-446-100-29	Sequence 29, Appl
30	57	15.9	454	3	US-08-446-100-30	Sequence 30, Appl
31	56	15.6	602	2	US-08-415-652A-6	Sequence 6, Appl1
32	56	15.6	763	1	US-07-923-976-6	Sequence 6, Appl1
33	56	15.6	763	1	US-07-923-976-6	Sequence 6, Appl1
34	56	15.6	895	1	US-07-923-976-6	Sequence 8, Appl1
35	56	15.6	863	1	US-08-117-362A-3	Sequence 8, Appl1
36	55.5	15.5	860	1	US-08-486-924-3	Sequence 3, Appl1
37	55.5	15.5	860	1	US-08-167-919A-11	Sequence 11, Appl
38	55	15.3	432	1	US-08-715-106-11	Sequence 11, Appl
39	55	15.3	432	1	US-08-715-106-11	Sequence 11, Appl
40	54	15.2	1713	3	US-08-600-982-24	Sequence 24, Appl
41	54	15.2	1713	3	US-08-600-982-24	Sequence 24, Appl
42	54	15.2	1713	3	US-08-600-982-24	Sequence 24, Appl
43	54	15.0	751	4	US-09-036-987A-24	Sequence 24, Appl
44	54	15.0	751	4	US-09-036-987A-24	Sequence 24, Appl
45	53.5	14.9	373	3	US-08-258-287B-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-08-838-151A-44
Sequence 44, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: SCOTT, John T
INVENTOR: Hanson, Steve
APPLICANT: Maxwell, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
NUMBER OF SEQUENCES: 63
COMBINATION: 63
ADDRESS: Rockey, Milwaukee & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838, 151A
FILING DATE: 800
PUBLICATION: 800
ATTORNEY INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ. ID:
SEQ. ID: 151A
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-44
Query Match 59.3%, Score 213; DB 4; Length 553;
Best Local Similarity 58.6%; Pred. No. 1.7e+20;
Matches 41; Conservative 17; Indels 0; Gaps 0;
QY 1 T1WGEFVDYRSGRCQCTNSDAAEMLASSEEALITREKIPKYLFPFHINLSAL 60

DB 110 TTEMGQFOVDRSANGQGSANDSVAKMLADSIESTLTIKEOPDYVLOHHNINSNL 169
 07 61 AAIPTKPP 70
 DB 170 ERIFVYKPP 179

RESULT 2

US-08-838-151A-46
 : Sequence 46, Application US/08838151A
 : Patent No. 6291743
 : GENERAL INFORMATION:
 : APPLICANT: Stout, John T
 : APPLICANT: Maxwell, Douglas
 : APPLICANT: Albquist, Paul
 : APPLICANT: Hanson, Steve
 : APPLICANT: Albquist, Paul
 : TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
 : NUMBER OF SEQUENCES: 63
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 : STREET: Two Prudential Plaza, Suite 4700
 : CITY: Chicago
 : STATE: Illinois
 : COUNTRY: U.S.A.
 : ZIP: 60601
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : FILING DATE: NUMBER: 05/08/838, 151A
 : CLASSIFICATION: 800
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Mueller, Lisa V
 : REGISTRATION NUMBER: 38,978
 : REFERENCE/DOCKET NUMBER: SVS3801P0260
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 312-616-5460
 : TELEFAX: 312-616-5460
 : INFORMATION FOR SEO ID NO: 46:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 353 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-838-151A-46

Query Match 59.3%; Score 213; DB 4; Length 353;

Best Local Similarity 58.6%; Pred. No. 1.7e-20;
 Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

07 1 TLVNGCFQVDRSANGQGSANDSVAKMLADSIESTLTIKEOPDYVLOHHNINSNL 60
 DB 110 TTEMGQFOVDRSANGQGSANDSVAKMLADSIESTLTIKEOPDYVLOHHNINSNL 169
 07 61 AAIPTKPP 70
 DB 170 ERIFVYKPP 179

RESULT 3

US-08-838-151A-49
 : Sequence 49, Application US/08838151A
 : Patent No. 6291743
 : GENERAL INFORMATION:
 : APPLICANT: Stout, John T
 : APPLICANT: Lau, Hang T

APPLICANT: Maxwell, Douglas
 APPLICANT: Albquist, Paul
 APPLICANT: Hanson, Steve
 APPLICANT: Albquist, Paul
 TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: NUMBER: 05/08/838, 151A
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5460
 TELEFAX: 312-616-5460
 INFORMATION FOR SEO ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 353 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-838-151A-49

Query Match 59.3%; Score 213; DB 4; Length 353;

Best Local Similarity 58.6%; Pred. No. 1.7e-20;
 Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

07 1 TLVNGCFQVDRSANGQGSANDSVAKMLADSIESTLTIKEOPDYVLOHHNINSNL 60
 DB 110 TTEMGQFOVDRSANGQGSANDSVAKMLADSIESTLTIKEOPDYVLOHHNINSNL 169
 07 61 AAIPTKPP 70
 DB 170 ERIFVYKPP 179

RESULT 4

US-08-838-151A-52
 : Sequence 52, Application US/08838151A
 : Patent No. 6291743
 : GENERAL INFORMATION:
 : APPLICANT: Stout, John T
 : APPLICANT: Lau, Hang T
 : APPLICANT: Albquist, Paul
 : APPLICANT: Hanson, Steve
 : APPLICANT: Albquist, Paul
 : TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
 : NUMBER OF SEQUENCES: 63
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 : STREET: Two Prudential Plaza, Suite 4700
 : CITY: Chicago
 : STATE: Illinois
 : COUNTRY: U.S.A.
 : ZIP: 60601
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SYS801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5400
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-52

Query Match
59.3%: Score 213; DB 4; Length 353;
Best Local Similarity 58.6%: Pred. No. 1.7e-20;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

OY 1 TLWGEFVGDSRANGCCTSNDAALMASSKEAQLIRKIPKYLQFHNLSAL 60
DB 110 TLWGEFVGDSRANGCCTSNDAALMASSKEAQLIRKIPKYLQFHNLSAL 169
OY 61 AAIKDKTPEP 70
DB 170 ERIFFVKPEP 179

RESULT 5
US-08-838-151A-55
Sequence 55, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stoult, John T
APPLICANT: Liu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Harrison, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milanow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago, Illinois
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SYS801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5400
INFORMATION FOR SEQ ID NO: 55:

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SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-55

Query Match
59.3%: Score 213; DB 4; Length 353;
Best Local Similarity 58.6%: Pred. No. 1.7e-20;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

OY 1 TLWGEFVGDSRANGCCTSNDAALMASSKEAQLIRKIPKYLQFHNLSAL 60
DB 110 TLWGEFVGDSRANGCCTSNDAALMASSKEAQLIRKIPKYLQFHNLSAL 169
OY 61 AAIKDKTPEP 70
DB 170 ERIFFVKPEP 179

RESULT 6
US-08-809-1038-2
Sequence 2, Application US/088091038
Patent No. 613505
GENERAL INFORMATION:
APPLICANT: GROENBORN, Bruno
TITLE OF INVENTION: PHYTOANTHROGENIC DNA VIRUS RESISTANT
TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,1038
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94,11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH AND WILSON
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: US94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 665-0573
FILER: 248425 EBNON
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-1038-2

Query Match
58.8%: Score 211; DB 4; Length 359;
Best Local Similarity 56.5%: Pred. No. 3.1e-20;
Matches 39; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

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OY 2 LWMEFQVDSNRAGGCGTSDNDAAEALNKSKEALQIREKIPKYLEFPHNLNSALA 61
DB 111 LEMGTPOIDGNSRAGGCGTANDANAAALNKSQALDIRELARQYVLIHFHNSIND 170
OY 62 AIFKXPREP 70
DB 171 KVFQVPEAP 179

RESULT 7
US-08-809-103B-4
Sequence 4: Application US/08809103B
Patent No. 6133505
GENERAL INFORMATION:
APPLICANT: GROENBORN, Bruno
TITLE OF INVENTION: PHYTOANTHOGENIC DNA VIRUS RESISTANT
TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: 31A
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REFERENCE/DOCKET NUMBER: US94AL CNR TOM
TELEPHONE: (703) 521-2297
TELEFAX: (703) 521-2297
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-4

Query Match
Best Local Similarity 58.8%, Score 211, DB 4, Length 359,
Matches 39, Conservative 10, Mismatches 20, Indels 0, Gaps 0,
OY 2 LWMEFQVDSNRAGGCGTSDNDAAEALNKSKEALQIREKIPKYLEFPHNLNSALA 61
DB 111 LEMGTPOIDGNSRAGGCGTANDANAAALNKSQALDIRELARQYVLIHFHNSIND 170
OY 62 AIFKXPREP 70
DB 171 KVFQVPEAP 179

RESULT 8
US-08-809-103B-6
Sequence 6: Application US/08809103B

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Patent No. 6133505
GENERAL INFORMATION:
APPLICANT: GROENBORN, Bruno
TITLE OF INVENTION: PHYTOANTHOGENIC DNA VIRUS RESISTANT
TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94,11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REFERENCE/DOCKET NUMBER: US94AL CNR TOM
TELEPHONE: (703) 521-2297
TELEFAX: (703) 521-2297
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-6

Query Match
Best Local Similarity 58.8%, Score 211, DB 4, Length 359,
Matches 39, Conservative 10, Mismatches 20, Indels 0, Gaps 0,
OY 2 LWMEFQVDSNRAGGCGTSDNDAAEALNKSKEALQIREKIPKYLEFPHNLNSALA 61
DB 111 LEMGTPOIDGNSRAGGCGTANDANAAALNKSQALDIRELARQYVLIHFHNSIND 170
OY 62 AIFKXPREP 70
DB 171 KVFQVPEAP 179

RESULT 9
US-08-809-103B-8
Sequence 8: Application US/08809103B
Patent No. 6133505
GENERAL INFORMATION:
APPLICANT: GROENBORN, Bruno
TITLE OF INVENTION: PHYTOANTHOGENIC DNA VIRUS RESISTANT
TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.

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? ZIP: 22202
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? FILING DATE: 17-MAR-1997
? CLASSIFICATION: 800
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: FR 94.11040
? FILING DATE: 15-SEP-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: NO PCT/FR95/01192
? FILING DATE: 15-SEP-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: PATCH, Andrew J.
? REGISTRATION NUMBER: 32,925
? REFERENCE/DOCKET NUMBER: US94AL CNR TOM
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 665-0537
? TELEFAX: (703) 665-0537
? INFORMATION FOR SEQ ID NO: 8:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 359 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-805-1038-8

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Query Match 58.8%; Score 211; DB 4; Length 359;
Best Local Similarity 56.5%; Pred. No. 3.1e-20;
Matches 39; Conservative 10; Mismatches 20; Indels 0; Caps 0;
OY 2 1TWGCEVDGSRAGCGCTSNDAAPALNASKRELAQIIRKTEKXIFQFNNHNSALA 61
DB 111 LKMTGTQIDGRSARGCGGTANDAVAKALNKGSKQALDYIKELAPROYLHFHNHNSLD 170
OY 62 AIFDKTPEP 70
DB 171 KYFQVPPAP 179

RESULT 10
US-08-838-151A-2
? Sequence 2, Application US/08838151A
? Patent No. 6291743
? GENERAL INFORMATION:
? APPLICANT: Stoult, John T
? APPLICANT: Liu, Jiaqing
? APPLICANT: Maxwell, Douglas
? APPLICANT: Ahlquist, Paul
? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
? TITLE OF INVENTION: Genes
? NUMBER OF SEQUENCES: 63
? CORRESPONDENCE ADDRESS:
? ATTORNEY/AGENT INFORMATION:
? STREET: Two Presidential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838.151A

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? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5400
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 361 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-838-151A-2

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Query Match 58.8%; Score 211; DB 4; Length 361;
Best Local Similarity 55.7%; Pred. No. 3.2e-20;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Caps 0;
OY 1 1TWGCEVDGSRAGCGCTSNDAAPALNASKRELAQIIRKTEKXIFQFNNHNSALA 60
DB 110 LKMTGTQIDGRSARGCGGTANDAVAKALNKGSKQALDYIKELAPROYLHFHNHNSLD 169
OY 61 AIFDKTPEP 70
DB 170 KYFQVPPAP 179

RESULT 11
US-08-838-151A-4
? Sequence 4, Application US/08838151A
? Patent No. 6291743
? GENERAL INFORMATION:
? APPLICANT: Stoult, John T
? APPLICANT: Liu, Jiaqing
? APPLICANT: Maxwell, Douglas
? APPLICANT: Ahlquist, Paul
? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
? TITLE OF INVENTION: Genes
? NUMBER OF SEQUENCES: 63
? CORRESPONDENCE ADDRESS:
? ATTORNEY/AGENT INFORMATION:
? STREET: Two Presidential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838.151A
? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? STREET: Two Presidential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5400
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 361 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein

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US-08-838-151A-4

Query Match 58.8%, Score 211; DB 4; Length 361;
 Best Local Similarity 55.7%; Pred. No. 3.2e-20;
 Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

OY 1 TWGDEPOJIDRGARGCOTSDAAREALMASSSEAFLOITREKIPKYLQPHINISAL 60
 DB 110 TTEMCDPJIDRGARGCOTSDAAREALMASSSEAFLOITREKIPKYLQPHINISAL 169
 OY 61 AAIETKPEP 70
 DB 170 ERTFAKAPP 179

RESULT 12

US-08-838-151A-6

Sequence 6, Application US/08838151A
 Patent No. 6291743
 GENERAL INFORMATION:

APPLICANT: Scout, John T
 APPLICANT: Lou, Hang T
 APPLICANT: Maxwell, Douglas
 APPLICANT: Ahlquist, Paul
 APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 TITLE OF INVENTION: Genes
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Rocky, Minamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 ZIP: 60601 U.S.A.

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA
 APPLICATION NUMBER: US/08/838,151A
 FILING DATE:

CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5460
 TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 361 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: protein
 US-08-838-151A-6

Query Match 58.8%, Score 211; DB 4; Length 361;
 Best Local Similarity 55.7%; Pred. No. 3.2e-20;

Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

OY 1 TWGDEPOJIDRGARGCOTSDAAREALMASSSEAFLOITREKIPKYLQPHINISAL 60
 DB 110 TTEMCDPJIDRGARGCOTSDAAREALMASSSEAFLOITREKIPKYLQPHINISAL 169
 OY 61 AAIETKPEP 70
 DB 170 ERTFAKAPP 179

RESULT 13

US-08-838-151A-8

Sequence 24, Application US/08838151A
 Patent No. 6291743
 GENERAL INFORMATION:

APPLICANT: Scout, John T
 APPLICANT: Lou, Hang T
 APPLICANT: Maxwell, Douglas
 APPLICANT: Ahlquist, Paul
 APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 TITLE OF INVENTION: Genes
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Rocky, Minamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 ZIP: 60601 U.S.A.

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA
 APPLICATION NUMBER: US/08/838,151A
 FILING DATE:

CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5460
 TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 361 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: protein
 US-08-838-151A-8

Query Match 58.8%, Score 211; DB 4; Length 361;
 Best Local Similarity 55.7%; Pred. No. 3.2e-20;

Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

OY 1 TWGDEPOJIDRGARGCOTSDAAREALMASSSEAFLOITREKIPKYLQPHINISAL 60
 DB 110 TTEMCDPJIDRGARGCOTSDAAREALMASSSEAFLOITREKIPKYLQPHINISAL 169
 OY 61 AAIETKPEP 70
 DB 170 ERTFAKAPP 179

RESULT 14

US-08-838-151A-24

Sequence 24, Application US/08838151A
 Patent No. 6291743
 GENERAL INFORMATION:

APPLICANT: Scout, John T
 APPLICANT: Lou, Hang T
 APPLICANT: Maxwell, Douglas
 APPLICANT: Ahlquist, Paul
 APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 TITLE OF INVENTION: Genes
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:

ADDRESSER: Dressler, Rocky, Milnamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: US/08/838,151A
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5460
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 357 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-838-151A-24

Query Match 53.8%; Score 193; DB 4; Length 357;
 Best Local Similarity 62.3%; Pred. No. 8e-18;
 Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Oy 4 MGFQVDGRSRRGGCQTSNDAAALANSSKEBALQIREKIPKYLPPFHNLSALAI 63
 DB 111 FVSDLSGHSRGGQSNMNYALALNGSGSBALNILEAKRYVLIQTHNLSSHLDR 170

Oy 64 F 64
 DB 171 F 171

RESULT 15
 US-08-838-151A-27
 Sequence 27 Application US/08838151A
 Patent No. 6291743
 GENERAL INFORMATION:
 APPLICANT: Stout, John T
 APPLICANT: Liu, Hang T
 APPLICANT: Maxwell, Douglas
 APPLICANT: Altmueller, Paul
 APPLICANT: Hengst, Peter
 TITLE OF INVENTION: transgenic Plants Expressing Gametolitus
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Dressler, Rocky, Milnamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: US/08/838,151A
 FILING DATE:
 CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5460
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 357 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-838-151A-27

Query Match 53.8%; Score 193; DB 4; Length 357;
 Best Local Similarity 62.3%; Pred. No. 8e-18;
 Matches 38; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Oy 4 MGFQVDGRSRRGGCQTSNDAAALANSSKEBALQIREKIPKYLPPFHNLSALAI 63
 DB 111 FVSDLSGHSRGGQSNMNYALALNGSGSBALNILEAKRYVLIQTHNLSSHLDR 170

Oy 64 F 64
 DB 171 F 171

Search completed: January 3, 2002, 15:38:51
 Job time: 228 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:37:37 ; Search time 144.17 Seconds
(without alignments)
35,965 Million cell updates/sec

Title: US-09-289-346a-8

Perfect score: 361
Sequence: 1 TLVMSAAVVDGRSFGGGCT.....PQPHNLNSNLDI:DKTTP 70

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Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74072390 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result NO.	Score	Query Match	Length	DB ID	Description
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2	350	97.0	70	21	AA19867
3	350	97.0	356	21	AA19887
4	342	94.7	70	21	AA19885
5	338	93.6	70	21	AA19886
6	338	93.6	70	21	AA19890
7	335	92.8	70	21	AA19878
8	335	92.8	70	21	AA19885
9	334	92.5	70	21	AA19889
10	334	92.0	70	21	AA19880
11	332	92.0	70	21	AA19880

SUMMARIES

RESULT	ID	Score	Query Match	Length	DB ID	Description
1	AA19864	361	100.0	70	21	AA19864
2	AA19867	350	97.0	70	21	AA19867
3	AA19887	350	97.0	356	21	AA19887
4	AA19885	342	94.7	70	21	AA19885
5	AA19886	338	93.6	70	21	AA19886
6	AA19890	338	93.6	70	21	AA19890
7	AA19878	335	92.8	70	21	AA19878
8	AA19885	335	92.8	70	21	AA19885
9	AA19889	334	92.5	70	21	AA19889
10	AA19880	334	92.0	70	21	AA19880
11	AA19880	332	92.0	70	21	AA19880

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	DB ID	Description
1	AA19864	361	100.0	70	21	AA19864
2	AA19867	350	97.0	70	21	AA19867
3	AA19887	350	97.0	356	21	AA19887
4	AA19885	342	94.7	70	21	AA19885
5	AA19886	338	93.6	70	21	AA19886
6	AA19890	338	93.6	70	21	AA19890
7	AA19878	335	92.8	70	21	AA19878
8	AA19885	335	92.8	70	21	AA19885
9	AA19889	334	92.5	70	21	AA19889
10	AA19880	334	92.0	70	21	AA19880
11	AA19880	332	92.0	70	21	AA19880

[illegible]

PT	encoding a mutant AUL protein with a mutation in the Rb binding region
FT	
PS	Disclosures: Page 18; 72pp; English.
XX	
CC	The present sequence is derived from a geminivirus replication (Rep)
CC	protein, which is also known as ALI. ALI binds double-stranded DNA,
CC	catalyzes cleavage and ligation of single-stranded DNA, and interacts
CC	with other viral and host proteins. Mutants of the ALI protein are used
CC	to produce transgenic plants. The mutation in ALI is present in a virus
CC	increased resistance to geminivirus infection in the plant. Mutant ALI
CC	proteins are useful for producing plants having increased resistance or
CC	reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
CC	tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
CC	virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
CC	yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
CC	bean curly top virus, Texas pepper virus, cotton leaf curl virus or
SQ	Sequence 70 AA:
DB	
OY	61 DRIETKPEP 70
Db	61 DRIETKPEP 70
Db	61 DRIETKPEP 70
RESULT 3	
AABI6687	
ID	AABI6687 standard; peptide: 356 AA.
AC	
AD	AABI6687:
DD	22-JAN-2001 (first entry)
DE	Amino acid sequence of a geminivirus replication protein of TMW.
XX	
KM	Geminiviruses: replication protein; Rep protein; ALI; transgenic plant;
KW	Ribosome binding region; resistance; geminivirus infection.
XX	
XX	Tomato golden mosaic virus.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 356 /note= "unspecified amino acid"
XX	
PX	WO200054573-A1.
PD	
PD	21-SEP-2000.
PP	15-MAR-2000; 2000MO-US06759.
PR	18-MAR-1999; 99US-0125004.
PR	09-APR-1999; 99US-0289346.
XX	
PA	(UYNC-) UNIV NORTH CAROLINA STATE.
XX	
XX	Banley-Bowdoin L, Orosco BM, Kong L;
DR	WPI: 2000-618651/59.
PT	Transgenic plants with increased resistance to geminivirus infection
FT	comprise a nucleic acid construct containing a nucleic acid sequence
TT	encoding a mutant ALI protein with a mutation in the Rb binding region

PT -
XX
PS Disclosure; Page 47-48; 73pp; English

The prest sequence represents a geminivirus replication (Rep) protein, which is also known as AL1. AL1 binds double-stranded DNA, catalyzes cleavage and ligation of single-stranded DNA, and interacts with other proteins involved in the replication cycle. The gene is used to produce transgenic plants. The mutation in AL1 is essential to produce transgenic plants. The expression of mutant AL1 protein impairs increased resistance to geminiviruses infection in the plant. Mutant AL1 reduced sensitivity to a geminivirus such as tomato golden mosaic virus. Tomato mottle virus, Tomato yellow leaf curl virus, Tomato leaf curl virus, Tomato yellow leaf curl virus, Tomato yellow leaf curl virus, Yellow mosaic virus, Tomato yellow leaf curl virus, Squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.

Sequence 356 AA:

Query Match	97.0%	Score 350;	DB 21;	Length 356;
Best Local Similarity	97.1%	Pred. No. 8.1e-36;		
Matches 68; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

QY	1	TLMWCEAAVDORSGACGCTSNDAAPFLMASSFEALQITREKTEPEKTLFGPHNINSL	60
QY			
db	110	tlvwgcelqygdzraagcgctmnaaaeanmaasskeeaqlitrektpexylfcmfinsnl	160
QY	61	DRIEDKTPPEP 70	
QY			
db	170	drifdktppep 179	

```

RESULT      4
AAB18685
ID  AAB18685 standard; peptide; 70 AA

```

22-JAN-2001 (first entry)
 Mutant peptide derived from amino acids 110-179 of Rep (Alt) protein.
 Geminivirus; replication protein; Rep protein; Alt; transgenic plant.
 Ribosome binding region; resistance; geminivirus infection.

OS	synthetic	
OS	Tomato golden mosaic virus.	
XX		
FH		
Key	Location/Qualifiers	
FT	Misc-difference 10	
PT	/note="wild type residue replaced with Ala"	

XX	PN	MO200054573-A1.
XX	PN	21-SEP-2000.
XX	PF	15-MAR-2000; 2000MO-US06759.
XX	PR	18-MAR-1999; 99US-0125004.
XX	PR	09-APR-1999; 99US-0289346.
XX	KA	(UTWC-) ONLY NORTH CAROLINA STATE.
XX	PI	Hanley-Bowdoin L. Orozco BM, Kong L.
XX	PR	WPI; 2000-618851/59.

PT Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant AUL protein with a mutation in the Rb binding region

PT	-
XX	
PS	Claim 53; Page 46; 73pp; English

CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and is involved in both replication and movement of the virus.
CC AL1 is related to other proteins, such as the nuclear protein AL1
CC present in a ribosome binding region, and expression of mutant AL1
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant AL1 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC cassava mosaic virus, cassava brown streak virus, and cassava
CC virus. Bean dwarf mosaic virus, squash leaf curl virus, Texas
CC virus, cotton leaf curl virus or beet curly top virus.
XX Sequence 70 AA:

Query Match	94.7%;	Score 342;	DB 21;	Length 70;
Best Local Similarity	95.7%;	Pred. NO. 1e-35;		
Matches 67;	Conservative	0;	Mismatches 3;	Indels 0;
			Gaps	0;

Accession	Protein	Length
Oy	1 TLWEEAADVCSNRGGCTSDAAAEFLAASSKEEAQLIIRKIPKYLPEQHNLSMT	61
Oy	1 TLWEEAADVCSNRGGCTSDAAAEFLAASSKEEAQLIIRKIPKYLPEQHNLSMT	61
Db	1 TLWEEGTVAGTSRGGCTSDAAAEFLAASSKEEAQLIIRKIPKYLPEQHNLSMT	61
Oy	61 DRLEFKTPEP 70	
Oy	61 DRLEFKTPEP 70	
Db	61 DRLEFKTPEP 70	

RESULT	5
AAB18688	
ID	AAB18688 standard; peptide; 70 AA

DT 22-JAN-2001 (first entry)
XX Mutant peptide derived from amino acids 110-179 of Rep (Alt) protein
XX
XX
XX Geminivirus; replication protein, Rep protein, Alt; transgenic plant
XX ribosome binding region; resistance; geminivirus infection.
XX

	Location/Qualifiers
OS	synthetic
OS	Tomato golden mosaic virus.
XX	
Key	
FM	
FT	Misc-difference 19
FT	/note- "wild type residue replaced with Ala"

FT		/note="wild type res
XT	MO2000054573-AL	
XX		
XX	21-SEP-2000	
XX		
PF	15-MAR-2000; 2000MO-US06759.	
PD		
PR	18-MAR-1999; 5905-0125004.	
PR	03-APR-1999; 99005-0893146.	
PA	(UYMC)- UNIV NORTH CAROLINA STATE.	
PI		
PI	Healey-Bowdoin L., Orozco BK., Kong L.	

DR WPI: 2000-618851/59.
XX
PT Transgenic plants with increased resistance to geminivirus infection

XX DB WPI: 2000-618851/59.

XX PT Transgenic plants with increased resistance to geminivirus infection

XX PT comprise a nucleic acid construct containing a nucleic acid sequence

XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region

XX PS

XX PS Disclosure: Page 49: 73pp: English.

XX CC The present sequence represents a mutant peptide, derived from a

CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds

CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded

CC DNA, and interacts with other viral and host proteins. Mutants of the AL1

CC protein are used to produce transgenic plants with resistance to AL1 is

CC present in a ribosome binding region, and expression of mutant AL1 is

CC protein imparts increased resistance to geminivirus infection in the

CC plant. Mutant AL1 proteins are useful for producing plants having

CC increased resistance or reduced sensitivity to a geminivirus such as

CC tomato golden mosaic virus, tomato yellow leaf curl virus, Indian

CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic

CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian

CC cassava mosaic virus, potato yellow mosaic virus, Texas pepper

CC virus, cotton leaf curl virus or beet curly top virus.

XX CC

XX Sequence 70 AA:

SQ

Query Match 93.1% Score 336 DB 21: Length 70:

Best Local Similarity 94.3% Pred. No. 5, 9e-35:

Matches 66: Conservative 0: Mismatches 4: Indels 0: Gaps 0:

OY 1 TLWGEAAYDGRSAGCQTSDNAAAEALMASSKEPAQLIIRKXIPKXITLDFPHNLSNLT 60

DB 1 TLVGEGLYDGRSAGCQTSDNAAAEALMASSKEPAQLIIRKXIPKXITLDFPHNLSNLT 60

OY 61 DRIPKTRPEP 70

DB 61 drifdktrpep 70

XX RESULT 8

XX AAAB18678 standard: peptide: 70 AA.

XX AC AAB18678:

XX DT 22-JAN-2001 (first entry)

XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

XX KW Geminivirus: replication protein; Rep protein; AL1; transgenic plant;

XX KW ribosome binding region; resistance; geminivirus infection.

XX OS Synthetic.

XX OS Tomato golden mosaic virus.

XX Key Location/Qualifiers

XX FT Misc-difference 12 /note= "wild type residue replaced with Ala"

XX FT Misc-difference 13 /note= "wild type residue replaced with Ala"

XX FT Misc-difference 19 /note= "wild type residue replaced with Ala"

XX FT Misc-difference 15 /note= "wild type residue replaced with Ala"

XX MO200054573-A1.

XX 21-SEP-2000.

XX 15-MAR-2000: 2000MO-US06759.

XX 18-MAR-1999: 9905-0125004.

XX 09-APR-1999: 9905-0289346.

XX XX (UNCL) UNIV NORTH CAROLINA STATE.

XX PI Hanley-Bowdoin L, Orozco BM, Kong L;

XX DB WPI: 2000-618851/59.

XX PT Transgenic plants with increased resistance to geminivirus infection

XX PT comprise a nucleic acid construct containing a nucleic acid sequence

XX PT encoding a mutant AL1 protein with a mutation in the Rb binding region

XX PS

XX PS Claim 53: Page 42-43: 73pp: English.

XX CC The present sequence represents a mutant peptide, derived from a

CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds

CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded

CC DNA, and interacts with other viral and host proteins. Mutants of the AL1

CC protein are used to produce transgenic plants. The mutation in AL1 is

CC present in a ribosome binding region, and expression of mutant AL1 is

CC protein imparts increased resistance to geminivirus infection in the

CC plant. Mutant AL1 proteins are useful for producing plants having

CC increased resistance or reduced sensitivity to a geminivirus such as

CC tomato golden mosaic virus, tomato yellow leaf curl virus, Indian

CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic

CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian

CC cassava mosaic virus, potato yellow mosaic virus, Texas pepper

CC virus, cotton leaf curl virus or beet curly top virus.

XX CC

XX Sequence 70 AA:

SQ

Query Match 92.8% Score 335 DB 21: Length 70:

Best Local Similarity 92.9% Pred. No. 7, 9e-35:

Matches 65: Conservative 1: Mismatches 4: Indels 0: Gaps 0:

OY 1 TLWGEAAYDGRSAGCQTSDNAAAEALMASSKEPAQLIIRKXIPKXITLDFPHNLSNLT 60

DB 1 TLVGEGLYDGRSAGCQTSDNAAAEALMASSKEPAQLIIRKXIPKXITLDFPHNLSNLT 60

OY 61 DRIPKTRPEP 70

DB 61 drifdktrpep 70

XX RESULT 9

XX AAB18686 standard: peptide: 70 AA.

XX AC AAB18686:

XX DT 22-JAN-2001 (first entry)

XX DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

XX KW Geminivirus: replication protein; Rep protein; AL1; transgenic plant;

XX KW ribosome binding region; resistance; geminivirus infection.

XX OS Synthetic.

XX OS Tomato golden mosaic virus.

XX Key Location/Qualifiers

XX FT Misc-difference 24 /note= "wild type residue replaced with Leu"

XX FT Misc-difference 25 /note= "wild type residue replaced with Leu"

XX FT Misc-difference 26 /note= "wild type residue replaced with Leu"

XX MO200054573-A1.

XX 21-SEP-2000.

PF 15-MAR-2000: 2000MO-US06759.
 XX 18-MAR-1999: 990US-0125004.
 XX 09-APR-1995: 990US-0289346.
 XX (UNNC-) UNIV NORTH CAROLINA STATE.
 PA Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI: 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 PF comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 XX
 XX Claim 53: Page 46: 73pp: English.
 XX
 XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 XX Sequence 70 AA:

Query Match 92.8%; Score 335; DB 21: Length 70;
 Best Local Similarity 92.9%; Pred. No. 7.9e-35;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLVGEAVDGRSAGCCGTSNDAAAEALNASSREAAQIRREKIPKYLTFORHNLNSL 60
 DB 1 TLVGEAVDGRSAGCCGTSNDAAAEALNASSREAAQIRREKIPKYLTFORHNLNSL 60
 QY 61 DRIDPKTPP 70
 DB 61 dridfktp 70

RESULT 10
 AAB18689
 ID AAB18689 standard: peptide: 70 AA.

AC AAB18689:
 XX 22-JAN-2001 (first entry)
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus: replication protein: Rep protein: AL1; transgenic plant:
 XX ribosome binding region; resistance: geminivirus infection.
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX
 XX Key Location/Qualifiers
 PF Misc-difference 22 /note= "wild type residue replaced with Ala"
 FT Misc-difference 23 /note= "wild type residue replaced with Ala"
 XX
 XX MO200054573-A1.

PD 21-SEP-2000.
 XX 15-MAR-2000: 2000MO-US06759.
 XX 18-MAR-1999: 990US-0125004.
 XX 09-APR-1995: 990US-0289346.
 XX (UNNC-) UNIV NORTH CAROLINA STATE.
 PA Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI: 2000-618851/59.
 XX Transgenic plants with increased resistance to geminivirus infection
 PF comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 XX
 XX Disclosure: Page 48-49: 73pp: English.

CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX
 XX Sequence 70 AA:

Query Match 92.5%; Score 334; DB 21: Length 70;
 Best Local Similarity 94.3%; Pred. No. 1.1e-34;
 Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLVGEAVDGRSAGCCGTSNDAAAEALNASSREAAQIRREKIPKYLTFORHNLNSL 60
 DB 1 TLVGEAVDGRSAGCCGTSNDAAAEALNASSREAAQIRREKIPKYLTFORHNLNSL 60
 QY 61 DRIDPKTPP 70
 DB 61 dridfktp 70

RESULT 11
 AAB18680
 ID AAB18680 standard: peptide: 70 AA.

AC AAB18680:
 XX 22-JAN-2001 (first entry)
 DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 XX Geminivirus: replication protein: Rep protein: AL1; transgenic plant:
 XX ribosome binding region; resistance: geminivirus infection.
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX
 XX Key Location/Qualifiers
 PF Misc-difference 42 /note= "wild type residue replaced with Ala"
 FT Misc-difference 43 /note= "wild type residue replaced with Ala"
 XX
 XX Misc-difference 44


```

FT      /note= "wild type residue replaced with Ala"
XX      W0200054573-A1.
XX      21-SEP-2000.
XX      15-MAR-2000: 2000MO-US06759.
XX      18-MAR-1999: 99US-0125004.
XX      09-APR-1999: 99US-0289346.
XX      (UYNC-) UNIV NORTH CAROLINA STATE.
XX      Hanley-Bowdoin L, Orozco BM, Kong L;
XX      WPI: 2000-618851/59.
XX      Transgenic plants with increased resistance to geminivirus infection
XX      comprise a nucleic acid construct containing a nucleic acid sequence
XX      encoding a mutant A11 protein with a mutation in the RB binding region
XX      -
XX      Claim 52: Page 43-44: 73pp: English.
XX      The present sequence represents a mutant peptide, derived from a
XX      geminivirus replication (Rep) protein, also known as A11. A11 binds
XX      double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX      DNA, and interacts with other viral and host proteins. Mutants of the A11
XX      protein are used to produce transgenic plants. The mutation in A11 is
XX      present in a ribosome binding region, and expression of mutant A11
XX      protein imparts increased resistance to geminivirus infection in the
XX      plant. Mutant A11 proteins are useful for producing plants having
XX      increased resistance or reduced sensitivity to a geminivirus such as
XX      cassava golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX      virus, tomato leaf curl virus, African cassava mosaic virus, bean golden mosaic
XX      virus, bean dwarf mosaic virus, potato yellow mosaic virus, Texas pepper
XX      virus, cotton leaf curl virus or beet curly top virus.
XX      Sequence 70 AA:
XX      50
XX      Query Match          92.0%: Score 332: DB 21: Length 70:
XX      Best Local Similarity 92.9%: Pred. No. 1,9c-34:
XX      Matches 65: Conservative 0: Mismatches 5: Indels 0: Gaps 0:
XX      Oy      1 TLVGSAAVDSRGANGCOTNSDAAEALMASKEEALQITREKIPKYLQFHHNLSNM: 60
XX      Db      1 LTVGSLTQVGRSARGCQTNSDAAEALMASKEEALQITREKIPKYLQFHHNLSNM: 60
XX      Oy      61 DRIFDKTREP 70
XX      Db      61 dRlfdktrep 70
XX      RESULT 12
XX      AAB18691
XX      AAB18691 standard: peptide: 70 AA.
XX      AAB18691:
XX      22-JAN-2001 (first entry)
XX      Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
XX      Geminivirus: replication protein; Rep protein; A11; transgenic plant;
XX      ribosome binding region; resistance; geminivirus infection.
XX      Synthetic.
XX      Tomato golden mosaic virus.
XX      Key Location/Qualifiers
XX      Misc-difference 34

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FT      /note= "wild type residue replaced with Ala"
XX      Misc-difference 35
XX      MISC-difference 36
XX      MISC-difference 36
XX      W0200054573-A1.
XX      21-SEP-2000.
XX      15-MAR-2000: 2000MO-US06759.
XX      18-MAR-1999: 99US-0125004.
XX      09-APR-1999: 99US-0289346.
XX      (UYNC-) UNIV NORTH CAROLINA STATE.
XX      Hanley-Bowdoin L, Orozco BM, Kong L;
XX      WPI: 2000-618851/59.
XX      Transgenic plants with increased resistance to geminivirus infection
XX      comprise a nucleic acid construct containing a nucleic acid sequence
XX      encoding a mutant A11 protein with a mutation in the RB binding region
XX      -
XX      Disclousure: Page 49: 73pp: English.
XX      The present sequence represents a mutant peptide, derived from a
XX      geminivirus replication (Rep) protein, also known as A11. A11 binds
XX      double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX      DNA, and interacts with other viral and host proteins. Mutants of the A11
XX      protein are used to produce transgenic plants. The mutation in A11 is
XX      present in a ribosome binding region, and expression of mutant A11
XX      protein imparts increased resistance to geminivirus infection in the
XX      plant. Mutant A11 proteins are useful for producing plants having
XX      increased resistance or reduced sensitivity to a geminivirus such as
XX      cassava golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX      virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX      cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX      virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
XX      virus, cotton leaf curl virus or beet curly top virus.
XX      Sequence 70 AA:
XX      50
XX      Query Match          92.0%: Score 332: DB 21: Length 70:
XX      Best Local Similarity 92.9%: Pred. No. 1,9c-34:
XX      Matches 65: Conservative 0: Mismatches 5: Indels 0: Gaps 0:
XX      Oy      1 TLVGSAAVDSRGANGCOTNSDAAEALMASKEEALQITREKIPKYLQFHHNLSNM: 60
XX      Db      1 LTVGSLTQVGRSARGCQTNSDAAEALMASKEEALQITREKIPKYLQFHHNLSNM: 60
XX      Oy      61 DRIFDKTREP 70
XX      Db      61 dRlfdktrep 70
XX      RESULT 13
XX      AAB18681
XX      AAB18681 standard: peptide: 70 AA.
XX      AAB18681:
XX      22-JAN-2001 (first entry)
XX      Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
XX      Geminivirus: replication protein; Rep protein; A11; transgenic plant;
XX      ribosome binding region; resistance; geminivirus infection.
XX      Synthetic.
XX      OS

```


DT 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

DE Geminivirus: replication protein; Rep protein; AL1; Transgenic plant;

KN ribosome binding region; resistance; geminivirus infection.

XX Synthetic.

OS Tomato golden mosaic virus.

XX Location/Qualifiers

FT Key MISC-difference 52/ote- "wild type residue replaced with Ala"

FT MISC-difference 54 /note- "wild type residue replaced with Ala"

FT MISC-difference 55 /note- "wild type residue replaced with Ala"

XX MO200054573-AL.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000MO-US06759.

XX 18-MAR-1999; 9905-0125004.

XX 09-APR-1999; 9905-0289346.

XX (UNCL-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence

PT encoding a mutant AL1 protein with a mutation in the Rb binding region

XX Claim 53; Page 44-45; 73pp; English.

XX The present sequence represents a mutant peptide, derived from a

CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds

CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded

CC DNA, and interacts with other viral and host proteins. Mutants of the AL1

CC protein have been used to engineer transgenic plants with increased resistance to geminivirus infection. AL1 is

CC present in a ribosome binding region and is essential for geminivirus

CC plant. Mutant AL1 proteins are useful for producing plants having

CC increased resistance or reduced sensitivity to a geminivirus such as

CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl

CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian

CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic

CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper

CC virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA:

Query Match 90.38; Score 326; DB 21; Length 70;

Best Local Similarity 32.98; Pred. No. 1; Le-33;

Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TLWGCALAVDGRAGCCGTNDAAAFALMASKEEAQIIRREKIPKTLPOPHNLNSNT. 60

Db 1 LTVWGEFYVDRYRGYCGTANDAAALNASKEEAQIIRREKIPKTLPOPHNLNSNT. 60

OY 61 DRIFDKTRPP 70

Db 61 DRIFDKTRPP 70

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:40:11 ; Search time 72.79 seconds

(without alignments)

73.255 Million cell updates/sec

Title: US-09-289-346a-8

Product score: 36.1

Sequence: 1 TLVWGMAMVDGSRAGGCGT.....FQTHNLSNLTIDETPEP 70

Scoring table:

gapop 10.0 , gapext 0.5

Searched: 219241 segs, 7617452 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: P111.*
2: P112.*
3: P113.*
4: P114.*

Pred. No. is the number of results predicted by chance to have a
score of 96.5 or higher. The score of the best result is printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	350	97.0	352	1	OCIYPT
2	250	69.3	361	1	OCIYPT
3	237	65.7	358	2	S07584
4	230	63.7	362	1	J01887
5	223	61.8	359	2	S39211
6	219	60.7	349	2	JQ2300
7	219	60.7	349	2	S31875
8	216	59.6	353	2	S22553
9	216	59.6	353	2	S22553
10	213	59.0	355	1	OCIYPT
11	212	58.7	357	1	OCIYPT
12	210	58.2	359	1	J01870
13	210	58.2	359	2	S39235
14	210	58.2	359	2	S28360
15	203	56.2	360	2	S59885
16	203	56.2	360	2	S59885
17	111	32.4	347	1	S43Y85
18	68.5	19.0	1713	2	A53437
19	68	18.8	587	2	OCIYPT
20	67	18.6	180	2	DB4082
21	66.5	18.4	201	2	A81380
22	64.5	17.9	299	2	B71967
23	63.5	17.6	1447	2	T12554
24	63.5	17.6	1447	2	T12554
25	63.5	17.6	1447	2	T12554
26	63.5	17.6	1447	2	T12554
27	63.5	17.6	1447	2	T12554
28	63.5	17.6	1447	2	T12554
29	62	17.2	295	2	D42452

ALIGNMENTS

```

RESULT
OCIYPT
1
A:Title: tomato golden mosaic virus
A:Species: tomato golden mosaic virus
A:Note: host Nicotiana sp. (tomacco)
A:Date: 28-Aug-1985 #sequence-revision 28-Aug-1985 #text-change 08-Apr-1994
A:Accession: A04170 Steinf. V.E.; Coutts, R.H.A.; Buck, K.W.
EMBL J 31 2157-2205 1984
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomo
A:Reference number: A04163
A:Molecule type: DNA
A:Accession: A04170
A:Residues: 1-352 <IAB>
C:Comments: The genome consists of two circular, single-stranded DNA components, DNA A
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus A11 protein

Query Match 97.0% Score 350; DB 1; Length 352;
Best local Similarity 97.1% Pred. No. 1,4e-31;
Matches 66; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 TLVWGMAMVDGSRAGGCGTSTNAAEALMAASKEEALQITREKIPKTYFQTHNLSNLT 60
DB 111 TLVWGFQVDSRAGGCGTSTNAAEALMAASKEEALQITREKIPKTYFQTHNLSNLT 170

OY 61 DRIEDKTEPP 70
DB 171 DRIEDKTEPP 180

RESULT 2
OCIYPT
A11 protein - potato yellow mosaic virus (Isolate Venezuela)
C:Species: potato yellow mosaic virus
C:Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #text-change 16-Jun-2000
R:Comments: R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato ye
J. Gen. Virol. 72, 1515-1520, 1991
A:Reference number: J00362; M7ID:91311403
A:Accession: J00364
A:Status: translation not shown
A:Molecule type: DNA
A:Accession: J00364
A:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus A11 protein

```


C:Date: 22-Nov-1993 #sequence-revision 26-May-1995 #text-change 20-Sep-1999
 A:Accession: S31875
 R:Forres-Pacheco, I.; Garzon-Tiznado, J.A.; Jimenez, B.; Herrera-Estrella, L.; Rivera-Bu
 submitted to the EMBL Data Library, February 1993
 A:Reference number: S31872
 A:Accession: S31875
 A:Reference number: S31872
 A:Molecule type: DNA
 A:Status: preliminary
 A:Cross-references: EMBL:X70418; NID:961023; PIDN:CAA9656.1; PID:961025
 A:Note: the source is designated as pepper huasteco virus
 C:Superfamily: tomato golden mosaic virus ALI protein

Query Match 60.7%; Score 219; DB 2; Length 349;
 Best Local Similarity 58.6%; Pred. NO. 6.3e-17;
 Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

Db 1 TLWGEAAVDRSGAGCCGTSNDAAEALMAASSKEEALQITREKIPKYLQFPHNLNSND 60
 |||||
 Db 110 TWKGEFQIDSRSGAGCCGTSNDAAEALMAASSKEEALQITREKIPKYLQFPHNLNSND 169
 |||||
 Db 61 DRIFDKTPEP 70
 |||||
 Db 170 NRIQTPPEP 179

RESULT 8
 S22593
 hypothetical protein C4 - tomato yellow leaf curl virus
 C:Species: tomato yellow leaf curl virus
 C:Date: 22-Nov-1993 #sequence-revision 10-Nov-1995 #text-change 20-Sep-1999
 C:Accession: S22593
 R:Kierf-Pou, A.; Bendahmane, M.; Metzelt, V.; Accotto, G.P.; Crespi, S.; Gronenborn, B.
 Nucleic Acids Res. 19, 6627-6769, 1991
 A:Title: Acids Res. 19, 6627-6769, 1991 from Sardinia is a whitefly-transmitted monopartit
 A:Reference number: S22588; MUID:92107660
 A:Accession: S22593
 A:Reference number: S22588; MUID:92107660
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-359 <KHE>
 A:Cross-references: EMBL:X61153; NID:962211; PIDN:CAA3466.1; PID:962217
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
 C:Superfamily: tomato golden mosaic virus ALI protein

Query Match 59.8%; Score 216; DB 2; Length 359;
 Best Local Similarity 56.5%; Pred. NO. 1.4e-16;
 Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Db 2 LWKGEAAVDRSGAGCCGTSNDAAEALMAASSKEEALQITREKIPKYLQFPHNLNSND 61
 |||||
 Db 111 LEMKTFQIDSRSGAGCCGTSNDAAEALMAASSKEEALQITREKIPKYLQFPHNLNSND 170
 |||||
 Db 62 RIFDKTPEP 70
 |||||
 Db 171 KVFQVPPAP 179

RESULT 9
 JO2327
 All protein - Indian cassava mosaic virus
 N:Alternate names: replication-associated protein
 C:Species: Indian cassava mosaic virus
 C:Date: 26-Aug-1995 #sequence-revision 07-Oct-1994 #text-change 20-Sep-1999
 A:Accession: J02327; S25083
 R:Kierf-Pou, A.; Bendahmane, M.; Metzelt, V.; Accotto, G.P.; Crespi, S.; Gronenborn, B.
 Nucleic Acids Res. 19, 6627-6769, 1991
 A:Title: Nucleic Acids Res. 19, 6627-6769, 1991 from Sardinia is a whitefly-transmitted monopartit
 A:Reference number: J02326; MUID:94065670
 A:Accession: J02327
 A:Molecule type: DNA

A:Residues: 1-351 <HON>
 A:Cross-references: EMBL:Z24758; NID:9395351; PIDN:CAA0891.1; PID:9584046
 C:Superfamily: tomato golden mosaic virus ALI protein

Query Match 59.0%; Score 213; DB 2; Length 351;
 Best Local Similarity 61.2%; Pred. NO. 3e-16;
 Matches 41; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Db 4 WGEAAVDRSGAGCCGTSNDAAEALMAASSKEEALQITREKIPKYLQFPHNLNSND 63
 |||||
 Db 113 WKFQIDSRSGAGCCGTSNDAAEALMAASSKEEALQITREKIPKYLQFPHNLNSND 172
 |||||
 Db 64 FQKTPPEP 70
 |||||
 Db 173 FTKPEP 179

RESULT 10
 Q00CWI
 protein - abutilon mosaic virus (isolate West India)
 C:Species: abutilon mosaic virus
 C:Date: 31-Mar-1992 #sequence-revision 31-Mar-1992 #text-change 08-Apr-1994
 C:Accession: A36214
 R:Pfischmuth, T.; Zimmat, G.; Joske, H.
 Virology 178, 461-468, 1990
 A:Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as
 A:Reference number: A36214; MUID:91020964
 A:Accession: A36214
 A:Reference number: A36214; MUID:91020964
 A:Residues: 1-355 <FPD>
 A:Cross-references: EMBL:X15983
 C:Genetics:
 A:Map position: segment A
 C:Superfamily: tomato golden mosaic virus ALI protein

Query Match 59.0%; Score 213; DB 1; Length 355;
 Best Local Similarity 57.1%; Pred. NO. 3e-16;
 Matches 40; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

Db 1 TLWGEAAVDRSGAGCCGTSNDAAEALMAASSKEEALQITREKIPKYLQFPHNLNSND 60
 |||||
 Db 110 TWKGEFQIDSRSGAGCCGTSNDAAEALMAASSKEEALQITREKIPKYLQFPHNLNSND 169
 |||||
 Db 61 DRIFDKTPEP 70
 |||||
 Db 170 ERIKAPPEP 179

RESULT 11
 Q00CWI
 protein - tomato yellow leaf curl virus
 N:Alternate names: CI protein
 C:Species: tomato yellow leaf curl virus
 C:Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #text-change 23-Jul-1999
 C:Accession: D40779
 R:Navot, N.; Pichersky, E.; Zeidan, M.; Zamir, D.; Czosnek, H.
 Virology 185, 151-161, 1991
 A:Title: tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a sin
 A:Accession: D40779
 A:Reference number: D40779; MUID:92024070
 A:Accession: D40779
 A:Reference number: D40779; MUID:92024070
 A:Molecule type: DNA
 A:Status: translation not shown
 A:Cross-references: GB:X15656; NID:962204; PIDN:CAA3688.1; PID:962207
 C:Superfamily: tomato golden mosaic virus ALI protein

Query Match 58.7%; Score 212; DB 1; Length 357;
 Best Local Similarity 65.6%; Pred. NO. 3.9e-16;
 Matches 40; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:57:17 ; Search time 43.68 Seconds
(without alignments)

58,758 Million cell updates/sec

Title: US-09-289-346a-8

Protein Sequence: 1 TLWGCAMVNGSRAGCCCT.....FORHNSNLDIDRTEPP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query	Match	Length	DB	ID	Description
1	350	97.0	352	1	VAL1_TGMV	P03567	tomato gold
2	250	69.3	361	1	VAL1_PPMV	P27258	potato yell
3	237	65.7	358	1	VAL1_CXKV	P14862	cassava lat
4	230	63.7	356	1	VAL1_CXNV	P14972	cassava lat
5	223	61.8	359	1	VAL1_TYCV	P3603	tomato yell
6	223	61.8	359	1	VAL1_TYCV	006523	pepper huss
7	219	60.7	349	1	VAL1_PPMV	P27260	tomato yell
8	216	59.8	359	1	VAL1_PPMV	P21947	bean golden
9	214	59.3	353	1	VAL1_PPMV	P05175	bean golden
10	213	59.0	355	1	VAL1_PPMV	P21947	bean golden
11	212	58.7	357	1	VAL1_PPMV	P27259	tomato yell
12	210	58.2	356	1	VAL1_PPMV	P03567	tomato gold
13	210	58.2	356	1	VAL1_PPMV	P27259	tomato yell
14	117	32.4	347	1	VAL1_PPMV	P03567	tomato gold
15	68.5	19.0	1713	1	VAL1_PPMV	P03567	tomato gold
16	64.5	17.6	299	1	VAL1_PPMV	P03567	tomato gold
17	63.5	17.6	447	1	VAL1_PPMV	P03567	tomato gold
18	63.5	17.6	1610	1	VAL1_PPMV	P03567	tomato gold
19	63.5	17.6	2161	1	VAL1_PPMV	P03567	tomato gold
20	63.5	17.6	2203	1	VAL1_PPMV	P03567	tomato gold
21	63.5	17.6	2203	1	VAL1_PPMV	P03567	tomato gold
22	61	16.6	1463	1	VAL1_PPMV	P03567	tomato gold
23	60	16.6	432	1	VAL1_PPMV	P03567	tomato gold
24	60	16.6	447	1	VAL1_PPMV	P03567	tomato gold
25	59.5	16.5	136	1	VAL1_PPMV	P03567	tomato gold
26	59.5	16.5	299	1	VAL1_PPMV	P03567	tomato gold
27	58.5	16.3	640	1	VAL1_PPMV	P03567	tomato gold
28	58.5	16.3	334	1	VAL1_PPMV	P03567	tomato gold
29	58.5	16.2	335	1	VAL1_PPMV	P03567	tomato gold
30	58.5	16.2	428	1	VAL1_PPMV	P03567	tomato gold
31	58.5	16.2	428	1	VAL1_PPMV	P03567	tomato gold
32	58.5	16.2	589	1	VAL1_PPMV	P03567	tomato gold
33	58.5	16.2	1044	1	VAL1_PPMV	P03567	tomato gold

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	352 AA.
VAL1_TGMV				
NC	P03567:1966 (rel. 01, Created)			
DE	21-JUL-1986 (rel. 01, last sequence update)			
DE	01-JUN-1994 (rel. 29, last annotation update)			
DE	ALI PROTEIN.			
GN	AC1.			
OS	Tomato golden mosaic virus (TGMV).			
CC	Virus; ssDNA viruses; Geminiviridae; Begomovirus.			
OX	NCBI_TaxID=10831:			
DE	SEQUENCE FROM N.A.			
RA	Hamilton M.D.O., Stein V.E., Coates R.H.A., Buck K.W.;			
RT	*Complete nucleotide sequence of the infectious cloned DNA components			
RT	of tomato golden mosaic virus: potential coding regions and regulatory			
RT	sequences.			
RE	EMBL J. 3:2197-2205(1984).			
CC	1. SIMILARITY: BELONGS TO GEMINIVIRUS ALL PROTEIN FAMILY			
CC	2. This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	entities requires a license agreement (see http://www.isb-sdb.ch/announce/			
CC	or send an email to license@sdb.ch).			
DR	EMBL: K02029; -; NOT_ANNOTATED_CDS.			
DR	PIR: A04170; QOCVLL.			
DR	InterPro: IPR001191; Gemin1_AL1.			
DR	PIR: PF00799; Gemin1_AL1.			
DR	PRINTS: PR00227; GEMINICATV.L			
DR	PROSITE: PS000736; Gemin1_AL1.			
DR	APP-Bind49_223			
FT	NP_BIND 223			
FT	SDOUENCE 352 AA: C303938964BBA4 CRC64:			
Query Match	97.0%	Score 350:	DB 1:	Length 352:
Best Local Similarity	97.1%	Pred. No. 8.2e-32:		
Matches	66:	Conservative	2:	Indels
OY	1 TLWGCAMVNGSRAGCCCTNSAAVAALNASEAALQIIIRKIPKYLEPFRHNSLN 170			
DB	111 TLWGCAMVNGSRAGCCCTNSAAVAALNASEAALQIIIRKIPKYLEPFRHNSLN 170			
OY	61 DRIIDRTEPP 70			
DB	171 DRIIDRTEPP 180			
RESULT	2			
VAL1_PPMV				

```

ID VAL1_PPMV STANDARD: PRT: 361 AA.
CC CC
DT 01-MAR-1992 (rel.: 23. Created)
DT 01-AUG-1992 (rel.: 23. Last sequence update)
DZ 01-MAR-1992 (rel.: 23. Last annotation update)
DE AII PROTEIN (rel.: 23).
OS Potato yellow mosaic virus [Isolate Venezuela].
OC Viruses::ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxId=10828;.
RN (1)
RP SEQUENCE FROM N.A.
RA PRODUCED BY J.H. DUBBEDAARD-JANSSEN; R.M.K. DE VRIES; F.J.F. HAMILTON W.D.O.; C.E. VAN DER KAMMEN AND S.G. MULLER.
RL "The nucleotide sequence of the infectious cloned DNA components of potato yellow mosaic virus."
RL J. Gen. Virol. 72:1515-1520(1991)..
CC -1-SIMILARITY: BELONGS TO GEMINVIRUSES ALL PROTEIN FAMILY..
CC --
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DR PFam: PF00640; pfam_782.L; -.
DR PfR: PF00640; OGCVP.
DR InterPro: IPR001191; Gemini.AL.II.
DR Pfam: PF00799; Gemini.AL.I.
DR PRINTS: PR00227; GENCOMATALL.
DR PRINTS: PR00228; GENCOMATCIVLI.
DR ProDom: PD000736; Gemini_AL_I.
AP Abinding: 322 AP (BOWENETAL.).
FW 322
SEQUENCE 361 AA; 40850 MW; 56273rBB126v383 CRC64;
QY Query Match 69.3%; Score 250; DB 1; Length 361;
DB BEE Local Similarity 68.1%; Pred. No. 1,2e+20;
Matches 47; Conservancy 11; Mismatches 11; Indels 0; Gaps 0;
OY 1 TTVGAGNNGNSRGCGSSNDAAEAIANSGKEPLOTITREKYPKYLPDPNNENN 60
||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: ||
Db 110 TTIMGIGFPIODGSRRGGGVVDNAADAEALNSGREAKMTIKELPERFLPGHNSCN 169
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 61 DRIFPKPTPE 69
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 170 DRLEMAPE 178
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
RESULT 3
VAL1_CLVK STANDARD: PRT: 358 AA.
ID VAL1_VALCK
CC CC
DT 01-APR-1990 (rel.: 19. Created)
DT 01-FEB-1990 (rel.: 19. Last sequence updates)
DZ 01-APR-1990 (rel.: 20. Last annotation update)
DE AII PROTEIN (rel.: 19).
OS Cassava latent virus (strain West Kenyan 844).
OC Viruses::ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxId=10818;.
RN (1)
RP SEQUENCE FROM N.A.
RA Produced by J.H. DUBBEDAARD-JANSSEN; R.M.K. DE VRIES; F.J.F. HAMILTON W.D.O.; C.E. VAN DER KAMMEN AND S.G. MULLER.
RL "Nucleotide sequence of cassava latent virus DNA."
RL Nature 301:260-262(1983).
CC -1-SIMILARITY: BELONGS NO GEMINVIRUSES ALL PROTEIN FAMILY..
CC --
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DR      DR     EMBL: J02057..-; NCBI: ANNOTATED_CDS.  
DR      DR     InterPro: IPRO01191; GEMINI_ALI:  
DR Pfam: PF00799; GEMINI_ALI: 1.  
DR PRINTS: PR00227; GEMCONTCV.L1.  
DR PRINTS: PR00228; GEMCONTCV.L1.  
DR ProDom: PD000736; GEMINI_ALI: 1.  
APR binding 220   APR (POTENTIAL)  
FM          FM    SQUONCE 358 AA: 40346 MW: EDJ7SEF55EEB92D0E CRC64;  
SQ  
  
OY       OY      Query Match           65.7%; Score 237; DB 1; Length 358;  
Best Local Similarity 61.4% Pred.: No, 3,4e-19;  
Matches         13; Mismatches        14; Indels      0; Gaps      0;  
OY            OY      1 TIVGANDNCSGGCGCSCSNDAENALNSKREGLITRKIDPEKTPOPNUNT 60  
DB            DB      109 TVMGSDPDIGRSARCCGSQANDAYAKALNSKSKEALTAVRELVPKHDFIQGFNNLSLT 168  
OY              OY      61 DRIEDFKTPEP 70  
DB              DB      169 DRIEDFPAPP 178  
  
RESULT_4  
VAL CLVN STANDA RD: PRT: 358 AA.  
ID VAL1 CLVN  
OC P14572:  
DT 01-AFR-1990 (Ref., 14, Created)  
AT -AFR-1990 (Ref., 14, Last sequence update)  
DE 01-AFR-1990  
DE A11 PROTEIN (40 kDa protein).  
AC1.  
GN Cassava latent virus (strain Nigerian).  
OS Viruses: SSINA viruses; Gemniviridae; Begomovirus.  
NCBI_TaxId=10819;. . .  
LN SEQUENCE FROM N.A.  
RN MEDLINE=46174370 PubMed=2308831;  
RL Morris B.; Coates L.; Lowe S.; Richardson K.; Eddy P.;  
FT Nucleotide sequence of the infectious cloned DNA components of  
RL African cassava mosaic virus (Nigerian strain)." ;  
NL Nucleic Acids Res. 18:197-198(1990).  
CC *- SIMILARITY: BELONGS TO GEMINVIRUSES AL1 PROTEIN FAMILY.  
CC  
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CC  
DR      DR     EMBL: X17055; CA334953.1 .  
DR      DR     PI R: S07594; S07594.  
DR      DR     InterPro: IPR001191; GEMINI_ALI:  
DR Pfam: PF00799; GEMINI_ALI: 1.  
DR PRINTS: PR00227; GEMCONTCV.L1.  
DR PRINTS: PR00228; GEMCONTCV.L1.  
DR ProDom: PD000736; GEMINI_ALI: 1.  
APR binding 220   APR (POTENTIAL)  
FM          FM    SQUONCE 358 AA: 40345 MW: IDBLIBHBOCBZBDZEC CRC64;  
SQ  
  
Query Match           65.7%; Score 237; DB 1; Length 358;  
Best Local Similarity 61.4% Pred.: No, 3,4e-19;  
Matches         13; Mismatches        14; Indels      0; Gaps      0;
```


ProDom: PD000736: Gemini_AL1.1.

ATP-binding: 221 ATP (BY SIMILARITY).

NP_BIND 349 AA: 39722 MW: 55476CD5370F4 CIGC4:

Query Match 60.7%: Score 219: DB 1: Length 349:

Best Local Similarity 58.6%: Pred. No. 3.4e-17:

Matches 41: Conservative 13: Mismatches 16: Indels 0: Gaps 0:

1 TLWGEAAVDGSRAGCOTSDAAEAALANSSKEEAALQIRKIPKYLFOFHNLNSN 60

110 TLWGEAAVDGSRAGCOTSDAAEAALANSSKEEAALQIRKIPKYLFOFHNLNSN 169

61 DRIDFKTPP 70

170 NRIFQTPP 179

RESULT 9

VAL1_TYICM STANDARD: PRT: 359 AA.

AC P27260:

01-AUG-1992 (Rel. 23, Created)

01-AUG-1992 (Rel. 23, Last sequence update)

01-JUN-1994 (Rel. 29, Last annotation update)

CL1 PROTEIN (C1 PROTEIN).

Tomato yellow leaf curl virus (strain Margaret).

Viruses: ssDNA viruses: Geminiviridae: Begomovirus.

NCBI_TaxID:10833:

EMBL: X61153: GMA456.1: -

PIR: S22593: S22593

InterPro: IPR001191: Gemini_AL1.

Pfam: PF00799: Gemini_AL1.

PRINTS: PR00227: GEMCOATL1.

PRINTS: PR00228: GEMCOATL1.

ProDom: PD000736: Gemini_AL1.1.

ATP-binding: 220 ATP (POTENTIAL)

SEQUENCE 359 AA: 40733 MW: 97194N07C3B87 CIGC4:

Query Match 59.8%: Score 216: DB 1: Length 359:

Best Local Similarity 56.5%: Pred. No. 7.6e-17:

Matches 39: Conservative 11: Mismatches 19: Indels 0: Gaps 0:

2 TLWGEAAVDGSRAGCOTSDAAEAALANSSKEEAALQIRKIPKYLFOFHNLNSN 61

110 TLWGEAAVDGSRAGCOTSDAAEAALANSSKEEAALQIRKIPKYLFOFHNLNSN 170

62 DRIDFKTPP 70

171 KYFQVPP 179

RESULT 9

VAL1_BGV STANDARD: PRT: 353 AA.

AC P2197:

01-AUG-1987 (Rel. 05, Created)

13-AUG-1987 (Rel. 05, Last sequence update)

01-OCT-1996 (Rel. 34, Last annotation update)

AL1 PROTEIN (40.2 KDA PROTEIN).

AC1.

Bean golden mosaic virus.

Viruses: ssDNA viruses: Geminiviridae: Begomovirus.

NCBI_TaxID:10833:

EMBL: X61153: GMA456.1: -

PIR: S22593: S22593

InterPro: IPR001191: Gemini_AL1.

Pfam: PF00799: Gemini_AL1.

PRINTS: PR00227: GEMCOATL1.

PRINTS: PR00228: GEMCOATL1.

ProDom: PD000736: Gemini_AL1.1.

ATP-binding: 222 ATP (POTENTIAL)

SEQUENCE 353 AA: 40190 MW: 80FA779DF029A34 CIGC4:

Query Match 59.3%: Score 214: DB 1: Length 353:

Best Local Similarity 58.6%: Pred. No. 1.3e-16:

Matches 41: Conservative 13: Mismatches 16: Indels 0: Gaps 0:

1 TLWGEAAVDGSRAGCOTSDAAEAALANSSKEEAALQIRKIPKYLFOFHNLNSN 60

110 TLWGEAAVDGSRAGCOTSDAAEAALANSSKEEAALQIRKIPKYLFOFHNLNSN 169

61 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

62 DRIDFKTPP 70

170 NRIFQTPP 179

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CC CC
DR DRL EMBL; X15983; -. NOT_ANNOTATED.CDS.
DR PIR; A36214; OOCVWL.
DR InterPro; IPR001191; Gemin_AAT1.
DR Pfam; PF007993; Gemin_AAT1; 1.
DR PRINTS; PR00228; GEMIN_AAT1; 1.
DR PROSITE; PS000736; Gemin_AAT1; 1.
DR ATP-binding.
FW KRP BINDING 221 228 ATP (POTENTIAL).
SQ SEQUENCE 355 AA: 405257 MW: 16A2JCA6B3251E95 CRC64;
GC GC
CC CC Query Match 59.0%; Score 213; DP 1; Length 355;
CC Best Local Similarity 57.1%; Pos Neg 1.6e-16;
CC Matches 40; Conservative 12; Mismatches 18; Indels 0; Gaps 0;
OY 1 TLVGEAAVDGNSARQCGCONSDNAAPALNANASKEEDALTITREKIPKYLTFEPHNLISNL 60
DB 110 TAMEEAFDIDGSNRGGQGTANDSYAKALANGDVQSALTITREKPKDYVLAQNHNITSNL 169
OY 61 DRIFPKRPP 70
DB :||| |||
DB 170 BRIFKAAPER 179
RESUL 11
FALL YTCVCV
TTL YTCVCV STANDARD: PERI 357 AA.
AC P27259;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN (C1 PROTEIN).
DE C1.
OS Tomato yellow leaf curl virus (TYLCV).
OS Virus eukaryota/Viruses/geminiviridae/Begomovirus.
OS NCBI_TaxId=10832.
RN R1
RP SEQUENCE FROM N.A.
RA MEDLINE:92024070; PubMed:1926771;
RA Navot N., Pleschsky R., Zeldin M., Zamit D., Czosnek H.;
RA "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
RT Virology 185:151-161(1999)."
RI 1 - SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC CC
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CC CC
DR DRL EMBL; X15566; CA33568.1; -.
DR PIR; D40779; OOCVCI.
DR InterPro; IPR001191; Gemin_AAT1.
DR Pfam; PF007993; Gemin_AAT1; 1.
DR PRINTS; PR00227; GEMIN_AAT1; 1.
DR PROSITE; PS00228; GEMIN_AAT1; 1.
DR ProDom; PD000736; Gemin_AAT1; 1.
DR ATP-binding.
FW KRP BINDING 219 226 ATP (POTENTIAL).
SQ SEQUENCE 357 AA: 40678 MW: 93BA6BE1AE332A7 CRC64;
```

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Qy      Query Match: 58.7% Score 210: DB 1: Length 357:
Db      Best Local Similarity 65.6% Pred. No. 2,je-16:
Matches 40: Conservative 11: Mismatches 10: Indels 0: Gaps 0:

Oy      4 WGAHVDGNSANGCCGTSSNDAAEALMAASSREBALDIKEKTYIDPFNNLSMDRT 63
Db      111 |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
          RYSDVSDANSHAGGGDGSNDNVADNALNSGSKSBALNLKRNADTILDFHMLSSHLDRI 170

Oy      Oy      64 F 64
Db      Db      171 F 171

RESULT_12
VALI_RCVY STANDARD: PRT: 359 AA.
ID VALI_ID VALI_RECVY
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DL ALI PROTEIN (40.8 KDa PROTEIN).
DS Beet curly top virus (BCTV).
OS VIRUSES: SEDSA Viruses; Geminiviridae; Curtovirus.
OC NCBI_TaxID=1040:
RN (1)
RF SEQUENCE FROM N.A.
RT RESECU OF THE BCTV BY P.G. CALLIS R.T. PINNER M.S.:
PT "The nucleotide sequence of an infectious clone of the geminivirus
   beet curly top virus."
RL EMBL J. 5:1761-1767(1986).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
CC CC This SMS-S-POR entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL: X01414: ? NOT ANNOTATED CODS.
DR InterPro: IP0001191; Gemin_ALI.
DR Pfam: PF00739; Gemin_ALI.1.
DR PRINTS: PR00227; GEMCONFALL.
DR PRINTS: PR00228; GEMCONFALL.1.
DN DR KEGG: D000736; Gemin_ALI.1.
DN ATP-Binding 222 229 AFP (POTENTIAL).
FT NE BINDING 358 AA: 40889 MW; 39k45PRC309C33 CRC64;
SQ SEQUENCE

Query Match 58.7% Score 210: DB 1: Length 358:
Best Local Similarity 54.3% Pred. No. 3,je-16:
Matches 38: Conservative 16: Mismatches 16: Indels 0: Gaps 0:

Oy      1 TTVWEPAYDNGSGCGGTSSNDAAEALMAASSREKALDIKEKYIDPFNNLSMNT 60
Db      111 |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
          RYSDVSDANSHAGGGDGSNDNVADNALNSGSKSBALNLKRNADTILDFHMLSSHLDRI 169

Oy      Oy      61 DRIFKPTEP 70
Db      Db      170 OKLTORPPDP 179

RESULT_13
ID VALI_ID VALI_RECVY STANDARD: PRT: 361 AA.
AC Q06657:
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)

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DE ALL PROTEIN.
CC ALL.
OS Tomato mottle virus (isolate Florida) (TMov).
CC VIRUSES: ssDNA viruses: Geminiviridae; Begomovirus.
CC NCBI:taxid=36443.
RN [1]
RE SEQUENCE FROM N.A.
RA MEDLINE-93107851; PubMed-1469361.
RA Aboudia A.M., Polston J.E., Hiebert E.:
RA "The nucleotide sequence of tomato mottle virus, a new geminivirus
RA isolated from tomatoes in Florida."
RA J. Gen. Virol. 73:231-234 (1992).
CC 1. SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
-----
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-----
DR EMBL: L14460; AAC32410.1; .
DR PIR: J01870; J01870.
DR InterPro: IPR001191; Gemin_LAM1.
DR Pfam: PF00799; Gemin_LAM1.1.
DR PRINTS: PR00227; GEMCOATALL.
DR PRINTS: PR00228; GEMCOATCIVL.
DR ProDom: PD000736; Gemin_LAM1.1.
RM ATP-binding: 222
RM NP_BIND
SQ SEQUENCE 361 AA; 40516 MW; 81388505EAC6950 CRC64;
-----
Query Match 58.28; Score 210; DB 1; Length 361;
Best Local Similarity 57.98; Pred. No. 8.3e-06;
Matches 38; Conservative 16; Mismatches 16; Indels 0; Gaps 0;
-----
OY 1 TIVNGEAVDGRSARGCOTSDNAAPALMASKEKALQIETKRIPEKLFQPHNLMSLN. 60
DB 110 TIVNGEAVDGRSARGCOTSDNAAPALMASKEKALQIETKRIPEKLFQPHNLMSLN. 169
OY 61 DPKETKTP 70
DB 111 DPKETKTP 70
DB 170 ERTAAAP 179
-----
RESULT 14
VALD_SICV STANDARD: PRT; 347 AA.
ID PACT_SICV
DR 01-DEC-1992 (rel. 24, Created)
DR 01-DEC-1992 (rel. 24, last sequence update)
DR 01-DEC-1992 (rel. 24, last annotation update)
DE A11 PROTEIN.
OS Squash leaf curl virus.
CC VIRUSES: ssDNA viruses: Geminiviridae; Begomovirus.
CC NCBI:taxid=10823.
RN [1]
RE SEQUENCE FROM N.A.
RA MEDLINE-91082449; PubMed-1984668.
RA Lazavovitz S.G., Lardino I.B.:
RA "Infectivity and complete nucleotide sequence of the cloned genomic
RA components of a bipartite squash leaf curl geminivirus with a broad
RA host range phenotype."
RA Virology 160:58-66 (1991).
CC 1. SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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DR EMBL: M38183; ACC32410.1; ALT_INT.
DR PIR: G67183; G67183.1; Gemin_LAM1.
DR InterPro: IPR001191; Gemin_LAM1.
DR Pfam: PF00799; Gemin_LAM1.1.
DR PRINTS: PR00227; GEMCOATALL.
DR PRINTS: PR00228; GEMCOATCIVL.
DR ProDom: PD000736; Gemin_LAM1.1.
RM ATP-binding: 218
RM NP_BIND
SQ SEQUENCE 347 AA; 39110 MW; AFD8BDE122110E CRC64;
-----
Query Match 32.44; Score 117; DB 1; Length 347;
Best Local Similarity 37.98; Pred. No. 8.3e-06;
Matches 25; Conservative 12; Mismatches 25; Indels 4; Gaps 1;
-----
OY 5 GCAVNGDSARGCOTSDNAAPALMASKEKALQIETKRIPEKLFQPHNLMSLN. 64
DB 116 GQYVSG-----GSKMKDQYVHAAVNAAGSAGALADIKADPKFVWNLIAVSRIF 171
OY 65 DKETP 70
DB 172 OKPEP 177
-----
RESULT 15
ID LAM3_HUMAN STANDARD: PRT; 1713 AA.
AC Q16787; Q1679; Q13680;
DR 01-NOV-1997 (rel. 35, Created)
DR 20-NOV-1997 (rel. 35, last sequence update)
DR 20-NOV-1997 (rel. 35, last annotation update)
DE LAM3_HUMAN ALPHA-3 CHAIN PRECURSOR (EPITHELIAL 170 KDa SUBUNIT) (E170).
CN LAM3
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eulheria; Primates; Catarrhini; Hominoidea; Homo.
CC NCBI:taxid=9606;
RN [1]
RE SEQUENCE FROM N.A.
RA MEDLINE-9457926; PubMed-8077230.
RA Ryan M.C., Tizard R., Vandevanter D.R., Carter W.G.:
RA "Cloning of the Lam3 gene encoding the alpha 3 chain of the adhesive
RA 119ad epiligrin. Expression in wound repair."
RA J. Biol. Chem. 269:22779-22787 (1994).
RN [2] JENSEN OF 1-1331 FROM N.A. (ISSOKNS A AND B).
RN [3] MEDLINE-96163880; PubMed-1556427.
RA Vidal F., Baudouin C., Miguel C., Galliano M.-F., Christiano A.M.,
RA Ulitz J., Ortonne J.-P., Menezes G.:
RA "Cloning of the laminin alpha 3 chain gene (LAM3) and identification
RA of a homozygous deletion in a patient with Herlitz junctional
RA epidermolysis bullosa."
RN [4] JENSEN OF 1-1331 FROM N.A. (ISSOKNS A AND B).
RN [5] MEDLINE-96163880; PubMed-1556427.
CC 1. SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
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009727 ID 009727 PRELIMINARY: PRT: 226 AA.
AC 009727:
DT 01-JUN-1997 (TRENBLER, 04, Created)
DT 01-JUN-1997 (TRENBLER, 04, Last sequence update)
DE REP. PROTEIN (FRAGMENT).
GN REP.
OS Leonturus mosaicivirus.
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=58177;
OX NCBI_TaxID=58177;
RN SEQUENCE FROM N.A.
RP STRAIN=CMV-Brazil.1;
RA Faria J.C., Maxwell D.P.;
RI Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL, U52532; AAB5157.1; -.
DR InterPro: IPR00191; Geminv_AL1.
DR Pfam: PF00799; Geminv_AL1.
DR PRINTS: PR00227; GEMCOATALL.
DR PRODOM: PD000736; Geminv_AL1.
PT NON_CODING_SEQUENCE.
SQ
SEQUENCE 226 AA: 25617 MW: 74CDBE676083PC5 CRC64:

Query Match
Best Local Similarity 78.1%; Score 282; DB 12; Length 226;
Matches 53; Conservative 4; Mismatches 11; Indels 0; Gaps 0:

OY 1 TLWGEAAVDSRGAGCGCTSDNAAEAALNASSKEAAIIRKIPKYLFOYHNLNSMDI 60
Db 111 TLWGEFVQDGRSARGCGCTSDNAAEAALNASSKEAAIIRKIPKYLFOYHNLNSMDI 170
|||||
Db 117 DRIENAFAP 180
|||||

RESULT 3
O9MHF6 PRELIMINARY: PRT: 226 AA.
ID O9MHF6:
AC O9MHF6:
DT 01-NOV-1999 (TRENBLER, 13, Created)
DT 01-NOV-1999 (TRENBLER, 13, Last sequence update)
DE 01-JUN-2001 (TRENBLER, 17, Last annotation update)
DE REPLICATION-ASSOCIATED PROTEIN (FRAGMENT).
GN REP.
OS tomato mild mottle geminivirus.
OC Viruses: ssDNA viruses; Geminiviridae; Unclassified Geminiviridae.
NCBI_TaxID=92943;
OX NCBI_TaxID=92943;
RN SEQUENCE FROM N.A.
RP STRAIN=HN95-HSKV;
RA Nahata M.K., Mejia L., Ramirez P., Karkashian J.P., Doyle M.M.,
RA Maxwell D.P.;
RI "Molecular characterization and DNA-based detection methods for
RI vegetable-infecting geminiviruses in Central America.";
RI Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL, U52532; AAB5157.1; -.
DR InterPro: IPR00191; Geminv_AL1.
DR Pfam: PF00799; Geminv_AL1.
DR PRINTS: PR00227; GEMCOATALL.
DR PRODOM: PD000736; Geminv_AL1.
PT NON_CODING_SEQUENCE.
SQ
SEQUENCE 226 AA: 25941 MW: 2EAL16712871A23 CRC64:

Query Match
Best Local Similarity 78.1%; Score 282; DB 12; Length 226;
Matches 52; Conservative 12; Mismatches 6; Indels 0; Gaps 0:

OY 1 TLWGEAAVDSRGAGCGCTSDNAAEAALNASSKEAAIIRKIPKYLFOYHNLNSMDI 60
RI Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.

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Db 111 TLWGEFVQDGRSARGCGCTSDNAAEAALNASSKEAAIIRKIPKYLFOYHNLNSMDI 170
OY 61 DRIENAFAP 70
|||||
Db 171 DRIENAFAP 180
|||||

RESULT 4
O67574 PRELIMINARY: PRT: 361 AA.
ID O67574:
AC O67574:
DT 01-NOV-1996 (TRENBLER, 01, Created)
DT 01-NOV-1996 (TRENBLER, 01, Last sequence update)
DE REP. PROTEIN (FRAGMENT).
GN REP.
OS Bean golden mosaic virus.
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=10839;
OX NCBI_TaxID=10839;
RN SEQUENCE FROM N.A.
RP STRAIN=CMV-Brazil.1;
RA Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RI Phytopathology 81:980-985(1991).
RI [2]
RN SEQUENCE FROM N.A.
RP STRAIN=CMV-Brazil.1;
RA Gilbertson R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RI Plant Dis. 75:356-362(1991).
RI [3]
RN SEQUENCE FROM N.A.
RP STRAIN=CMV-Brazil.1;
RA Gilbertson R.L., Faria J.C., Ahlquist P.G., Maxwell D.P.;
RI Submitted (MAR-1992) to the EMBL/Genbank/DBJ databases.
DR EMBL, M86866; AAA6512.1; -.
DR InterPro: IPR00191; Geminv_AL1.
DR Pfam: PF00799; Geminv_AL1.
DR PRINTS: PR00227; GEMCOATALL.
DR PRODOM: PD000736; Geminv_AL1.
PT NON_CODING_SEQUENCE.
SQ
SEQUENCE 361 AA: 41041 MW: 0094C7ACAF06B788 CRC64:

Query Match
Best Local Similarity 77.6%; Score 280; DB 12; Length 361;
Matches 52; Conservative 9; Mismatches 6; Indels 0; Gaps 0:

OY 4 WEAAVDSRGAGCGCTSDNAAEAALNASSKEAAIIRKIPKYLFOYHNLNSMDI 63
Db 113 WOHVQDGRSARGCGCTSDNAAEAALNASSKEAAIIRKIPKYLFOYHNLNSMDI 172
|||||
OY 64 FDKTREP 70
|||||
Db 173 FDKTREP 179
|||||

RESULT 5
O9ODB1 PRELIMINARY: PRT: 225 AA.
ID O9ODB1:
AC O9ODB1:
DT 01-MAY-2000 (TRENBLER, 13, Created)
DT 01-MAY-2000 (TRENBLER, 13, Last sequence update)
DE 01-JUN-2001 (TRENBLER, 17, Last annotation update)
DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
GN REP.
OS cowpea golden mosaic geminivirus.
OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=69263;
OX NCBI_TaxID=69263;
RN SEQUENCE FROM N.A.
RP STRAIN=CGMV-BR;
RA Faria J.C.;
RI "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
RI Brazil.";
RI Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.

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DR EMBL: AF188708.1; AF06318.1; -
 DR InterPro: IPR001191; Gemini.AL1.
 DR Pfam: PF00799; Gemini.AL1; 1.
 DR PRINTS: PR00227; GEMCOATALL.
 DR PROSITE: PS00736; GEMCOATALL.
 DR NON_TER 225 AA; 225 AA; 1.
 SO SEQUENCE 225 AA; 25766 MW; 10896CBBD015850 CRC64;

Query Match 77.0%: Score 278; DB 12; Length 225;
 Best Local Similarity 77.6%: Pred. No. 26-22;

Matches 52; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

OY 4 WCGAAYDGRSARGCQOTNDAAEAALNASSKEEALQITREKIPERYLPOFHNLNSNI 63
 DB 113 WGHPTDGRSARGCQOTNDAAEAALNASSKEEALQITREKIPERYLPOFHNLNSNI 172
 64 DPKTPEP 70
 DB 173 RKPPEP 179

RESULT 6
 ID Q98178 PRELIMINARY; PRT: 314 AA.

AC 01-MAR-2001 (TRENBLER). 16, Created)
 DT 01-MAR-2001 (TRENBLER). 15, Last sequence update)
 DE 01-MAR-2001 (TRENBLER). 15, Last annotation update)
 DE REPLICATION ASSOCIATION PROTEIN.
 AC1.
 OS Sweet potato leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OC NCBI_TaxID:100755;

OX NCBI_TaxID:100755;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA R. Valverde R.A., Clark C.A., Sim J., De La Torre R.;
 RA "Detection of a geminivirus infecting sweet potato in the United
 States."
 RL Plant Dis. 82:1253-1257(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lotrakul P., Valverde R.A.;
 RA Submitted (2001-2000) to the EMBL/GenBank/DBJ databases.
 RA InterPro: IPR001191; Gemini.AL1.
 RA Pfam: PF00799; Gemini.AL1; 1.
 DR PRINTS: PR00227; GEMCOATALL.
 DR PROSITE: PS00736; Gemini.AL1; 1.
 SO SEQUENCE 314 AA; 35153 MW; 686220613046934 CRC64;

Query Match 77.0%: Score 278; DB 12; Length 314;
 Best Local Similarity 80.9%: Pred. No. 2-96-22;

Matches 55; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

OY 1 TLWGCAYVDGRSARGCQOTNDAAEAALNASSKEEALQITREKIPERYLPOFHNLNSNI 60
 DB 110 TLWGCAYVDGRSARGCQOTNDAAEAALNASSKEEALQITREKIPERYLPOFHNLNSNI 169
 61 DPKTPEP 68
 DB 170 DPKTPEP 177

RESULT 7

ID Q98555 PRELIMINARY; PRT: 364 AA.

AC 01-MAY-2000 (TRENBLER). 13, Created)
 DT 01-MAY-2000 (TRENBLER). 13, Last sequence update)
 DT 01-JUN-2001 (TRENBLER). 17, Last annotation update)
 DE REPLICATION INITIATION PROTEIN AC1.

CN AC1.
 OS Sweet potato leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OC NCBI_TaxID:100755;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lotrakul P., Valverde R.A., Clark C.A., Sim J., De La Torre R.;
 RA "Detection of a geminivirus infecting sweet potato in the United
 States."
 RL Plant Dis. 82:1253-1257(1998).
 DR EMBL: AF104036; AACD17173.1; -
 DR InterPro: IPR001191; Gemini.AL1.
 DR PRINTS: PR00227; GEMCOATALL.
 DR PROSITE: PS00736; GEMCOATALL.
 SO SEQUENCE 364 AA; 40680 MW; 5F79752431A09D6E CRC64;

Query Match 77.0%: Score 278; DB 12; Length 364;
 Best Local Similarity 80.9%: Pred. No. 3-46-22;

Matches 55; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

OY 1 TLWGCAYVDGRSARGCQOTNDAAEAALNASSKEEALQITREKIPERYLPOFHNLNSNI 60
 DB 110 TLWGCAYVDGRSARGCQOTNDAAEAALNASSKEEALQITREKIPERYLPOFHNLNSNI 169
 61 DPKTPEP 68
 DB 170 DPKTPEP 177

RESULT 8
 ID Q98693 PRELIMINARY; PRT: 185 AA.

AC 01-FEB-1997 (TRENBLER). 02, Created)
 DT 01-FEB-1997 (TRENBLER). 02, Last sequence update)
 DT 01-JUN-2001 (TRENBLER). 17, Last annotation update)
 DE REP PROTEIN (FRAGMENT).
 GN AC1.
 OS sida golden mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OC NCBI_TaxID:51034;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-TAMATCHA.
 RA Roye M.E., McLaughlin W.A., Nakha N.K., Maxwell D.P.;
 RA Plant Dis. 81:1251-1258(1997).
 DR EMBL: U67926; AAB97865.1; -
 DR InterPro: IPR001191; Gemini.AL1.
 DR Pfam: PF00799; Gemini.AL1; 1.
 DR PRINTS: PR00227; GEMCOATALL.
 DR PROSITE: PS00736; Gemini.AL1; 1.
 SO SEQUENCE 185 AA; 20975 MW; 3913850A025A5EB1 CRC64;

Query Match 76.2%: Score 275; DB 12; Length 185;
 Best Local Similarity 71.4%: Pred. No. 3-46-22;

Matches 50; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

OY 1 TLWGCAYVDGRSARGCQOTNDAAEAALNASSKEEALQITREKIPERYLPOFHNLNSNI 60
 DB 89 TLWGCAYVDGRSARGCQOTNDAAEAALNASSKEEALQITREKIPERYLPOFHNLNSNI 148
 61 DPKTPEP 70
 DB 149 DPKTPEP 158

RESULT 9

ID P88975

ID P88975 PRELIMINARY: PRT: 149 AA.
 AC P88975; (1997) (TRENDEL: 03, Created)
 DT 01-MAY-1997 (TRENDEL: 03, Last sequence update)
 DT 01-MAY-1997 (TRENDEL: 03, Last sequence update)
 DT 01-MAY-2001 (TRENDEL: 03, Last sequence update)
 DE REPLICATION-ASSOCIATED PROTEIN (FRAGMENT).
 GN ACI.
 OS Macropitium golden mosaic geminivirus.
 OS Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
 OC NCBI_TaxID=51676;
 RN [1] SOURCE FROM N.A.
 RC STRAIN-JAMAICA.
 RA ROYE M.E.;
 RL Thesis (1996). Biochemistry. University of the West Indies, Jamaica.
 DR EMBL: U75278; AAB3619.1; -.
 DR InterPro: IPR001191; Gemin1_AL1.
 DR Pfam: PF00799; Gemin1_AL1; 1.
 DR PRINTS: PR00073; GEMCOAT1.
 DR PROSITE: PS00073; Gemin1_AL1; 1.
 FT NON_TER 1 149
 FT NON_TER 149 149
 SQ SEQUENCE 149 AA: 16785 MW: 64CF5EDD4C9CD508 CRC64:

Query Match 74.0%; Score 267; DB 12; Length 149;
 Best Local Similarity 70.0%; Pred. No. 1, 3e-21;
 Matches 49; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
 Oy 1 TTVGCAVAVGNSRAGCCGTGNDAAAEALNASSKEAALQIIRKIPKYLQPHNLNSN. 60
 Db 52 TTEGCFVQIDRSRAGCGGTGNDAAAEALNASSKEAALQIIRKIPKYLQPHNLNSN. 111
 Oy 61 DRIFDKTEP 70
 Db 112 DRIFDKTEP 121

RESULT 10
 ID 09YL44 PRELIMINARY: PRT: 233 AA.
 AC 09YL44; (1999) (TRENDEL: 10, Created)
 DT 01-MAY-1999 (TRENDEL: 10, Last sequence update)
 DT 01-MAY-1999 (TRENDEL: 10, Last sequence update)
 DT 01-JUN-2001 (TRENDEL: 17, Last annotation update)
 DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
 GN REP.
 OS Macropitium golden mosaic geminivirus.
 OS Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
 OC NCBI_TaxID=51676;
 RN [1] SOURCE FROM N.A.
 RC STRAIN-JAMAICA STRAIN 1;
 RA ROYE M.E.;
 RL "Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RC STRAIN-JAMAICA STRAIN 1;
 RN [1] SOURCE FROM N.A.
 RC STRAIN-JAMAICA STRAIN 1;
 RA ROYE M.E.; McLaughlin W.A.; Maxwell D.P.;
 RL "Molecular characterization of two distinct geminiviruses infecting M. lathyroides from Jamaica.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF009940; AAO17850.1; -.
 DR EMBL: AF009940; AAO17850.1; -.
 DR EMBL: AF009940; AAO17850.1; -.
 DR PRINTS: PR00073; GEMCOAT1.
 DR PROSITE: PS00073; Gemin1_AL1; 1.
 FT NON_TER 233 233
 SQ SEQUENCE 233 AA: 26355 MW: AAA90AFAD216A02 CRC64:

Query Match 74.0%; Score 267; DB 12; Length 233;
 Best Local Similarity 70.0%; Pred. No. 3, 2e-21;
 Matches 49; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
 Oy 1 TTVGCAVAVGNSRAGCCGTGNDAAAEALNASSKEAALQIIRKIPKYLQPHNLNSN. 60
 Db 110 TTEGCFVQIDRSRAGCGGTGNDAAAEALNASSKEAALQIIRKIPKYLQPHNLNSN. 169
 Oy 61 DRIFDKTEP 70
 Db 170 DRIFDKTEP 179

RESULT 11
 ID 039180 PRELIMINARY: PRT: 234 AA.
 AC 039180;
 DT 01-JAN-1998 (TRENDEL: 05, Created)
 DT 01-JAN-1998 (TRENDEL: 05, Last sequence update)
 DT 01-JAN-1998 (TRENDEL: 05, Last sequence update)
 DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
 OS Potato yellow mosaic virus.
 OS Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
 OC NCBI_TaxID=10827;
 RN [1] SOURCE FROM N.A.
 RC STRAIN-TOKYO STRAIN;
 RA KIMURA T.; KIMURA R.; Kimata D.; Portillo R.J.; Gilbertson R.L.;
 RL Plant Dis. 81:312-312(1997).
 DR EMBL: AF026553; AAB82605.1; -.
 DR InterPro: IPR001191; Gemin1_AL1.
 DR Pfam: PF00799; Gemin1_AL1; 1.
 DR PRINTS: PR00073; GEMCOAT1.
 DR PROSITE: PS00073; Gemin1_AL1; 1.
 FT NON_TER 234 234
 FT NON_TER 234 234
 SQ SEQUENCE 234 AA: 26486 MW: 9E08F0697105CD19 CRC64:

Query Match 72.3%; Score 261; DB 12; Length 234;
 Best Local Similarity 68.6%; Pred. No. 1, 4e-20;
 Matches 48; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 Oy 1 TTVGCAVAVGNSRAGCCGTGNDAAAEALNASSKEAALQIIRKIPKYLQPHNLNSN. 60
 Db 110 TTEGCFVQIDRSRAGCGGTGNDAAAEALNASSKEAALQIIRKIPKYLQPHNLNSN. 169
 Oy 61 DRIFDKTEP 70
 Db 170 DRIFDKTEP 179
 RESULT 12
 ID 09Z089 PRELIMINARY: PRT: 190 AA.
 AC 09Z089;
 DT 01-MAY-1999 (TRENDEL: 10, Created)
 DT 01-MAY-1999 (TRENDEL: 10, Last sequence update)
 DT 01-JUN-2001 (TRENDEL: 17, Last annotation update)
 DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
 GN C1.
 OS Tobacco leaf curl virus.
 OS Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
 OC NCBI_TaxID=67762;
 RN [1] SOURCE FROM N.A.
 RC STRAIN-TOKYO STRAIN;
 RA KIMURA T.; KIMURA R.; Kimata D.; Portillo R.J.; Gilbertson R.L.;
 RL Plant Res. 110:247-257(1997).
 DR EMBL: AB001315; BAA34033.1; -.
 DR InterPro: IPR001191; Gemin1_AL1.
 DR Pfam: PF00799; Gemin1_AL1; 1.

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DR PRINTS: PR00227; GEMCONFALL.
DR Prodom: PD000736; GEMINT.1.
FT NON-TER 1
FT NON-TER 1
SO SEQUENCE 190 AA; 21432 MW; AAC093D1D1610FAD CRC64;

OY 1 TLVGEAAVDGDSARCCGCONSDAAAPALMASSKEEALOTIREKIPKXYLFOFPHINLSNL 60
DB 95 TLKMGITQIDGSRHGGCCONNADACAPALNSKKEALATIRENLPKDFIYHINLSNL 144

OY 61 DRI-----FDKTPK 69
DB 145 DRIAPFLVFCVCFPAASSDPOVE 169

RESULT 13
OY0827 ID 092084 PRELIMINARY: PRT: 190 AA.
AC 092084;
DT 01-MAY-1999 (TREMBL) 10. (Created)
DY 01-MAY-1999 (TREMBL) 10. (Last sequence update)
DE 01-JUN-2001 (TREMBL) 17. (Last annotation update)
DE C1 AND C4 GENES, CLOVE YOKOHAMA-2, PARTIAL AND COMPLETE CDS (FRAGMENT).
DE
DE C1 tobacco leaf curl virus.
DE C1 viruses: ssRNA viruses; Gemintoviridae; Begomovirus.
DE C1 NCBI_ProtID=67762;
DE C1 [1]
DE C1 SEQUENCE FROM N.A.
DE C1 STRAIN-YOKOHAMA-2, Isoli T. Yahara T.;
DE C1 Molecular biology of geminiviruses infecting wild plants in Japan.
DE C1 J. Plant Res. 110:247-257(1997).
DE C1 EMBL: AA001318; BAA34039.1; -
DE C1 InterPro: IPR001191; Gemin_Atl.
DE C1 Pfam: PF00799; Gemin_Atl; 1.
DE C1 PRINTS: PR00227; GEMCONFALL.
DE C1 Prodom: PD000736; GEMINT.1.
DE C1 NON-TER 190 190
DE C1 FT NON-TER 190 190
DE C1 SEQUENCE 190 AA; 21444 MW; AAC1C2943E3F01AD CRC64;

Query Match
Best Local Similarity 71.5%; Score 258; DB 12; Length 190;
Matches 51; Conservative 8; Mismatches 10; Indels 16; Gaps 1
OY 1 TLVGEAAVDGDSARCCGCONSDAAAPALMASSKEEALOTIREKIPKXYLFOFPHINLSNL 60
DB 95 TLKMGITQIDGSRHGGCCONNADACAPALNSKKEALATIRENLPKDFIYHINLSNL 144

OY 61 DRI-----FDKTPK 69
DB 145 DRIAPFLVFCVCFPAASSDPOVE 169

RESULT 14
OY0827 ID 092084 PRELIMINARY: PRT: 190 AA.
AC 092084;
DT 01-MAY-1999 (TREMBL) 12. (Created)
DY 01-MAY-1999 (TREMBL) 11. (Last sequence update)
DE 01-JUN-2001 (TREMBL) 17. (Last annotation update)
DE C1 PROTEIN (FRAGMENT).
DE C1 tobacco leaf curl virus.
DE C1 viruses: ssDNA viruses; Gemintoviridae; Begomovirus.

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OX NCBI_TaxID=67762;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=CGR1.
RA Ooi K., Oshiba S., Ishii T., Yahara T.;
RT Nucleic Acids Res. 2004;32(25):7597-7601.
RI PubMed: 15034725(1997).
DR EMBL: AB001303; BAA34010.1; -
DR InterPro: IP000191; Gemini_Atl.
DR Pfam: PF00799; Gemini_Atl.1.
DR PRINTS: PR00227; GEMCONTALL.
DR ProDom: PD00736; Gemini_Atl.1.
DR NON-TER 199 1
FT MISC_FEATURES 199 1
FT SOURCE 190 AA; 21444 MW; 9303742ABEBD7EB CAC64;
SQ
Query Match 71.2% Score 257; DB 12; Length 190;
Best Local Similarity 60.0% Pred. No. 3.1e-20;
Matches 51; Conservative 6; Mismatches 10; Indels 16; Gaps 1;
Qy 1 TWMEBAAYDGSARGGCGSNDAAALMALNSKREGLQITREKIPDKYIPQFININSL 60
Db 85 ITLMTGTFVGVGSHSARGGCGQANDACABALNASKREGLSITREKIPDKYIPQFININSL 144
Qy 61 DRI-----FDKTPG 69
Db 145 DRIAPLEFLVFCPSNSFDPOVE 169
RESULT 15
ID 0920C4 PRELIMINARY; PRT: 208 AA.
AC 0920C4
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Annotation update)
DR NCBI AND CC GENES, CLONE AB00435.1, PARTIAL AND COMPLETE CDS (FRAGMENT).
GN C1
OS tobacco leaf curl virus.
OC Viruses; ssDNA viruses; Geminitoviridae; Begomovirus.
OX NCBI_TaxID=67762;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=AB0516.
RA Ooi K., Oshiba S., Ishii T., Yahara T.;
RT Molecular phylogeny of geminivirus infecting wild plants in Japan.
RI Plant Res. 110:247-257(1997).
DR EMBL: AB001294; BAA33952.1; -
DR InterPro: IP000191; Gemini_Atl.
DR Pfam: PF00799; Gemini_Atl.1.
DR PRINTS: PR00227; GEMCONTALL.
DR ProDom: PD00736; Gemini_Atl.1.
DR NON-TER 208 1
FT MISC_FEATURES 208 1
FT SOURCE 208 AA; 23526 MW; 249CC31DB8729C72D CRC64;
SQ
Query Match 71.2% Score 257; DB 12; Length 208;
Best Local Similarity 60.0% Pred. No. 3.4e-20;
Matches 51; Conservative 6; Mismatches 10; Indels 16; Gaps 1;
Qy 1 TWMEBAAYDGSARGGCGSNDAAALMALNSKREGLQITREKIPDKYIPQFININSL 60
Db 102 ITLMTGTFVGVGSHSARGGCGQANDACABALNASKREGLSITREKIPDKYIPQFININSL 161
Qy 61 DRI-----FDKTPG 69
Db 162 DRIAPLEFLVFCPSNSFDPOVE 186

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Fri Jan 4 09:39:52 2002

us-09-289-346a-8.rpt

Page 6

Job time: 1122 sec

Genome version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:38:51 Search time 65.28 seconds
(without alignments)
24.130 Million cell updates/sec

Title: US-09-289-346a-8

Sequence: 1 TLWGEAAVVGSRAGGCGCT.....PQTHN/NSLDRFDTRP 70

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Gapop 10.0, Cpept 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: Issued Patents, AA.*

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- 2: /cgm2.6/pctdata/2/1aa/5A_COMB.pep.*
- 3: /cgm2.6/pctdata/2/1aa/6A_COMB.pep.*
- 4: /cgm2.6/pctdata/2/1aa/6B_COMB.pep.*
- 5: /cgm2.6/pctdata/2/1aa/PTCUS_COMB.pep.*
- 6: /cgm2.6/pctdata/2/1aa/backfillseq1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	216	59.8	353	4	US-08-838-151A-44	Sequence 44, App
2	216	59.8	353	4	US-08-838-151A-46	Sequence 46, App
3	216	59.8	353	4	US-08-838-151A-49	Sequence 49, App
4	216	59.8	353	4	US-08-838-151A-52	Sequence 52, App
5	216	59.8	353	4	US-08-838-151A-55	Sequence 55, App
6	216	59.8	359	4	US-08-809-103B-6	Sequence 2, App
7	216	59.8	359	4	US-08-809-103B-6	Sequence 6, App
8	216	59.8	359	4	US-08-809-103B-6	Sequence 6, App
9	216	59.8	359	4	US-08-838-151A-4	Sequence 2, App
10	214	59.3	361	4	US-08-838-151A-4	Sequence 2, App
11	214	59.3	361	4	US-08-838-151A-6	Sequence 6, App
12	214	59.3	361	4	US-08-838-151A-6	Sequence 6, App
13	214	59.3	361	4	US-08-838-151A-6	Sequence 6, App
14	212	58.7	357	4	US-08-838-151A-27	Sequence 27, App
15	212	58.7	357	4	US-08-838-151A-30	Sequence 30, App
16	204	56.5	357	4	US-08-838-151A-20	Sequence 20, App
17	178	19.0	1713	3	US-08-600-982-24	Sequence 24, App
18	68.5	19.0	1713	3	PCR-US94-10251A-24	Sequence 24, App
19	63.5	17.6	2161	1	US-07-745-4206A-2	Sequence 2, App
20	63.5	17.6	2161	1	US-08-455-543A-49	Sequence 49, App
21	63.5	17.6	2161	1	US-08-223-105C-49	Sequence 49, App
22	63.5	17.6	2161	1	US-08-223-105C-51	Sequence 51, App
23	63.5	17.6	2161	2	US-08-111-663-2	Sequence 2, App
24	60	16.6	446	4	US-07-677-814D-11	Sequence 11, App
25	60	16.6	446	4	US-09-333-696-11	Sequence 11, App

28	58	16.1	171 2 US-08-609-049A-22	Sequence 22, Appl
29	58	16.1	171 4 US-09-170-996-22	Sequence 22, Appl
30	58	16.1	844 4 US-09-029-267-20	Sequence 20, Appl
31	57.2	15.9	6 229059-937-870-9	Patent No 9, 3520630
32	57.2	15.9	439 1 US-07-637-399-6	Sequence 6, Appl
33	57.5	15.9	439 1 US-08-113-703-6	Sequence 6, Appl
34	57.5	15.9	439 1 US-08-113-703-6	Sequence 6, Appl
35	57	15.8	165 4 US-08-995-369-4	Sequence 4, Appl
36	57	15.8	165 5 PCR-US95-10075-4	Sequence 4, Appl
37	56	15.5	454 3 US-08-466-100-31	Sequence 31, Appl
38	56	15.2	384 4 US-08-928-442-3	Sequence 3, Appl
39	54.5	15.1	497 2 US-08-576-311A-13	Sequence 2, Appl
40	54.5	15.1	497 2 US-08-576-311A-13	Sequence 2, Appl
41	54.5	15.1	497 2 US-08-353-486-2	Sequence 2, Appl
42	54.5	15.1	2628 2 US-08-570-311-14	Sequence 14, Appl
43	54	15.0	454 3 US-08-466-100-30	Sequence 30, Appl
44	54	15.0	602 2 US-08-419-652-6	Sequence 6, Appl
45	54	15.0	771 1 US-07-923-976-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-838-151A-44
Sequence 44, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION: John T
APPLICANT: John T
APPLICANT: John T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiViruses
NUMBER OF SEQUENCES: 63
SEQUENCE LENGTH: 70
ADDRESS: Rockey, Milinow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
AND/OR OTHER FORM: disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838, 151A
FILING DATE: 800
ATTORNEY/INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38, 978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INVENTOR: YOUNG, JAMES
SEQUENCE CHARACTERISTICS: 44:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-44
Query Match 59.8%; Score 216; DB 4; Length 353;
Best Local Similarity 58.6%; Pred. No. 3.9e+20;
Matches 41; Conservative 13; Mismatches 16; Indels 0;

Db 110 TTEMGOPOVDNSAGQGSANDSVAKALMADSIESTALTILKEOPDQVYLOHHNRSNL 169
 Oy 61 DRIFDKTPEP 70
 Db 170 ERITVYKPEP 179

RESULT 2

US-08-838-151A-46
 : Sequence 46, Application US/08838151A
 : Patent No. 6291743
 : GENERAL INFORMATION:
 : APPLICANT: Scout, John T
 : APPLICANT: Lou, Hang T
 : APPLICANT: Maxwell, Douglas
 : APPLICANT: Ahlquist, Paul
 : APPLICANT: Hanson, Steve
 : TITLE OF INVENTION: Transgenic Plants Expressing GeminiViruses
 : TITLE OF INVENTION: Genes
 : NUMBER OF SEQUENCES: 63
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Dressier, Rocky, Milnamow & Katz
 : STREET: Two Prudential Plaza, Suite 4700
 : CITY: Chicago
 : STATE: Illinois
 : COUNTRY: U.S.A.
 : ZIP: 60601
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentln Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : FILING DATE: 05/08/83B,151A
 : CLASSIFICATION: 800
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Mueller, Lisa V
 : REGISTRATION NUMBER: 38,978
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 312-616-5460
 : TELEFAX: 312-616-5460
 : INFORMATION FOR SEQ ID NO: 46:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 353 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-838-151A-46

Query Match 59.8%, Score 216; Db 4; Length 353;
 Best Local Similarity 58.6%, Pred. No. 3.9e-20;

Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

Oy 1 TLVWGEAVDNGSAGCOTSNDAAELPLAASSKEEAQLIRKTPKTLTQPRHNSUN 60
 Db 110 TTEMGOPOVDNSAGQGSANDSVAKALMADSIESTALTILKEOPDQVYLOHHNRSNL 169
 Oy 61 DRIFDKTPEP 70
 Db 170 ERITVYKPEP 179

RESULT 3

US-08-838-151A-49
 : Sequence 49, Application US/08838151A
 : Patent No. 6291743
 : GENERAL INFORMATION:
 : APPLICANT: Scout, John T
 : APPLICANT: Lou, Hang T

APPLICANT: Maxwell, Douglas
 APPLICANT: Ahlquist, Paul
 APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing GeminiViruses
 TITLE OF INVENTION: Genes
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressier, Rocky, Milnamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentln Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 05/08/83B,151A
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5460
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 353 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-838-151A-49

Query Match 59.8%, Score 216; Db 4; Length 353;
 Best Local Similarity 58.6%, Pred. No. 3.9e-20;

Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

Oy 1 TLVWGEAVDNGSAGCOTSNDAAELPLAASSKEEAQLIRKTPKTLTQPRHNSUN 60
 Db 110 TTEMGOPOVDNSAGQGSANDSVAKALMADSIESTALTILKEOPDQVYLOHHNRSNL 169
 Oy 61 DRIFDKTPEP 70
 Db 170 ERITVYKPEP 179

RESULT 4

US-08-838-151A-52
 : Sequence 52, Application US/08838151A
 : Patent No. 6291743
 : GENERAL INFORMATION:
 : APPLICANT: Scout, John T
 : APPLICANT: Lou, Hang T
 : APPLICANT: Maxwell, Douglas
 : APPLICANT: Ahlquist, Paul
 : APPLICANT: Hanson, Steve
 : TITLE OF INVENTION: Transgenic Plants Expressing GeminiViruses
 : TITLE OF INVENTION: Genes
 : NUMBER OF SEQUENCES: 63
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Dressier, Rocky, Milnamow & Katz
 : STREET: Two Prudential Plaza, Suite 4700
 : CITY: Chicago
 : STATE: Illinois
 : COUNTRY: U.S.A.
 : ZIP: 60601
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentln Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 05/08/83B,151A
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5460
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 353 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-83B-151A-52

Query Match 59.8%; Score 216; DB 4; Length 353;
 Best Local Similarity 58.6%; Pred. No. 3.9e-20;
 Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
 Oy 1 TLVGEANVDSAGGCGTSDNAAEALMASSEKALQITREKIPKYLQTHINLSN 60
 Db 110 TLVGEQVDSRAGGGSQNSYVAKMLADSTFALTLKREQPDVYVLOHNIRSN 169
 Oy 61 DRIFDKTPP 70
 Db 170 ERIIVKPEP 179

RESULT 5
 US-08-83B-151A-55
 Sequence 55, Application US/0883B151A
 Patent No. 6291743
 GENERAL INFORMATION:
 APPLICANT: Stout, John T
 APPLICANT: Liu, Hong T
 APPLICANT: Hanson, Douglas
 APPLICANT: Ahlquist, Paul
 APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing Geminitovirus
 TITLE OF INVENTION: Genes
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Rocky, Milwaukee & Katz
 ATTORNEY/AGENT INFORMATION:
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentln Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 05/08/83B,151A
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5460
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 55:

SEQUENCE CHARACTERISTICS:
 LENGTH: 353 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-83B-151A-55

Query Match 59.8%; Score 216; DB 4; Length 353;
 Best Local Similarity 58.6%; Pred. No. 3.9e-20;
 Matches 41; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
 Oy 1 TLVGEANVDSAGGCGTSDNAAEALMASSEKALQITREKIPKYLQTHINLSN 60
 Db 110 TLVGEQVDSRAGGGSQNSYVAKMLADSTFALTLKREQPDVYVLOHNIRSN 169
 Oy 61 DRIFDKTPP 70
 Db 170 ERIIVKPEP 179

RESULT 6
 US-08-809-103B-2
 Sequence 2, Application US/08809103B
 Patent No. 6133505
 GENERAL INFORMATION:
 APPLICANT: GONENBORN, Bruno
 TITLE OF INVENTION: PHOTOKINOGENIC DNA VIRUS RESISTANT
 TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: YOUNG & THOMPSON
 STREET: 745 South 23rd Street
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentln Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 08/809,103B
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 94,11040
 FILING DATE: 15-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: NO PCT/FR95/01192
 ATTORNEY/AGENT INFORMATION:
 NAME: PATCH, Andrew J
 REGISTRATION NUMBER: 32,925
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 521-2297
 TELEFAX: (703) 521-2573
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 359 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-809-103B-2

Query Match 59.8%; Score 216; DB 4; Length 359;
 Best Local Similarity 56.5%; Pred. No. 3.9e-20;
 Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

OY 2 LWMGAADVGRSGCGGCTNDAAAEALNNSKREALOTIREKIPERYLFOFHNLNSMD 61
 DB 111 LEMGTQIDGRSGCGGCTNDAAAEALNNSKREALOTIREKIPERYLFOFHNLNSMD 170
 OY 62 RIFKPTPEP 70
 DB 171 KVFQVPPAP 179

RESULT 7

US-08-809-103B-4
 Sequence 4, Application US/08809103B
 Sequence 8, Application US/08809103B
 GENERAL INFORMATION:
 APPLICANT: GROENBORN, Bruno
 TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 STREET: 745 South 23rd Street
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION NUMBER: US/08/809,103B
 APPLICATION NUMBER: US/08/809,103B
 FILING DATE: 17-MAR-1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 94,11040
 PRIORITY DATE: 15-SEP-1995
 APPLICATION NUMBER: WO PCT/FR95/01192
 FILING DATE: 15-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: PATCH, Andrew J.
 REGISTRATION NUMBER: 32,925
 TELEPHONE: (703) 521-2297
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 521-2297
 TELEFAX: (703) 685-0573
 TELEFAX: 248425 EMBON
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 359 amino acids
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-809-103B-4

Query Match 59.8%; Score 216; DB 4; Length 359;
 Best Local Similarity 56.5%; Pred. No. 3.9e-20;
 Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;
 OY 2 LWMGAADVGRSGCGGCTNDAAAEALNNSKREALOTIREKIPERYLFOFHNLNSMD 61
 DB 111 LEMGTQIDGRSGCGGCTNDAAAEALNNSKREALOTIREKIPERYLFOFHNLNSMD 170
 OY 62 RIFKPTPEP 70
 DB 171 KVFQVPPAP 179

RESULT 8
 US-08-809-103B-6
 Sequence 6, Application US/08809103B

Patent No. 6133505
 GENERAL INFORMATION:
 APPLICANT: GROENBORN, Bruno
 TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESS: YOUNG & THOMPSON
 STREET: 745 South 23rd Street
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION NUMBER: US/08/809,103B
 APPLICATION NUMBER: US/08/809,103B
 FILING DATE: 15-SEP-1994
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 94,11040
 FILING DATE: 15-SEP-1994
 APPLICATION NUMBER: WO PCT/FR95/01192
 FILING DATE: 15-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: PATCH, Andrew J.
 REGISTRATION NUMBER: 32,925
 TELEPHONE: (703) 521-2297
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 521-2297
 TELEFAX: (703) 685-0573
 TELEFAX: 248425 EMBON
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 359 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-809-103B-6

Query Match 59.8%; Score 216; DB 4; Length 359;
 Best Local Similarity 56.5%; Pred. No. 3.9e-20;
 Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;
 OY 2 LWMGAADVGRSGCGGCTNDAAAEALNNSKREALOTIREKIPERYLFOFHNLNSMD 61
 DB 111 LEMGTQIDGRSGCGGCTNDAAAEALNNSKREALOTIREKIPERYLFOFHNLNSMD 170
 OY 62 RIFKPTPEP 70
 DB 171 KVFQVPPAP 179

RESULT 9
 US-08-809-103B-8
 Sequence 8, Application US/08809103B
 Patent No. 6133505
 GENERAL INFORMATION:
 APPLICANT: GROENBORN, Bruno
 TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESS: YOUNG & THOMPSON
 STREET: 745 South 23rd Street
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.

ADDRESS: Dressler, Rocky, Milnamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838,151A
 PRIORITY NUMBER:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5460
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 357 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-838-151A-24

Query Match 58.7%: Score 212; DB 4; Length 357;

Best Local Similarity 65.6%; Pred. No. 1.3e-19;
 Matches 40; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 4 MGEAVDGRSANGCGQTSNDAAEALNASSKREALOITREKIPKYLDPFHNSNDRI 63
 DB 111 FVSQIDRSNAGQSANADYVNALNSGSKSEALNITKKXPNKYILOPHNSNDRI 170

QY 64 F 64

DB 171 F 171

RESUME 15
 US-08-838-151A-27
 Sequence 27, Application US/08838151A
 Patent No. 6291743
 GENERAL INFORMATION:
 APPLICANT: Stout, John T
 APPLICANT: Luu, Hang T
 APPLICANT: Maxwell, Douglas
 APPLICANT: Miquel, Paul
 APPLICANT: Rando, Ryan
 TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838,151A
 PILING DATE:
 CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5460
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 357 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-838-151A-27

Query Match 58.7%: Score 212; DB 4; Length 357;

Best Local Similarity 65.6%; Pred. No. 1.3e-19;
 Matches 40; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 4 MGEAVDGRSANGCGQTSNDAAEALNASSKREALOITREKIPKYLDPFHNSNDRI 63
 DB 111 FVSQIDRSNAGQSANADYVNALNSGSKSEALNITKKXPNKYILOPHNSNDRI 170

QY 64 F 64

DB 171 F 171

Search completed: January 3, 2002, 15:38:51
 Job time: 228 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:37:38 ; Search time 144.17 Seconds

(without alignments) 35.965 Million cell updates/sec

Title: US-09-289-346a-9

Sequence: 1 TLWMGEFQVAGNRSGCCQT.....FQFHMSNLDIRLTKTPR 70

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 7407290 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database:

A_Genecol_1101.*

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2: /SIDSB/gcgdata/geneseq/geneseqp/AA1191.DAT.*
3: /SIDSB/gcgdata/geneseq/geneseqp/AA1192.DAT.*
4: /SIDSB/gcgdata/geneseq/geneseqp/AA1193.DAT.*
5: /SIDSB/gcgdata/geneseq/geneseqp/AA1194.DAT.*
6: /SIDSB/gcgdata/geneseq/geneseqp/AA1195.DAT.*
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9: /SIDSB/gcgdata/geneseq/geneseqp/AA1198.DAT.*
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21: /SIDSB/gcgdata/geneseq/geneseqp/AA2001.DAT.*
22: /SIDSB/gcgdata/geneseq/geneseqp/AA2001.DAT.*

prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

Result Query SUMMARIES

NO	Score	Match	Length	DB	ID	Description
1	362	100.0	70	21	AA116685	Mutant peptide der
2	356	98.3	70	21	AA116677	Peptide fragment f
3	356	98.3	356	21	AA116687	Amino acid sequenc
4	345	95.3	70	21	AA116688	Mutant peptide der
5	344	95.0	70	21	AA116692	Mutant peptide der
6	344	94.5	70	21	AA116694	Mutant peptide der
7	342	94.5	70	21	AA116690	Mutant peptide der
8	341	94.2	70	21	AA116678	Mutant peptide der
9	341	94.2	70	21	AA116686	Mutant peptide der
10	340	93.9	70	21	AA116689	Mutant peptide der
11	338	93.4	70	21	AA116680	Mutant peptide der

12	338	93.4	70	21	AA116691	Mutant peptide der
13	335	92.5	70	21	AA116681	Mutant peptide der
14	334	92.3	70	21	AA116683	Mutant peptide der
15	332	91.7	70	21	AA116682	Mutant peptide der
16	324	89.5	70	21	AA116679	Mutant peptide der
17	323	89.3	353	18	AAW34336	Beau golden mosaic
18	323	89.3	353	18	AAW34337	Beau golden mosaic
19	322	89.3	353	18	AAW34338	Beau golden mosaic
20	322	89.3	353	18	AAW34339	Beau golden mosaic
21	322	89.3	353	18	AAW34340	Beau golden mosaic
22	322	89.3	353	18	AAW34341	Beau golden mosaic
23	322	89.3	353	18	AAW34342	Beau golden mosaic
24	322	89.3	353	18	AAW34343	Beau golden mosaic
25	322	89.3	353	18	AAW34344	Beau golden mosaic
26	322	89.3	353	18	AAW34345	Beau golden mosaic
27	322	89.3	353	18	AAW34346	Beau golden mosaic
28	322	89.3	353	18	AAW34347	Beau golden mosaic
29	322	89.3	353	18	AAW34348	Beau golden mosaic
30	322	89.3	353	18	AAW34349	Beau golden mosaic
31	322	89.3	353	18	AAW34350	Beau golden mosaic
32	322	89.3	353	18	AAW34351	Beau golden mosaic
33	322	89.3	353	18	AAW34352	Beau golden mosaic
34	322	89.3	353	18	AAW34353	Beau golden mosaic
35	322	89.3	353	18	AAW34354	Beau golden mosaic
36	322	89.3	353	18	AAW34355	Beau golden mosaic
37	322	89.3	353	18	AAW34356	Beau golden mosaic
38	322	89.3	353	18	AAW34357	Beau golden mosaic
39	322	89.3	353	18	AAW34358	Beau golden mosaic
40	322	89.3	353	18	AAW34359	Beau golden mosaic
41	322	89.3	353	18	AAW34360	Beau golden mosaic
42	322	89.3	353	18	AAW34361	Beau golden mosaic
43	322	89.3	353	18	AAW34362	Beau golden mosaic
44	322	89.3	353	18	AAW34363	Beau golden mosaic
45	322	89.3	353	18	AAW34364	Beau golden mosaic

ALIGNMENTS

RESULT 1	AA116685	standard; peptide: 70 AA.
ID	AA116685	
XX	AA116685:	
XX	22-JAN-2001 (first entry)	
DE	Mutant peptide derived from amino acids 110-179 of Rep (Alt) protein.	
KW	Geminivirus; replication protein; Rep protein; Alt; Transgenic Plant;	
KM	ribosome binding region; resistance; geminivirus infection.	
XX	Synthetic.	
OS	Tomato golden mosaic virus.	
XX	Tomato golden mosaic virus.	
XX	Key	Location/Qualifiers
FT	Misc-difference 10	/note="wild type residue replaced with Ala"
XX	W0200054573-AL.	
XX	21-SEP-2000.	
XX	15-MAR-2000; 2000MO-US06759.	
XX	18-MAR-1999; 99US-0125004.	
XX	09-APR-1999; 99US-0289346.	
XX	(GYN-) UNIV NORTH CAROLINA STATE.	
XX	Hanley-Bowdoin L, Orozco BM, Koo L;	
XX	WPI: 2000-618851/59.	

```

XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant A11 protein with a mutation in the Rb binding region
XX
XX
PS Claim 53: Page 46: 73pp: English.
XX
CC The present sequence represents a mutant peptide, derived from a
CC geminivirus replication (Rep) protein, also known as A11. A11 binds
CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
CC DNA, and is involved in the replication of the geminivirus. A11 is
CC present in a ribosome binding region, and expression of mutant A11 is
CC protein imparts increased resistance to geminivirus infection in the
CC plant. Mutant A11 proteins are useful for producing plants having
CC increased resistance or reduced sensitivity to a geminivirus such as
CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC virus, bean dwarf mosaic virus, bean golden mosaic virus, Texas
CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC virus, cotton leaf curl virus or beet curly top virus.
XX
SQ Sequence 70 AA:
XX
Query Match 100.0% Score 362: DB 21: Length 70:
Best Local Similarity 100.0%: Pred. No. 3.1e-30:
Matches 70: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
OY 1 TLVGEFVAGRSARAGCCTSNDAAEALNASSKEPALQITREKIPKYLEFOFHNLNSNL 60
DB 1 TLVGEITGVGRTSARIGYCTINDAAAEALNASSKEPALQITREKIPKYLEFHNLNSNL 60
OY 61 DHIPDKTRPEP 70
DB 61 dHIdKtRpep 70
XX
RESULT 2
AAB18677
ID AAB18677 standard: peptide: 70 AA.
AC AAB18677:
XX
XX 22-JAN-2001 (first entry)
XX
DB Peptide fragment from Rep protein of TGMV (amino acids 110-179).
XX
XX Geminivirus: replication protein: Rep protein: A11; transgenic plant:
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Tomato golden mosaic virus.
XX
XX WC200054573-A1.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000: 2000MO-US06759.
XX
XX 18-MAR-1999: 990US-0125004.
XX
XX 09-APR-1999: 990US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX
XX WPI: 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant A11 protein with a mutation in the Rb binding region

```

```

XX
XX Disclosure: Page 18: 73pp: English.
XX
CC The present sequence is derived from a geminivirus replication (Rep)
CC protein, also known as A11. A11 binds double-stranded DNA and
CC catalyzes cleavage and ligation of single-stranded DNA and interacts
CC with other viral and host proteins. Mutants of the A11 protein are used
CC to produce transgenic plants. The mutation in A11 is present in a
CC ribosome binding region, and expression of mutant A11 protein imparts
CC increased resistance to geminivirus infection in the plant. Mutant A11
CC proteins are useful for producing plants having increased resistance or
CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
CC tomato mottle virus, tomato yellow leaf curl virus, African cassava
CC virus, African cassava mosaic virus, Indian cassava mosaic virus, potato
CC yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus,
CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
CC beet curly top virus.
XX
SQ Sequence 70 AA:
XX
Query Match 98.3% Score 356: DB 21: Length 70:
Best Local Similarity 98.6%: Pred. No. 3.1e-37:
Matches 69: Conservative 0: Mismatches 1: Indels 0: Gaps 0:
OY 1 TLVGEFVAGRSARAGCCTSNDAAEALNASSKEPALQITREKIPKYLEFOFHNLNSNL 60
DB 1 TLVGEITGVGRTSARIGYCTINDAAAEALNASSKEPALQITREKIPKYLEFHNLNSNL 60
OY 61 DHIPDKTRPEP 70
DB 61 dHIdKtRpep 70
XX
RESULT 3
AAB18687
ID AAB18687 standard: peptide: 356 AA.
AC AAB18687:
XX
XX 22-JAN-2001 (first entry)
XX
XX Amino acid sequence of a geminivirus replication protein of TGMV.
XX
XX Geminivirus: replication protein: Rep protein: A11; transgenic plant:
XX ribosome binding region; resistance; geminivirus infection.
XX
XX Tomato golden mosaic virus.
XX
XX Key location/qualifiers
XX Misc-difference /note= "unspecified amino acid"
XX
XX WC200054573-A1.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000: 2000MO-US06759.
XX
XX 18-MAR-1999: 990US-0125004.
XX
XX 09-APR-1999: 990US-0289346.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong L;
XX
XX WPI: 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
PT comprise a nucleic acid construct containing a nucleic acid sequence
PT encoding a mutant A11 protein with a mutation in the Rb binding region

```

PS Disclosure: Page 47-48: 73pp: English.

XX The present sequence represents a geminivirus replication (Rep)
 CC protein, which is also known as AL1. AL1 binds double-stranded DNA,
 CC catalyzes cleavage and ligation of single-stranded DNA, and interacts
 CC with the host cell's replication machinery. The mutation in AL1 is used
 CC to produce transgenic plants. The mutation in AL1 is present in a
 CC ribosome binding region, and expression of mutant AL1 protein imparts
 CC increased resistance to geminivirus infection in the plant. Mutant AL1
 CC proteins are useful for producing plants having increased resistance or
 CC reduced sensitivity to a geminivirus such as tomato golden mosaic virus,
 CC tomato mottle virus, tomato yellow leaf curl virus, tomato leaf curl
 CC virus, African cassava mosaic virus, indian cassava mosaic virus, potato
 CC yellow mosaic virus, squash leaf curl virus, bean golden mosaic virus,
 CC squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or
 CC beet curly top virus.

XX Sequence 356 AA:

Query Match 98.3%: Score 356; DB 21; Length 356;
 Best Local Similarity 98.6%: Pred. No. 2.4e-36;
 Matches 69; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TLVGEFVAGRSARGCCTSDAALANSSKEBALQITREKIPKYLEPQFNHLSML 60
 DB 110 TLVGEFVAGRSARGCCTSDAALANSSKEBALQITREKIPKYLEPQFNHLSML 169
 OY 61 DRIEDKTPPEP 70
 DB 170 dRIEdKtPeP 179
 |||||

Db 170 dRIEdKtPeP 179

Db 61 dRIEdKtPeP 70

RESULT 4
 AAB18688 standard; peptide; 70 AA.

XX AAB18688;

DT 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;

XX ribosome binding region; resistance; geminivirus infection.

OS Synthetic.

XX Tomato golden mosaic virus.

XX Key Location/Qualifiers

FT Misc-difference 19 /note="wild type residue replaced with Ala"

FT Misc-difference 69 /note="wild type residue replaced with Ala"

PN MO200054573-AL1.

PD 21-SEP-2000.

XX 15-MAR-2000; 2000OMO-US06759.

PR 18-MAR-1999; 990US-0125004.

PR 09-APR-1999; 990US-0289346.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

PT Transgenic plants with increased resistance to geminivirus infection

PS Disclosure: Page 48: 73pp: English.

XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication protein, as of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, African cassava mosaic virus, indian cassava mosaic virus,
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA:

Query Match 95.3%: Score 345; DB 21; Length 70;
 Best Local Similarity 95.7%: Pred. No. 7.5e-36;
 Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TLVGEFVAGRSARGCCTSDAALANSSKEBALQITREKIPKYLEPQFNHLSML 60
 DB 1 TLVGEFVAGRSARGCCTSDAALANSSKEBALQITREKIPKYLEPQFNHLSML 60
 OY 61 DRIEDKTPPEP 70
 DB 61 dRIEdKtPeP 70
 |||||

Db 61 dRIEdKtPeP 70

RESULT 5
 AAB18692 standard; peptide; 70 AA.

XX AAB18692;

DT 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

XX Geminivirus; replication protein; Rep protein; AL1; transgenic plant;

XX ribosome binding region; resistance; geminivirus infection.

OS Synthetic.

XX Tomato golden mosaic virus.

XX Key Location/Qualifiers

FT Misc-difference 69 /note="wild type residue replaced with Ala"

FT Misc-difference 69 /note="wild type residue replaced with Ala"

PN MO200054573-AL1.

PD 21-SEP-2000.

XX 15-MAR-2000; 2000OMO-US06759.

PR 18-MAR-1999; 990US-0125004.

PR 09-APR-1999; 990US-0289346.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

PT Transgenic plants with increased resistance to geminivirus infection

XX DR WPI: 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection

XX complete a nucleic acid construct containing a nucleic acid sequence

XX encoding a mutant A11 protein with a mutation in the Rb binding region

XX PS Disclosure: Page 49; 73pp: English.

XX The present sequence represents a mutant peptide, derived from a

XX geminivirus replication (Rep) protein, also known as A11. A11 binds

XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded

XX DNA, and interacts with other viral and host proteins. Mutants of the A11

XX present in a ribosome binding region, and expression of mutant A11 is

XX protein impacts increased resistance to geminivirus infection in the.

XX plant. Mutant A11 proteins are useful for producing plants having

XX increased resistance or reduced sensitivity to a geminivirus such as

XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl

XX virus, bean dwarf mosaic virus, African cassava mosaic virus, Indian

XX cassava mosaic virus, squash leaf curl virus, Texas pepper

XX virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA:

SO

Query Match 94.5%: Score 342; DB 21; Length 70;

Best Local Similarity 95.7%: Pred. No. 1, 8e-35;

Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TLVGEFQVAGRSARGCCTSNDAAEALNASSKEEAQLITREKTPKTYLQFHNINSNL 60

DB 1 TLVGEFQVdgraragcqtlnsdanaaalaasskeeaqlitrekipekyltqfhnlnsl 60

OY 61 drrpdkrpep 70

DB 61 drrltdkrpep 70

RESULT 8

AA18678 standard: peptide: 70 AA.

AC AA18678:

XX 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.

XX Geminivirus: replication protein; Rep protein; A11; Transgenic plant;

XX ribosome binding region; resistance; geminivirus infection.

OS Synthetic.

XX Tomato golden mosaic virus.

XX Key Location/Qualifiers

FT Misc-difference 12 /note= "wild type residue replaced with Ala"

FT Misc-difference 13 /note= "wild type residue replaced with Ala"

FT Misc-difference 15 /note= "wild type residue replaced with Ala"

FT Misc-difference 26 /note= "wild type residue replaced with Leu"

XX MO200054573-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000MO-US05759.

XX 18-MAR-1999; 9905-0125004.

XX 09-APR-1999; 9905-0289346.

XX (UNCL-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI: 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection

XX complete a nucleic acid construct containing a nucleic acid sequence

XX encoding a mutant A11 protein with a mutation in the Rb binding region

XX PS Claim 53; Page 42-43; 73pp: English.

XX The present sequence represents a mutant peptide, derived from a

XX geminivirus replication (Rep) protein, also known as A11. A11 binds

XX double-stranded DNA, catalyzes cleavage and ligation of single-stranded

XX DNA, and interacts with other viral and host proteins. Mutants of the A11

XX present in a ribosome binding region, and expression of mutant A11 is

XX protein impacts increased resistance to geminivirus infection in the

XX plant. Mutant A11 proteins are useful for producing plants having

XX increased resistance or reduced sensitivity to a geminivirus such as

XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl

XX virus, bean dwarf mosaic virus, African cassava mosaic virus, Indian

XX cassava mosaic virus, squash leaf curl virus, Texas pepper

XX virus, cotton leaf curl virus or beet curly top virus.

XX Sequence 70 AA:

SO

Query Match 94.2%: Score 341; DB 21; Length 70;

Best Local Similarity 94.3%: Pred. No. 2, 4e-35;

Matches 66; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 TLVGEFQVAGRSARGCCTSNDAAEALNASSKEEAQLITREKTPKTYLQFHNINSNL 60

DB 1 TLVGEFQVdgraaagcqtlnsdanaaalaasskeeaqlitrekipekyltqfhnlnsl 60

OY 61 drrpdkrpep 70

DB 61 drrltdkrpep 70

RESULT 9

AA18686 standard: peptide: 70 AA.

AC AA18686:

XX 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.

XX Geminivirus: replication protein; Rep protein; A11; Transgenic plant;

XX ribosome binding region; resistance; geminivirus infection.

OS Synthetic.

XX Tomato golden mosaic virus.

XX Key Location/Qualifiers

FT Misc-difference 24 /note= "wild type residue replaced with Leu"

FT Misc-difference 25 /note= "wild type residue replaced with Leu"

FT Misc-difference 26 /note= "wild type residue replaced with Leu"

XX MO200054573-A1.

XX 21-SEP-2000.

PF 15-MAR-2000: 2000MO-US06759.
 XX 18-MAR-1999: 99US-0125004.
 PR 09-APR-1999: 99US-0289346.
 XX (UNNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 PI WPI: 2000-618851/59.
 DR Transgenic plants with increased resistance to geminivirus infection
 XX encoding a nucleic acid construct containing a nucleic acid sequence
 PT comprising a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 PS Claim 53: Page 46; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance to geminivirus infection, such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX Sequence 70 AA:
 SQ

Query Match 94.28; Score 341; DB 21: Length 70;
 Best Local Similarity 94.3%; Pred. No. 2,4e-35;

Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TLVNGEYVACRGAGCCGTSTNMAALEALNASSKEEAQITIREKIPKYLPOFHNLNSNI 60
 Db 1 TLVNGEYVACRGAGCCGTSTNMAALEALNASSKEEAQITIREKIPKYLPOFHNLNSNI 60
 OY 61 DRIFDKTEP 70
 Db 61 drifdktep 70

RESULT 10
 AABI8689 ID AABI8689 standard; peptide: 70 AA.

XX AABI8689:
 AC
 XX 22-JAN-2001 (first entry)
 DT
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 KM Geminivirus: replication protein; Rep protein; AL1; transgenic plant;
 KM ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 OS Tomato golden mosaic virus.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 22 /note= "wild type residue replaced with Ala"
 FT Misc-difference 23 /note= "wild type residue replaced with Ala"
 FT
 FT Misc-difference 23 /note= "wild type residue replaced with Ala"
 FT
 XX W0200054573-AL.

XX 21-SEP-2000.
 XX 15-MAR-2000: 2000MO-US06759.
 XX 18-MAR-1999: 99US-0125004.
 PR 09-APR-1999: 99US-0289346.
 XX (UNNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 PI WPI: 2000-618851/59.
 DR Transgenic plants with increased resistance to geminivirus infection
 XX encoding a nucleic acid construct containing a nucleic acid sequence
 PT comprising a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 XX
 PS Disclosure: Page 48-49; 73pp; English.
 XX
 CC The present sequence represents a mutant peptide, derived from a
 CC double-stranded DNA, catalyses cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance to geminivirus infection, such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX Sequence 70 AA:
 SQ

Query Match 93.9%; Score 340; DB 21: Length 70;
 Best Local Similarity 95.7%; Pred. No. 3,2e-35;

Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TLVNGEYVACRGAGCCGTSTNMAALEALNASSKEEAQITIREKIPKYLPOFHNLNSNI 60
 Db 1 TLVNGEYVACRGAGCCGTSTNMAALEALNASSKEEAQITIREKIPKYLPOFHNLNSNI 60
 OY 61 DRIFDKTEP 70
 Db 61 drifdktep 70

RESULT 11
 AABI8680 ID AABI8680 standard; peptide: 70 AA.

XX AABI8680:
 AC
 XX 22-JAN-2001 (first entry)
 DT
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 KM Geminivirus: replication protein; Rep protein; AL1; transgenic plant;
 KM ribosome binding region; resistance; geminivirus infection.
 XX
 XX Synthetic.
 OS Tomato golden mosaic virus.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 42 /note= "wild type residue replaced with Ala"
 FT Misc-difference 43 /note= "wild type residue replaced with Ala"
 FT
 FT Misc-difference 44 /note= "wild type residue replaced with Ala"
 FT

FT /note= "wild type residue replaced with Ala"
 PN W0200054573-AL.
 XX 21-SEP-2000.
 PD 15-MAR-2000; 2000MO-US06759.
 PR 18-MAR-1999; 99US-0125004.
 XX 09-APR-1999; 99US-0289346.
 PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI: 2000-618851/59.
 DR Transgenic plants with increased resistance to geminivirus infection
 PT compile a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT
 PS
 XX
 PS Claim 52; Page 43-44; 73pp; English.
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants with increased resistance to
 CC present in a ribosome binding region. The mutation in AL1 is
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomatillo golden mosaic virus, tomatillo mottle virus, tomatillo leaf curl
 CC virus, tomatillo leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, tomatillo leaf curl virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 CC
 XX
 SQ Sequence 70 AA:
 Query Match 93.4%; Score 338; DB 21; Length 70;
 Best Local Similarity 94.3%; Pred. No. 5.6e-35;
 Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 TLWGEFVNGSRAGCGCTSNDAALAAALMASSKEEALQIREKIPERYLPORHMLNSM 60
 Db 1 TLVGEFVNGSRAGCGCTSNDAALAAALMASSKEEALQIREKIPERYLPORHMLNSM 60
 OY 61 DRIFDKTEP 70
 Db 61 drifdktep 70
 RESULT 12
 ID AAB18691 standard; peptide; 70 AA.
 AC AAB18691.
 XX 22-JAN-2001 (first entry)
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KM ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.
 OS Tomato golden mosaic virus.
 XX Key Location/Qualifiers
 FH Misc-difference 34

FT /note= "wild type residue replaced with Ala"
 PN Misc-difference 35
 FT /note= "wild type residue replaced with Ala"
 FT Misc-difference 36
 FT /note= "wild type residue replaced with Ala"
 PN W0200054573-AL.
 XX 21-SEP-2000.
 PD 15-MAR-2000; 2000MO-US06759.
 PR 18-MAR-1999; 99US-0125004.
 XX 09-APR-1999; 99US-0289346.
 PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX Hanley-Bowdoin L, Orozco BM, Kong L;
 XX WPI: 2000-618851/59.
 DR Transgenic plants with increased resistance to geminivirus infection
 PT compile a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PT
 PS
 XX
 PS Disclosure; Page 49; 73pp; English.
 CC The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to a geminivirus such as
 CC tomatillo golden mosaic virus, tomatillo mottle virus, tomatillo leaf curl
 CC virus, tomatillo leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, tomatillo leaf curl virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 CC
 XX
 SQ Sequence 70 AA:
 Query Match 93.4%; Score 338; DB 21; Length 70;
 Best Local Similarity 94.3%; Pred. No. 5.6e-35;
 Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 TLWGEFVNGSRAGCGCTSNDAALAAALMASSKEEALQIREKIPERYLPORHMLNSM 60
 Db 1 TLVGEFVNGSRAGCGCTSNDAALAAALMASSKEEALQIREKIPERYLPORHMLNSM 60
 OY 61 DRIFDKTEP 70
 Db 61 drifdktep 70
 RESULT 13
 ID AAB18681 standard; peptide; 70 AA.
 AC AAB18681.
 XX 22-JAN-2001 (first entry)
 XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
 DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
 KM ribosome binding region; resistance; geminivirus infection.
 XX Synthetic.

DT 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

DE Geminivirus; replication protein; Rep protein; AL1; transgenic plant;

KW ribosome binding region; resistance; geminivirus infection.

XX Synthetic.

OS Tomato golden mosaic virus.

XX Key Location/Qualifiers

FT Misc-difference 52 /note= "wild type residue replaced with Ala"

FT Misc-difference 54 /note= "wild type residue replaced with Ala"

FT Misc-difference 55 /note= "wild type residue replaced with Ala"

XX MO200054573-AL.

XX 21-SEP-2000.

XX 15-MAR-2000: 2000MO-US06759.

XX 18-MAR-1999: 9905-0125004.

PR 09-APR-1999: 9905-0289346.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L. Orozco BM, Kong L;

DR WPI: 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 PT encoding a mutant AL1 protein with a mutation in the Rb binding region
 PS

XX Claim 53: Page 44-45: 73pp: English.

XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (rep) protein, also known as AL1. AL1 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and is involved in the replication of the geminivirus. The AL1
 CC protein are used to produce transgenic plants. The mutation in AL1 is
 CC present in a ribosome binding region, and expression of mutant AL1
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant AL1 proteins are useful for producing plants having
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, cassava brown streak virus, golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas popper
 CC virus, cotton leaf curl virus or beet curly top virus.
 XX

SQ Sequence 70 AA:

Query Match 91 74: Score 332, DB 21: Length 70;
 Best Local Similarity 94 38: Percent 73, 28-34;
 Matches 66: Conservative 0: Mismatches 4: Indels 0: Gaps 0;

OY 1 TLWGEFVVGSRAGCGGTNDAAEAALNLSKEBALQIREKIPKYLFOFHNTNSNL 60
 Db 1 LTVGGEIVGYSRGCGTNDAAEAALNLSKEBALQIREKIPKYLFOFHNTNSNL 60

OY 61 DRIFDKRPP 70
 Db 61 DRIFDKRPP 70

Search completed: January 3, 2002, 15:37:38

Job time: 155 sec

GenCode version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:40:11 ; Search time 72.79 Seconds

(Without alignments)
73.255 Million cell updates/sec

Title: US-09-289-346a-9

Sequence: 1 TIVMGEFQVAGKSNAGCCCT.....FQFHLNLSNLDRTDTEP 70

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq Length: 0

Maximum DB seq Length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Print No. is the number of results predicted by chance to have a score greater than or equal to the score of the best hit, as printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	356	98.3	352	1	QOCVU1
2	256	70.7	361	1	QOCVPT
3	243	67.1	358	2	S07594
4	236	65.2	362	1	J01887
5	229	63.3	359	2	S39211
6	225	62.2	349	2	J02300
7	223	62.2	349	2	S31875
8	215	60.5	353	2	S02327
9	212	60.5	355	2	S02327
10	219	60.5	355	1	QOCVW1
11	216	59.7	358	1	J01670
12	216	59.7	359	2	S39235
13	216	59.7	385	2	S28360
14	209	57.7	360	2	S59885
15	207	57.2	357	1	QOCVU1
16	207	57.2	357	1	QOCVU1
17	182	54.7	347	1	QOCVU1
18	182	54.7	347	1	QOCVU1
19	67	18.5	840	2	T31675
20	64.5	17.8	299	2	B71967
21	62.5	17.3	447	2	T12544
22	62.5	17.1	285	2	D14552
23	61.3	17.0	281	2	A51380
24	61.3	17.0	281	2	A51380
25	61.3	16.9	1502	1	RGVH1
26	60.5	16.7	1713	2	A55347
27	60.5	16.7	2137	2	A55347
28	60	16.6	160	2	G82060
29	60	16.6	447	2	S52437

30	60	16.6	988	2	P86316	protein T10022.13
31	59	16.3	397	2	B71078	probable NADH oxid
32	59	16.3	416	2	A82892	hypothetical prote
33	59	16.3	862	2	H82182	conserved hypothet
34	59	16.3	1287	2	S55954	viral mRNA transla
35	59	16.3	1341	2	S55954	translational prote
36	58	16.2	1400	2	S00063	hypothetical prote
37	58.5	16.2	230	2	S46332	homocytic protein G
38	58.5	16.2	297	1	MMVNRV	nonstructural prot
39	58.5	16.2	289	2	G64541	cell binding facto
40	58.5	16.2	589	2	D64125	hypothetical prote
41	58.5	16.2	1044	2	T33800	protein kinase sub
42	58.5	16.2	1285	2	T47625	structural main ten
43	58.5	16.2	1285	2	T47625	hypothetical prote
44	58	16.0	256	2	S79324	hypothetical prote
45	58	16.0	488	2	B84197	antiribulate synth

ALIGNMENTS

```

RESULT 1
QOCVU1
All protein - tomato golden mosaic virus
C:Species: tomato golden mosaic virus
A:Note: host: Nicotiana sp. (tobacco)
C:Date: 28-Aug-1985 #sequence-revision 28-Aug-1985 #taxL-change 08-Apr-1994
C:Accession: A04170
EMBL: 12197-2205
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of toma
A:Reference number: A04163
A:Molecule type: DNA
A:Accession: A04170
A:Residues: 1-352 <RAN>
C:Comments: The genome consists of two circular, single-stranded DNA components, DNA A
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus All protein

Query Match      98.3% Score 356; DB 1; Length 352;
Best Local Similarity 98.6% ; Pred. No. 2,1e-32;
Matches 69; Conservative 1; Indels 0; Gaps 0;

Ox 1
|||||
111 TIVMGEFQVAGKSNAGCCCTSNMAAENASKEBAKQIITEKIPKYLQFHLNLSN 60
Db 111 TIVMGEFQVAGKSNAGCCCTSNMAAENASKEBAKQIITEKIPKYLQFHLNLSN 170
Ox 61 DRFDKTEP 70
Db 171 DRFDKTEP 180

RESULT 2
QOCVPT
All protein - potato yellow mosaic virus (Isolate Venezuela)
C:Species: potato yellow mosaic virus
C:Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #taxL-change 16-Jun-2000
R:Contact: R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
J. Gen. Virol. 72, 1515-1520, 1991
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato ye
A:Reference number: J00362; M00D:91311403
A:Accession: J00364
A>Status: translation not shown
A:Molecule type: DNA
A:Accession: J00364
A:Residues: 1-361 <RAN>
C:Comments:
A:Cross-references: GB:D00940; NID:g222458; PIDW:MAA00782.1; PID:g222459
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus All protein

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Query Match          70.7%: Score 256; DB 1; Length 361;
Best Local Similarity 69.6%: Prid. No. 3-7a-21;
Matches 46: Conservative 11; Mismatches 10; Indels 0; Gaps 0;

OY 1 TLWGFQVAGRSARGCQTSNDAAEAALNASSKEALQIREKIPKYLQPHNLNSML 60
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 110 TLEMGFQIDGRSARGCQOTVNDAAEAALNASSKEALQIREKIPKYLQPHNLNSML 169
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 DRFDKTEP 69
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 170 DRFDKTEP 178
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
507594
Hypothetical protein, 40.4k - cassava latent virus (Nigerian isolate)
C:Species: Cassava Latent Virus
C:Accession: F007594
C:Date: 07-Sep-1999 #sequence_revision 07-Sep-1990 #texL_change 20-Sep-1999
R:Morris, B.; Coates, L.; Lowe, S.; Richardson, K.; Eddy, P.
Nucleic Acids Res. 18: 197-198, 1990
A:Title: Nucleotide sequence of the infectious cloned DNA components of African cassava
A:Reference number: S07590; MUID: 90174930
A:Accession: S07594
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-358 <DB>
A:Cross-references: EMBL:X17095; NID:g59371; PIDN:CAA34953.1; PID:g59376
C:Genetics:
A:Map position: segment DN1
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match          67.1%: Score 243; DB 2; Length 358;
Best Local Similarity 62.9%: Prid. No. 1-1e-19;
Matches 44: Conservative 13; Mismatches 13; Indels 0; Gaps 0;

OY 1 TLWGFQVAGRSARGCQTSNDAAEAALNASSKEALQIREKIPKYLQPHNLNSML 60
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 109 TLEMGFQIDGRSARGCQOSNDATKALNASSKEALNATRELVPRDVLQPHNLNSML 168
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 DRFDKTEP 70
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 169 DRFDKTEP 178
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
J01887
AL1 protein - tomato yellow leaf curl virus (strain Australia)
N:Alternate names: C1 protein
C:Species: tomato yellow leaf curl virus
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #texL_change 07-May-1999
C:Accession: J01887
R:Dray, L.B.; Ridsden, J.E.; Krahe, L.R.; Mullineux, P.M.; Rezaian, M.A.
A:Title: Nucleotide sequence and genome organization of tomato leaf curl geminivirus.
A:Reference number: J01885; MUID: 93139778
A:Accession: J01887
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-362 <DB>
A:Cross-references: GB:S53251
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match          65.2%: Score 236; DB 1; Length 362;
Best Local Similarity 55.3%: Prid. No. 6-7e-19;
Matches 47: Conservative 9; Mismatches 13; Indels 16; Gaps 1;

OY 1 TLWGFQVAGRSARGCQTSNDAAEAALNASSKEALQIREKIPKYLQPHNLNSML 60
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

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DB 110 TLEMGFQIDGRSARGCQOSNDAAEAALNASSKEALNATRELVPRDVLQPHNLNSML 169
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 DRFDKTEP 69
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 170 DRFDKTEP 178
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
S39211
gene C1 protein - tomato yellow leaf curl virus
C:Species: tomato yellow leaf curl virus
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #texL_change 20-Sep-1999
R:Morris, B.; Coates, L.; Lowe, S.; Richardson, K.; Eddy, P.
Nucleic Acids Res. 18: 197-198, 1990
A:Title: Nucleotide sequence of the infectious cloned DNA components of African cassava
A:Reference number: S39209
A:Accession: S39211
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-362 <DB>
A:Cross-references: EMBL:Z25751; NID:g433655; PIDN:CAA81026.1; PID:g433658
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match          63.3%: Score 229; DB 2; Length 359;
Best Local Similarity 60.9%: Prid. No. 4e-18;
Matches 42: Conservative 9; Mismatches 10; Indels 0; Gaps 0;

OY 2 TLWGFQVAGRSARGCQTSNDAAEAALNASSKEALQIREKIPKYLQPHNLNSML 61
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 111 LEMQTFQIDGRSARGCQOTVNDAAEAALNASSKEALQIREKIPKYLQPHNLNSML 170
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 62 DRFDKTEP 70
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 171 DRFDKTEP 179
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
J02300
replicase - pepper huasteco virus (component A)
N:Alternate names: ORF AL1 protein
C:Species: pepper huasteco virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #texL_change 20-Sep-1999
C:Accession: J02300
R:Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Herrera-Estrella, L.; Rivera-Bustamante,
J. Gen. Virol. 74: 2225-2231, 1993
A:Title: Complete nucleotide of pepper huasteco virus: Analysis and comparison with b
A:Reference number: J02399; MUID: 94015007
A:Accession: J02300
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-349 <DB>
A:Cross-references: GB:X70418; NID:g61023; PIDN:CAA9856.1; PID:g61025
C:Superfamily: tomato golden mosaic virus AL1 protein

Query Match          62.2%: Score 225; DB 2; Length 349;
Best Local Similarity 60.0%: Prid. No. 1-1e-15;
Matches 42: Conservative 13; Mismatches 15; Indels 0; Gaps 0;

OY 1 TLWGFQVAGRSARGCQTSNDAAEAALNASSKEALQIREKIPKYLQPHNLNSML 60
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 110 TLEMGFQIDGRSARGCQOSNDATVAAALNASSKEALQIREKIPKYLQPHNLNSML 169
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 DRFDKTEP 70
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 170 DRFDKTEP 179
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
S31875
AL1 protein - pepper rizado amarillo virus
C:Species: pepper rizado amarillo virus

```

C|Date: 22-Nov-1993 #sequence-revision 26-May-1995 #text-change 20-Sep-1999
C|Accession: S11875
R|Porter-Racheco, I.: Garzon-Tiznado, J.A.; Jimenes, B.; Herrera-Estrella, L.; Rivera-Bautista,
F.R. In: The Arabidopsis Thaliana Library, February 1995.
A:Molecular type: complete nucleotide sequence Of pepper huastec virus; analysis and compe
A|Reference number: S11872
A|Accession: S11875
A|Molecule type: DNA
A|status: preliminary
A:Molecule type: DNA
A:Residues: 1..349 <TOR>
G|Cross-references: EMBL:X70418; NID:961023; PIDN:CAM49856.1; PTD:961025
A>Note: The source is designated as pepper huasteca virus
C|Superfamily: tomato golden mosaic virus Adl protein

Dbl Query Match 62.2% | Score 225; DB 2; Length 349;
Best Local Similarity 60.0% | Pred.No. 1,1e-17;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Oy 1 TLVWGCVAGNSARGCOITSDNAALANSSKEBALQIQIKPEKYLEYDFHNLNSL 60
 :||| |||
Db 110 TVMGSPFDIHSARSGQSNDOTVALANSMEBAQLIKEPDPHFPIFNYSVA 159

Oy 61 DRIFDKTPEP 70
 :||| |||
Db 170 NRIPDPTPER 179

RESULT 8
S22593
hypothetical protein C4 - tomato yellow leaf curl virus
C|Species: tomato yellow leaf curl virus
C|Date: 22-Nov-1993 #sequence-revision 10-Nov-1995 #text-change 20-Sep-1999
C|Accession: S22593
R|hayer-Pour, A.; Bendahmane, M.; Matzelt, V.; Accotto, G.P.; Crespi, S.; Gronenborn, B.
Molecular Acids Res 19, 6763-6769, 1995 from Sardinia is a whitefly-transmitted monopartite
A|Reference number: S22588; MIDB:J92107660
A|Accession: S22593
A|status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1..359 <KRH>
G|Cross-references: EMBL:X61153; NID:962211; PIDN:CAM43466.1; PTD:962217
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
C|Superfamily: tomato golden mosaic virus Adl protein

Dbl Query Match 61.3% | Score 222; DB 2; Length 359;
Best Local Similarity 58.0% | Pred.No. 2,5e-17;
Matches 40; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Oy 2 LVNGEVOANGSRRCGCSTSNDAABALANSSREBALQIREKIPEKYLFPHMLNSLD 61
 :||| |||
Db 111 LEKPQTIDSRSRGCGTANDAAIALINSGKSGLADLTIELAPRODVLPFHMSIND 170

Oy 62 RIPEKTPER 70
 :||| |||
Db 171 KVFVEPPAP 179

RESULT 9
J02327
Adl protein - Indian cassava mosaic virus
A|Alternate names: replication-associated protein
C|Species: indian cassava mosaic virus
C|Date: 28-Jul-1995 #sequence-revision 07-Oct-1994 #text-change 20-Sep-1999
C|Accession: J02327; SS3683
R|Johnson, D.B.; Harrison, B.D.
J Gen Virol 74, 2437-2443, 1993
A>Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-tran
A|Reference name: J02326; MIDB:94065670
A|Accession: J02327
A:Molecule type: DNA

```

A:Residues: 1,351 <NON>
A:Cross-references: EMBL:424756; NID:9395531; PIDN:CA40891.1; PID:9584046
C:Superfamily: tomato golden mosaic virus A11 protein

Query Match
Query Match Similarity 62.5%; Score 219; DB 1; Length 351;
Best Local Similarity 55.7%; Pred. No. 5,2e-17;
Matches 42; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

Oy 4 WGEVYAGRSARAGCGCOTSDAAAEALNNSKDEALQITREKTEPKYFPOFINLSMDRI 63
Db 113 WGTQIDRSNRAGQGSANDANAAALNNSKSEAKLTRELAAPROTLDPRHNSMDRI 172
Oy 64 PKPKPPP 70
Db 173 PKPKPPP 179

RESULT 10
A:Map position: segment A
A:Protein - abutilon mosaic virus (isolate West India)
C:Species: abutilon mosaic virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #ext_change 08-Apr-1994
C:Accession: A36214
R:Frischmuth, T.; Zilmat, G.; Jesse, H.
Virology 178, 461-468, 1990
A:Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as
A:Reference number: A36214; MUID:91020994
A:Molecule: cDNA
A:Residues: 1,355 <EMBL>
A:Cross-references: EMBL:X15983
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus A11 protein

Oy 1 TLWGEFYVAGRSARGCGCOTSDAAAEALNNSKDEALQITREKTEPKYFPOFINLSNL 60
Db 110 TAWGEFYVAGRSARGCGCOTSDAAAEALNNSKDEALQITREKTEPKYFPOFINLSNL 169
Oy 61 DRPKDPTPP 70
Db 170 DRPKAAPP 179

RESULT 11
A:Map position: segment A
A:Protein - tomato mottle virus (isolate Florida)
C:Species: tomato mottle virus
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #ext_change 07-May-1999
C:Accession: JQ1870
R:Abouzid, A.M.; Polston, J.E.; Hiebert, E.
J. Gen. Virol. 73, 3225-3229, 1992
A:Title: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated
A:Reference number: JQ1869; MUID:93107858
A:Molecule: cDNA
A:Residues: 1,358 <ABO>
A:Cross-references: GR:114460
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus A11 protein

Query Match
Query Match Similarity 59.7%; Score 216; DB 1; Length 358;
Best Local Similarity 55.7%; Pred. No. 1,2e-16;
Matches 39; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

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Gencore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:57:17 ; Search time 43.68 seconds
(without alignments)
58,758 Million cell updates/sec

Title: US-09-289-346a-9

Perfect score: 362
Sequence: 1 TLVWSEFVGNRSGRCGCT.....FGRHNSNLDITDTEEP 70

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	Length	ID	Description
1	356	98.3	352	1 VAL1_TGMV	P03567 tomato gold
2	256	70.7	361	1 P27558	potato gold
3	243	67.1	358	1 VAL1_CIVR	P14982 castanea lat
4	236	65.2	362	1 VAL1_TYCA	P36772 castanea lat
5	229	63.3	359	1 VAL1_TYCU	P38609 tomato yell
6	225	62.2	349	1 VAL1_PHYU	Q06523 pepper huas
7	222	61.3	359	1 VAL1_TYCM	P27260 tomato yell
8	220	60.8	353	1 VAL1_BGVV	P21547 bean golden
9	219	60.5	355	1 VAL1_AAMW	P21947 abutilon mo
10	218	60.1	359	1 VAL1_PHYV	P21451 beet curly
11	216	59.7	358	1 VAL1_PHYV	P21451 beet curly
12	216	59.7	358	1 VAL1_PHYV	P21451 beet curly
13	207	57.2	357	1 VAL1_TYCV	P27259 tomato yell
14	125	34.5	347	1 VAL1_SICV	P29048 squash leaf
15	64.5	17.8	299	1 Y175_HELPJ	Q29mg7 heliochacte
16	62.5	17.3	447	1 TBL2_HUMAN	Q5Yqg3 homo sapien
17	62	17.1	295	1 VAL1_TYDA	P31617 tobacco yell
18	60.1	16.9	1483	1 CYP1_TYAT	P12551 saccharomy
19	60.1	16.9	1483	1 CYP1_TYAT	P12551 saccharomy
20	60.1	16.9	1483	1 CYP1_TYAT	P12551 saccharomy
21	59	16.3	1287	1 SKI2_TYAT	P35079 saccharomyc
22	58.5	16.2	297	1 RREP_RABVP	P06747 rabbit vifu
23	58.5	16.2	299	1 Y175_HELPJ	P53112 heliochacte
24	58.5	16.2	367	1 LHX4_MOUSE	P33776 mus musculu
25	58.5	16.2	367	1 Y667_HAEIN	P45521 haemophilus
26	58.5	16.2	367	1 Y667_HAEIN	P45521 haemophilus
27	58.5	16.2	367	1 Y667_HAEIN	P45521 haemophilus
28	58	16.0	256	1 YK19_TYAT	P31424 saccharomyc
29	58	16.0	617	1 YACR_ECOLI	P36682 escherichia
30	58	16.0	874	1 STAP_BACI	P49052 bacillus th
31	57.5	15.9	136	1 Y452_CABEL	O62250 caenorhabdi
32	57	15.7	355	1 CRTB_RROSH	P34905 rhodobacter
33	57	15.7	492	1 MOT3_MOUSE	O35308 mus musculu

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	352 AA.
VAL1_TGMV				
1 VAL1_TGMV				
AC P03567	1986 (Rel. 01, Created)			
DC 21-JUL-1986 (Rel. 01, last sequence update)				
DE 01-JUN-1994 (Rel. 29, last annotation update)				
DE ALL PROTEIN.				
OS Tomato golden mosaic virus (TGMV).				
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.				
ON NCBI_TaxID=10831;				
OR SEQUENCE FROM N.A.				
RP Hamilton M.D.O., Stejn V.E., Courts R.H.A., Buck K.W.;				
RT *Complete nucleotide sequence of the infectious cloned DNA components				
RF of tomato golden mosaic virus: potential coding regions and regulatory				
RE sequences. ;				
RL EMO J. 3:2197-2205(1984).				
RC				
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CC				
DR EMBL: K02029 ; NOT_ANNOTATED_CDS.				
DR PIR: A04170; Q0CVL1.				
DR InterPro: IP001191; Gemin1_A1.				
DR Pfam: PF00799; Gemin1_A1.				
DR PRINTS: PR00227; GEMINOCAT1.				
DR PROSITE: PS00251; GEMINOCAT1.				
DR PROSITE: PS000736; Gemin1_A1.1.				
DR ATP-binding: 223				
FT NP-BIND				
SQ SEQUENCE 352 AA: 40332 MM: C3C03B864B4A4 CRC64;				
Query Match	98.3%	Score 356	DB 1:	Length 352;
Matches 69;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
1 TLVWSEFVGNRSGRCGCTSNDAAEALNAKSEKALQITREKIPKYLPOFHNLSNL 60				
111 TLVWSEFVGNRSGRCGCTSNDAAEALNAKSEKALQITREKIPKYLPOFHNLSNL 170				
61 DRITDTEEP 70				
171 DRITDTEEP 180				
RESULT 2				
VAL1_PMYV				

```

ID VAL1.PYMW STANDARD: PRT: 361 AA.
AC P27258:
CC 01-AUG-1992 (rel. 23, Created)
CC 01-AUG-1992 (rel. 23, Last sequence update)
CC 01-AUG-1992 (rel. 23, Last annotation update)
CC 01-AUG-1992 (rel. 23, Last modification update)
CC ALL PROTEIN
CC Potaro yellow mosaic virus (Isolate Venezuela).
CC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
CC NCBI_TaxID=10828;
CC [1]
RN SEQUENCE FROM N.A.
RN MEDLINE=911105; PubMed=1856590.
RN PMID=911105; PubMed=1856590.
RN "The nucleotide sequence of the infectious cloned DNA components of
RN potaro yellow mosaic virus."
RN J. Gen. Virol. 72:1515-1520(1991).
RL J.
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J03067; GenBank: F02182.1;
CC PIR: J03064; SwissProt: P00799.
CC InterPro: IPR001191; Geminl.AL1.
CC Pfam: PF00799; Geminl.AL1; 1.
CC PRINTS: PR00227; GEMCOATC.VL.
CC PRINTS: PR00228; GEMCOATC.VL.
CC PRODOM: PD000736; Geminl.AL1; 1.
CC AFIP00736; Geminl.AL1; 1.
CC AFIP00736; Geminl.AL1; 1.
CC NP_00736.222
CC SEQUENCE 361 AA: 40850 MW: 562743BP2164383 CMC64:

Query Match
Best Local Similarity: 70.7%; Score 256; DB 1; Length 361;
Matches 48; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
OY 1 TVNCEGYVAGSANGCOTSNAAKPLASGEALOTIERPKYVGFHNLNSN: 60
DB 110 TLEMGFQIDGSRANGCQOTVNDAAALNSKTEAKKIKRKLPEKTLQYHNLNSN: 169
OY 61 DRIFDKEP 69
DB 170 DRIFDKEP 178

RESULT 3
VAL1.CLVN STANDARD: PRT: 358 AA.
AC P14982:
CC 01-APR-1990 (rel. 14, Created)
CC 01-APR-1990 (rel. 14, Last sequence update)
CC 01-JUN-1994 (rel. 28, Last annotation update)
CC 01-JUN-1994 (rel. 28, Last modification update)
CC ALL PROTEIN (40.4 KDA PROTEIN)
CC ACI.
CC Cassava latent virus (strain West Kenya 844).
CC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
CC NCBI_TaxID=10818;
CC [1]
RN SEQUENCE FROM N.A.
RN MEDLINE=911105; PubMed=1856590.
RN PMID=911105; PubMed=1856590.
RN "The nucleotide sequence of the infectious cloned DNA components of
RN potaro yellow mosaic virus."
RN J. Gen. Virol. 72:1515-1520(1991).
RL J.
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X17005; GenBank: F02182.1;
CC PIR: S07594; SwissProt: P00799.
CC InterPro: IPR001191; Geminl.AL1.
CC Pfam: PF00799; Geminl.AL1; 1.
CC PRINTS: PR00227; GEMCOATC.VL.
CC PRINTS: PR00228; GEMCOATC.VL.
CC PRODOM: PD000736; Geminl.AL1; 1.
CC AFIP00736; Geminl.AL1; 1.
CC AFIP00736; Geminl.AL1; 1.
CC NP_00736.222
CC SEQUENCE 358 AA: 40436 MW: 108156BP225252C CMC64:

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CC -----
CC EMBL: J03067; GenBank: F02182.1;
CC PIR: J03064; SwissProt: P00799.
CC InterPro: IPR001191; Geminl.AL1.
CC Pfam: PF00799; Geminl.AL1; 1.
CC PRINTS: PR00227; GEMCOATC.VL.
CC PRINTS: PR00228; GEMCOATC.VL.
CC PRODOM: PD000736; Geminl.AL1; 1.
CC AFIP00736; Geminl.AL1; 1.
CC AFIP00736; Geminl.AL1; 1.
CC NP_00736.222
CC SEQUENCE 358 AA: 40436 MW: 108156BP225252C CMC64:

Query Match
Best Local Similarity: 67.1%; Score 243; DB 1; Length 358;
Matches 44; Conservative 13; Mismatches 13; Indels 0; Gaps 0;
OY 1 TVNCEGYVAGSANGCOTSNAAKPLASGEALOTIERPKYVGFHNLNSN: 60
DB 109 TLEMGFQIDGSRANGCQOTVNDAAALNSKTEAKKIKRKLPEKTLQYHNLNSN: 168
OY 61 DRIFDKEP 70
DB 169 DRIFDKEP 178

RESULT 4
VAL1.CLVN STANDARD: PRT: 358 AA.
AC P14972:
CC 01-APR-1990 (rel. 14, Created)
CC 01-APR-1990 (rel. 14, Last sequence update)
CC 01-JUN-1994 (rel. 28, Last annotation update)
CC 01-JUN-1994 (rel. 28, Last modification update)
CC ALL PROTEIN (40.4 KDA PROTEIN)
CC ACI.
CC Cassava latent virus (strain Nigerian).
CC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
CC NCBI_TaxID=10819;
CC [1]
RN SEQUENCE FROM N.A.
RN MEDLINE=90174930; PubMed=2308831.
RN PMID=90174930; PubMed=2308831.
RN "Nucleotide sequence of the infectious cloned DNA components of
RN African cassava mosaic virus (Nigerian strain)."
RN Nucleic Acids Res. 18:197-198(1990).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES ALL PROTEIN FAMILY.
CC
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CC -----
CC EMBL: X17005; GenBank: F02182.1;
CC PIR: S07594; SwissProt: P00799.
CC InterPro: IPR001191; Geminl.AL1.
CC Pfam: PF00799; Geminl.AL1; 1.
CC PRINTS: PR00227; GEMCOATC.VL.
CC PRINTS: PR00228; GEMCOATC.VL.
CC PRODOM: PD000736; Geminl.AL1; 1.
CC AFIP00736; Geminl.AL1; 1.
CC AFIP00736; Geminl.AL1; 1.
CC NP_00736.222
CC SEQUENCE 358 AA: 40435 MW: 108156BP225252C CMC64:

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QY 1 TWMEGFQVAGRSARGCCGTSNDAAAEALNNSKEEALQIREKIPKYLDFQPHNLNSML 60
DB 109 TWMEGFQIDGSRNAGSGQSDANAYAKALNNSGSEALVIRELAPROVYLDFPHNLNSML 168
QY 61 DRPFOKTPRP 70
DB 169 DRPFOPEPAP 178

RESULT 5
VAL1_TYLCU STANDARD: PRT: 362 AA.
AC P36279.
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE A11 PROTEIN (C1 PROTEIN).
OS C1.
OS Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OS Genus: Tombusviruses; Geminiviridae; Begomovirus.
OS NCBI_TaxID=36447.
RX MEDLINE=93139778; PubMed=8423446;
RA Dry I.B., Ridgen J.E., Krake L.R., Mullineux P.M., Rezaian M.A.:
RA "Nucleotide sequence and genome organization of tomato leaf curl
RT geminivirus (TLCV): 74,147-151(1993)
RT C1.
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
DR InterPro: IPR001191; GenInfo.A11.
DR Pfam: PF00799; GenInfo.A11.
DR PRINTS: PR00227; GEMCOAT.A11.
DR PRODOM: PD000736; Gemin_A11.1.
KW ATP-binding 221 228 ATP (POTENTIAL).
FT NP_BIND 362 AA: 41197 MW: 343871844704098 CMC64.
SO SEQUENCE

Query Match 65.2% Score 236; DB 1; Length 362;
Best Local Similarity 55.3% Pred. No. 7e-19;
Matches 47; Conservative 9; Mismatches 13; Indels 16; Gaps 1;

QY 1 TWMEGFQVAGRSARGCCGTSNDAAAEALNNSKEEALQIREKIPKYLDFQPHNLNSML 60
DB 110 TWMEGFQIDGSRNAGSGQSDANAYAKALNNSGSEALVIRELAPROVYLDFPHNLNSML 169
QY 61 DRP- PDKTPE 69
DB 170 DRPTEPLEVYVSPVSSFRPPE 194

RESULT 6
VAL1_TYLCU STANDARD: PRT: 359 AA.
AC P38609.
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE A11 PROTEIN (C1 PROTEIN).
OS C1.
OS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OS Genus: ssDNA viruses; Geminiviridae; Begomovirus.
OS NCBI_TaxID=37159;
RX MEDLINE=4256836; PubMed=8198442;
RA Morris E., Hidalgo E., Accotto G., Moriones E.:
RA "High similarity among the tomato yellow leaf curl virus isolates
RT infectious clone from Spain."

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RL Arch. Virol. 135:165-170(1994).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
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CC
CC EMBL: Z23751; CAA81026.1; -
CC F1R: S3521; IPR001191; GenInfo.A11.
CC Pfam: PF00799; Gemin_A11.1.
CC PRINTS: PR00227; GEMCOAT.A11.
CC PRODOM: PD000736; Gemin_A11.1.
KW ATP-binding 221 228 ATP (POTENTIAL).
FT NP_BIND 359 AA: 41065 MW: 20170A51EF0A3EC CMC64.
SO SEQUENCE

Query Match 63.3% Score 229; DB 1; Length 359;
Best Local Similarity 60.9% Pred. No. 4.1e-18;
Matches 42; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 2 TWMEGFQVAGRSARGCCGTSNDAAAEALNNSKEEALQIREKIPKYLDFQPHNLNSML 61
DB 111 TWMEGFQIDGSRNAGSGQSDANAYAKALNNSGSEALVIRELAPROVYLDFPHNLNSML 170
QY 62 RIFOKTPRP 70
DB 171 RVEQVEPAP 179

RESULT 7
VAL1_PHVU STANDARD: PRT: 349 AA.
AC Q06923.
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE A11 PROTEIN.
OS C1.
OS Pepper huasteco virus (PHV).
OS Genus: ssDNA viruses; Geminiviridae; Begomovirus.
OS NCBI_TaxID=28349;
RX MEDLINE=94015007; PubMed=8409944;
RA Torres-Pacheco F., Garzon-Tiznado J.A., Herrera-Estrella L.,
RA "Nucleotide sequence of pepper huasteco virus: analysis and
RT comparison with bipartite geminiviruses."
RT J. Gen. Virol. 74:2225-2231(1993).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
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CC
CC EMBL: X70418; CAA49856.1; -
CC F1R: S31300; S31875.
CC F1R: S31300; S31875.
CC InterPro: IPR001191; Gemin_A11.
CC Pfam: PF00799; Gemin_A11.1.
CC PRINTS: PR00228; GEMCOAT.C1.A1.

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CC
DR      EMBL: X15983; -; NOT_ANNOTATED_CDS.
DR      PIR: A56214; OOCVW1.
DR      InterPro: IPR001191; GemIn1.AL1.
DR      PRINTS: PR00228; GEMCOATV1.
DR      PRINTS: PR00228; GEMCOATV1.
DR      ProDom: PD000736; GemIn1.AL1; 1.
KW      ATP-binding.
FT      NP-BIND.
SQ      SEQUENCE 355 AA; 40257 MW; 16A2CA8A63251E95 CRC64;

Query Match
Best Local Similarity 58.6%; Score 219; DB 1; Length 355;
Matches 41; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

OY      1 TLWGEFVGARSGAGCGTSDNPAAEALNASSSEALQITREKPYLPFPHNLNSL 60
DB      110 TLWGEFVGARSGAGCGTSDNPAAEALNASSSEALQITREKPYLPFPHNLNSL 169
OY      61 DRIPDKTPEP 70
DB      170 ERIFAKAPEP 179

RESUME 11
YALL.TYICV STANDARD: PRT: 358 AA.
AC P14991.
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE A11 PROTEIN (40.8 KDA PROTEIN).
OS Beet curly top virus (BCTV).
CC Viruses: ssDNA viruses; Gemnivalitidae; Curtovirus.
CC NCBI.Taxid=10940.
RN 111.
RP SEQUENCE FROM N.A.
RA Stanley J., Markham P.G., Callis R.J., Pinner M.S.;
RT "The nucleotide sequence of an infectious clone of the geminivirus
RT beet curly top virus."
RL EMBL J. 5:1761-1767(1986).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC
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CC
DR      EMBL: X04144; -; NOT_ANNOTATED_CDS.
DR      InterPro: IPR001191; GemIn1.AL1.
DR      Pfam: PF00799; GemIn1.AL1; 1.
DR      PRINTS: PR00227; GEMCOATV1.
DR      PRINTS: PR00228; GEMCOATV1.
DR      ProDom: PD000736; GemIn1.AL1; 1.
FT      NP-BIND.
SQ      SEQUENCE 358 AA; 40889 MW; 39A5FE3CB8C33 CRC64;

Query Match
59.7%; Score 216; DB 1; Length 358;

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CC      Best Local Similarity 55.7%; Pred. No. 1,1e-16;
CC      Matches 33; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

OY      1 TLWGEFVGARSGAGCGTSDNPAAEALNASSSEALQITREKPYLPFPHNLNSL 60
DB      110 TLWGEFVGARSGAGCGTSDNPAAEALNASSSEALQITREKPYLPFPHNLNSL 169
OY      61 DRIPDKTPEP 70
DB      170 ORTFOPEP 179

RESUME 12
YALL.TMOV STANDARD: PRT: 361 AA.
AC Q06657.
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE A11 PROTEIN.
OS Tomato mottle virus (Isolate Florida) (TMV).
CC Viruses: ssDNA viruses; Gemnivalitidae; Begomovirus.
CC NCBI.Taxid=36449;
RN 111.
RP SEQUENCE FROM N.A.
RA MEDLINE-9:3107856; PubMed-1469361;
RA Abouid A.M., Polston J.E., Herbert E.;
RT "Isolate Florida: a new geminivirus, a new geminivirus
RT isolated from tomatoes in Florida."
RL J. Gen. Virol. 73:3225-3229(1992).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC
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CC
DR      EMBL: L14460; AAC32414.1; -
DR      PIR: J01870; J01870.
DR      InterPro: IPR001191; GemIn1.AL1.
DR      Pfam: PF00799; GemIn1.AL1; 1.
DR      PRINTS: PR00227; GEMCOATV1.
DR      PRINTS: PR00228; GEMCOATV1.
DR      ProDom: PD000736; GemIn1.AL1; 1.
FT      NP-BIND.
SQ      SEQUENCE 361 AA; 40516 MW; 8138B65CEBAC6950 CRC64;

Query Match
59.7%; Score 216; DB 1; Length 361;
Matches 33; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

OY      1 TLWGEFVGARSGAGCGTSDNPAAEALNASSSEALQITREKPYLPFPHNLNSL 60
DB      110 TLWGEFVGARSGAGCGTSDNPAAEALNASSSEALQITREKPYLPFPHNLNSL 169
OY      61 DRIPDKTPEP 70
DB      170 ERIFAKAPEP 179

RESUME 13
YALL.TYICV STANDARD: PRT: 357 AA.
AC P27259.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)

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DE AL1 PROTEIN (C1 PROTEIN).
 GN C1.
 OS Tomato yellow leaf curl virus (TYLCV).
 CC Viruses: ssRNA viruses; Geminiviridae; Begomovirus.
 NR EMBL: X65241.1; GenBank: AF001911.
 CC [1] NCBI:taxid:108321.
 RN [1] NCBI:taxid:108321.
 RP SEQUENCE FROM N.A.
 RA MEDLINE:92042070; PubMed:1926771.
 RA Navot N., Pichersky E., Zeldin M., Zamir D., Czosnek H.
 "Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
 with a single genomic component." Virology 235:1-10 (1998).
 CC -1- SIMILARITY BELONGS TO GEMINIVIRUS AL1 PROTEIN FAMILY.
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 CC
 CC EMBL: X15656; CA33688.1; -
 DR PIR: D40779; Q00VC1.
 DR InterPro: IPR001191; GeminL_AL1.
 DR Pfam: PF00799; GeminL_AL1.1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR PRINTS: PR00228; GEMCOATL1.
 DR PRODOM: PD000736; GeminL_AL1.1.
 RM ATP-binding: 219
 FM NP_BIND
 FT SEQUENCE 357 AA: 40678 MW: 939AB68B1AB32A7 CRC64:
 50
 Query Match 57.2% Score 207; DB 1; Length 357;
 Best Local Similarity 65.6% Pred. No. 1,3e-15;
 Matches 40; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
 4 MEEYVAGSARSGCCQTSNDAAALANSSKEEALIIREKIPKXYLPFHINLSMDRI 63
 DB 111 FGVSQIDGSAKRGQOSANDAYABALNSSSEALINKEAKQYITDPIHLSMDRI 170
 64 F 64
 DB 171 F 171
 RESULT 14
 VALD_SLOC STANDARD; PRT; 347 AA.
 AC P250148.
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE AL1 PROTEIN.
 OS Squash leaf curl virus.
 CC Viruses: ssRNA viruses; Geminiviridae; Begomovirus.
 NR EMBL: X15656; CA33688.1; -
 CC [1] NCBI:taxid:108321.
 RN [1] NCBI:taxid:108321.
 RP SEQUENCE FROM N.A.
 RA MEDLINE:91082449; PubMed:199468;
 RA Lazarowitz S.G., Lazdins I.B.
 "Infectivity and complete nucleotide sequence of the cloned genomic
 components of a bipartite squash leaf curl geminivirus with a broad
 host range phenotype." Virology 235:1-10 (1998).
 CC -1- SIMILARITY BELONGS TO GEMINIVIRUS AL1 PROTEIN FAMILY.
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 CC
 CC EMBL: X65241.1; ALT_INT.
 DR PIR: D40779; Q00VC1.
 DR InterPro: IPR001191; GeminL_AL1.
 DR Pfam: PF00799; GeminL_AL1.1.
 DR PRINTS: PR00227; GEMCOATL1.
 DR PRINTS: PR00228; GEMCOATL1.
 DR PRODOM: PD000736; GeminL_AL1.1.
 RM ATP-binding: 219
 FM NP_BIND
 FT SEQUENCE 347 AA: 39110 MW: A4B8EDDE122110E CRC64:
 50
 Query Match 34.5% Score 125; DB 1; Length 347;
 Best Local Similarity 37.9% Pred. No. 1,3e-06;
 Matches 25; Conservative 15; Mismatches 22; Indels 4; Gaps 1;
 5 GFEYVAGSARSGCCQTSNDAAALANSSKEEALIIREKIPKXYLPFHINLSMDRI 64
 DB 111 FGVSQIDGSAKRGQOSANDAYABALNSSSEALINKEAKQYITDPIHLSMDRI 170
 65 DKTRPP 70
 DB 172 QKPEP 177
 RESULT 15
 VALD_SLOC STANDARD; PRT; 299 AA.
 AC Q92M07.
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE HYPOTHETICAL PROTEIN JHP0161 PROCONSQR.
 OS Helicobacter pylori J99 (campylobacter pylori J99).
 CC Bacteria: Proteobacteria; epsilon subdivision; Helicobacter group;
 CC Helicobacter.
 NR EMBL: X65241.1; GenBank: AF001911.
 CC [1] NCBI:taxid:108321.
 RN [1] NCBI:taxid:108321.
 RP SEQUENCE FROM N.A.
 RA MEDLINE:99120557; PubMed:99234682;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
 RA Smith D.R., Noonan B., Gould B.C., deJonghe B.L., Carmel G.,
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Merberg D., Mills S.D., Jiang O., Taylor D.E., Voyis G.F.,
 RA Trust R.J.
 "Genomic sequence comparison of two unrelated isolates of the human
 pathogen Helicobacter pylori." J. Bacteriol. 193:176-180 (1999).
 CC -1- SIMILARITY BELONGS TO THE PTC/PAVULIN FAMILY OF ROTAMASES.
 CC
 CC STRONG, TO C.JEUNI CBF2.
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 CC
 CC EMBL: AE001454; AAD05744.1; -
 DR HSSP: J13526; J1N.
 DR InterPro: IPR006379; rotamase.
 DR PROSITE: PS01096; PTC_P1ASE.1; 1
 KM Hypothetical protein: Isomerase: Rotamase: Signal: Complete proteome.
 FT SIGNAL 21
 FT CHAIN 22 299 POTENTIAL
 FT DOMAIN 154 253 HYPOTHETICAL PROTEIN JHP0161.
 FT SEQUENCE 299 AA: 34040 MW: 9C037BDC1110143 CRC64:
 50

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009727
ID 009727 PRELIMINARY: PRT; 226 AA.
AC 009727;1997 (TREMBLrel. 04, Created)
DT 01-JUN-1997 (TREMBLrel. 04, Last sequence update)
DE REP PROTEIN (FRAGMENT). 17, Last annotation update)
GN REP.
OS Leonturus mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
RN 111 TaxID=58177;
RP SEQUENCE FROM N.A.
RC STRAIN-LEWY-BRAZIL 1;
RA Faria J.C., Maxwell D.P.,
EMBL: U92532; AAB5157.1;
DR Interp: IPR001191; GeminI_AL1.
DR Interp: IPR001191; GeminI_AL1.
DR PRINTS: PR00227; GEMIN1_AL1.
DR Prodom: PD000736; GeminI_AL1; 1.
FT NON_TER 226
SQ SEQUENCE 226 AA; 25617 MW; 73CDB6F6083FC5 CRC64;

Query Match 79.6%; Score 288; DB 12; Length 226;
Best Local Similarity 75.7%; Pred. No. 3,9e-24;
Matches 56; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 1 TLWGEFVAGSARAGCGTSDAAEAALMASSKEEALQITREKIPKYLQFPHNLNSL 60
Db 111 TLWGEFVAGSARAGCGTSDAAEAALMASSKEEALQITREKIPKYLQFPHNLNSL 170
OY 61 DRIFKTRPP 70
Db 171 DRIFKTRPP 180
RESULT 3
OSUNTER
ID 09WHF6 PRELIMINARY: PRT; 226 AA.
AC 09WHF6
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
GN REPLICATION-ASSOCIATED PROTEIN (FRAGMENT).
OS Tomato mild mottle geminivirus.
OC Viruses; ssDNA viruses; Geminiviridae; Unclassified Geminiviridae.
RN NCBI_TaxID=92943;
RP SEQUENCE FROM N.A.
RC STRAIN-H96-HSKV
RA Maxwell D.P., Mejia L., Ramirez P., Karkashian J.P., Boyle M.M.,
RT "Molecular characterization and DNA-based detection methods for
vegetable-infecting geminiviruses in Central America.
Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
EMBL: AF131071; AAB33471.1;
DR Interp: IPR001191; GeminI_AL1.
DR Interp: IPR001191; GeminI_AL1.
DR PRINTS: PR00227; GEMIN1_AL1.
DR Prodom: PD000736; GeminI_AL1; 1.
FT NON_TER 226
SQ SEQUENCE 226 AA; 25941 MW; 2EA4116712871A23 CRC64;

Query Match 79.6%; Score 288; DB 12; Length 226;
Best Local Similarity 75.7%; Pred. No. 3,9e-24;
Matches 53; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
OY 1 TLWGEFVAGSARAGCGTSDAAEAALMASSKEEALQITREKIPKYLQFPHNLNSL 60
Db 111 TLWGEFVAGSARAGCGTSDAAEAALMASSKEEALQITREKIPKYLQFPHNLNSL 170

Db 111 TLWGEFVAGSARAGCGTSDAAEAALMASSKEEALQITREKIPKYLQFPHNLNSL 170
OY 61 DRIFKTRPP 70
Db 171 DRIFKTRPP 180

RESULT 4
OSUNTER
ID 067574 PRELIMINARY: PRT; 361 AA.
AC 067574
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE PUTATIVE REPLICATIVE PROTEIN.
GN AL1.
OS Vein golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
RN 111 NCBI_TaxID=10839;
RP SEQUENCE FROM N.A.
RC GILBERTSON R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
EMBL: M88686; A446312.1;
DR Interp: IPR001191; GeminI_AL1.
DR Interp: IPR001191; GeminI_AL1.
DR PRINTS: PR00227; GEMIN1_AL1.
DR Prodom: PD000736; GeminI_AL1; 1.
SQ SEQUENCE 361 AA; 41041 MW; 0094C7ACAF06B788 CRC64;

Query Match 79.0%; Score 286; DB 12; Length 361;
Best Local Similarity 79.1%; Pred. No. 1,1e-23;
Matches 53; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

OY 4 KCEPFAAGSARAGCGTSDAAEAALMASSKEEALQITREKIPKYLQFPHNLNSL 63
Db 113 KCEPFAAGSARAGCGTSDAAEAALMASSKEEALQITREKIPKYLQFPHNLNSL 172
OY 64 DRIFKTRPP 70
Db 173 DRIFKTRPP 179

RESULT 5
OSUNTER
ID 090DB1 PRELIMINARY: PRT; 225 AA.
AC 090DB1
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
GN REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
OS Cowpea golden mosaic geminivirus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
RN NCBI_TaxID=69263;
RP SEQUENCE FROM N.A.
RC STRAIN-CGW-BR;
RA Faria J.C.;
RT "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF188708; AAF06318.1; -
 DR InterPro: IPR001191; Gemini.AL1.
 DR Pfam: PF00799; Gemini.AL1.1.
 DR PRINTS: PR00227; GEMCOATALL.
 DR NCBI: F000226; Gemini.AL1.1.
 DR NCBI: F000225; Gemini.AL1.1.
 SO SEQUENCE 225 AA; 25766 MW; 1099C6HD0158D5 CRC64;

Query Match 78.5%; Score 284; DB 12; Length 225;
 Best Local Similarity 79.1%; Pred. No. 1, 1e-23;
 Matches 56; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 4 TTYGFEVQGRSARGGCGTNDAAALNSKEEALQITREKIPERYLPOPHNLNSNL 63
 DB 110 TTYGFEVQGRSARGGCGTNDAAALNSKEEALQITREKIPERYLPOPHNLNSNL 172
 DB 64 DRIKTPP 70
 DB 173 FRKPEP 179

RESULT 6
 ID 09ELT8 PRELIMINARY; PRT: 314 AA.
 AC 09ELT8;
 DT 01-MAR-2001 (TRENHUREL. 16, Created)
 DT 01-MAR-2001 (TRENHUREL. 15, Last sequence update)
 DT 01-JUN-2001 (TRENHUREL. 2, Last annotation update)
 DE REPLICATION ASSOCIATION PROTEIN.
 GN ACI.
 OS sweet potato leaf curl virus.
 CX Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
 NC NCBI_TaxID=100755;

RA SEQUENCE FROM N.A.
 RA LECTAKUL P., VALVERDE R.A., CLARK C.A., SIM J., DE LA TORRE R.;
 RT "Detection of a geminivirus infecting sweet potato in the United
 States.";
 RL Plant Dis. 82:1253-1257(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RA LECTAKUL P., VALVERDE R.A.;
 RA Submitted (2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF068227; AAF06318.1; -
 DR InterPro: IPR001191; Gemini.AL1.
 DR Pfam: PF00799; Gemini.AL1.1.
 DR PRINTS: PR00227; GEMCOATALL.
 DR PRODOM: PD000736; Gemini.AL1.1.
 SO SEQUENCE 314 AA; 35153 MW; 686220613049634 CRC64;

Query Match 78.5%; Score 284; DB 12; Length 314;
 Best Local Similarity 82.4%; Pred. No. 1, 1e-23;
 Matches 56; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 TTYGFEVQGRSARGGCGTNDAAALNSKEEALQITREKIPERYLPOPHNLNSNL 60
 DB 110 TTYGFEVQGRSARGGCGTNDAAALNSKEEALQITREKIPERYLPOPHNLNSNL 169
 QY 61 DRIKTPP 68
 DB 170 DRIKTPP 177

RESULT 7
 ID 09GS55 PRELIMINARY; PRT: 364 AA.
 AC 09GS55;
 DT 01-MAY-2000 (TRENHUREL. 13, Created)
 DT 01-MAY-2000 (TRENHUREL. 13, Last sequence update)
 DT 01-JUN-2001 (TRENHUREL. 17, Last annotation update)
 DE REPLICATION INITIATION PROTEIN ACI.

GN ACI.
 OS sweet potato leaf curl virus.
 CX Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
 NC NCBI_TaxID=100755;

RA SEQUENCE FROM N.A.
 RA LECTAKUL P., VALVERDE R.A., CLARK C.A., SIM J., DE LA TORRE R.;
 RT "Detection of a geminivirus infecting sweet potato in the United
 States.";
 RL Plant Dis. 82:1253-1257(1998).
 DR EMBL: AF104036; AAF06318.1; -
 DR InterPro: IPR001191; Gemini.AL1.
 DR PRINTS: PR00227; GEMCOATALL.
 DR PRODOM: PD000736; Gemini.AL1.1.
 SO SEQUENCE 364 AA; 40680 MW; 5F79752431A09D6E CRC64;

Query Match 78.5%; Score 284; DB 12; Length 364;
 Best Local Similarity 82.4%; Pred. No. 1, 1e-23;
 Matches 56; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 TTYGFEVQGRSARGGCGTNDAAALNSKEEALQITREKIPERYLPOPHNLNSNL 60
 DB 110 TTYGFEVQGRSARGGCGTNDAAALNSKEEALQITREKIPERYLPOPHNLNSNL 169
 QY 61 DRIKTPP 68
 DB 170 DRIKTPP 177

RESULT 8
 ID 098693 PRELIMINARY; PRT: 185 AA.
 AC 098693;
 DT 01-FEB-1997 (TRENHUREL. 02, Created)
 DT 01-FEB-1997 (TRENHUREL. 2, Last sequence update)
 DT 01-JUN-2001 (TRENHUREL. 17, Last annotation update)
 DE REP. PROTEIN (FRAGMENT).
 GN ACI.
 OS sida golden mosaic virus.
 CX Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
 NC NCBI_TaxID=51034;

RA SEQUENCE FROM N.A.
 RA STRAIN: JAMAICA.
 RA ROYE M.E., McLAUGHLIN M.A., NEKHLE M.K., MAXWELL D.P.;
 RA Plant Dis. 81:1251-1258(1997).
 DR EMBL: U67926; AAB97865.1; -
 DR InterPro: IPR001191; Gemini.AL1.
 DR Pfam: PF00799; Gemini.AL1.1.
 DR PRINTS: PR00227; GEMCOATALL.
 DR PRODOM: PD000736; Gemini.AL1.1.
 DR NCBI: F000226; Gemini.AL1.1.
 FT NON-TER
 SO SEQUENCE 185 AA; 20975 MW; 3913850A025A5E61 CRC64;

Query Match 77.6%; Score 281; DB 12; Length 185;
 Best Local Similarity 72.9%; Pred. No. 1, 1e-23;
 Matches 51; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 TTYGFEVQGRSARGGCGTNDAAALNSKEEALQITREKIPERYLPOPHNLNSNL 60
 DB 89 TTYGFEVQGRSARGGCGTNDAAALNSKEEALQITREKIPERYLPOPHNLNSNL 148
 QY 61 DRIKTPP 70
 DB 149 DRIKTPP 158

RESULT 9
 ID 098975 PRELIMINARY; PRT: 364 AA.
 AC 098975;
 DT 01-MAY-2000 (TRENHUREL. 13, Created)
 DT 01-MAY-2000 (TRENHUREL. 13, Last sequence update)
 DT 01-JUN-2001 (TRENHUREL. 17, Last annotation update)
 DE REPLICATION INITIATION PROTEIN ACI.

Query Match 75.4% Score 273; DB 12; Length 149;
 Best Local Similarity 71.4% Pred. No. 1, 1e-22;
 Matches 50; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

AC P88975 PRELIMINARY: PRT: 149 AA.
 DT 01-MAY-1997 (TEMBLrel. 03, Created)
 DT 01-MAY-1997 (TEMBLrel. 03, Last sequence update)
 DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
 DT REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
 GN AC1 REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
 OS Macropellium golden mosaic geminivirus.
 OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
 NCBI_TaxID=51676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-JAMAICA;
 RL Thesis (1996). Biochemistry, University of the West Indies, Jamaica.
 DR EMBL: U75278; AA836913.1;
 DR Interpro: IP001191; GeminI_AL1.
 DR Pfam: PF00799; GeminI_AL1.1.
 DR PRINTS: PR00227; GEMCOATALL.
 DR PRODOM: PD000736; GeminI_AL1.1.
 DR NCBI: NC001361; GeminI_AL1.1.
 FT NON-TER 149 149
 SQ SEQUENCE 149 AA; 16785 MW; E4CF5BED4C9D508 CRC64;

Query Match 75.4% Score 273; DB 12; Length 149;
 Best Local Similarity 71.4% Pred. No. 1, 1e-22;
 Matches 50; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

OY 1 TLVNGEPVAGSGARCGCGTNNMAAALNASSKEPALITREKTIPEKYLDFPHNLSNL 60
 DB 52 TLVNGEPVAGSGARCGCGTNNMAAALNASSKEPALITREKTIPEKYLDFPHNLSNL 111
 OY 61 DRIFDXTPEP 70
 DB 112 DRIFDXTPEP 121

RESULT 10
 OY104 PRELIMINARY: PRT: 233 AA.
 DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
 DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
 GN REP.
 OS Macropellium golden mosaic geminivirus.
 OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
 NCBI_TaxID=51676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-JAMAICA STRAIN 1;
 DT from Jamaica.
 DT Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.
 DT Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.
 RC STRAIN-JAMAICA STRAIN 1;
 RP SEQUENCE FROM N.A.
 RA Roye M.E.;
 DT "Genetic diversity and phylogeny of whitefly-transmitted geminiviruses
 DT latyviridites from Jamaica.";
 DT Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.
 DT Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Roye M.E., McLaughlin W.A., Maxwell D.P.;
 DT "Molecular characterization of two distinct geminiviruses infecting M.
 DT latyviridites from Jamaica.";
 DT Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.
 DT Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfam: PF00799; GeminI_AL1.1.
 DR PRINTS: PR00227; GEMCOATALL.
 DR PRODOM: PD000736; GeminI_AL1.1.
 DR NCBI: NC001361; GeminI_AL1.1.
 FT NON-TER 233 233
 SQ SEQUENCE 233 AA; 26355 MW; AAA90AFAD216A02 CRC64;

Query Match 75.4% Score 273; DB 12; Length 233;
 Best Local Similarity 71.4% Pred. No. 1, 1e-22;
 Matches 50; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

OY 1 TLVNGEPVAGSGARCGCGTNNMAAALNASSKEPALITREKTIPEKYLDFPHNLSNL 60
 DB 110 TLVNGEPVAGSGARCGCGTNNMAAALNASSKEPALITREKTIPEKYLDFPHNLSNL 169
 OY 61 DRIFDXTPEP 70
 DB 170 DRIFDXTPEP 179

Query Match 73.8% Score 267; DB 12; Length 234;
 Best Local Similarity 70.0% Pred. No. 8, 4e-22;
 Matches 49; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

OY 1 TLVNGEPVAGSGARCGCGTNNMAAALNASSKEPALITREKTIPEKYLDFPHNLSNL 60
 DB 110 TLVNGEPVAGSGARCGCGTNNMAAALNASSKEPALITREKTIPEKYLDFPHNLSNL 169
 OY 61 DRIFDXTPEP 70
 DB 170 DRIFDXTPEP 179

RESULT 12
 OY2089 PRELIMINARY: PRT: 190 AA.
 AC O92089
 DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
 DE C1 AND C4 GENES, CLONE YOKOHAMA3-1, PARTIAL AND COMPLETE CDS
 DE (FRAGMENT).
 GN C1.
 OS tobacco leaf curl virus.
 OC Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
 NCBI_TaxID=67762;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-YOKOHAMA3.
 RA Ooi K., Ohshita S., Ishii I., Yahara T.;
 DT "Molecular phylogeny of geminiviruses infecting wild plants in Japan.";
 DT J. Plant Res. 110:247-257(1997).
 DR EMBL: AB001315; BAA34033.1;
 DR Interpro: IP001191; GeminI_AL1.
 DR Pfam: PF00799; GeminI_AL1.1.

DR	PRINTS:	PR00227;	GEMCOATALL.
DR	PRODOM:	P000736;	Gemini1.ALL; 1.
FT	NON_TER	1	
FT	NON_TER	190	190
SQ	SEQUENCE	190 AA:	21432 MW; AAC093DID1610FAD CXC64;
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Oy	Query Match	72.9%	Score 264; DB 12; Length 190;
Oy	Best Local Similarity	61.2%;	Pred. No. 1,4e-21;
Oy	Matches	52; Conservative	8; Mismatches 9; Indels 16; Gaps 1;
Dy	1	TIVMGEPVAGSRARSGCCGTSDAAALNALNSKEEALQIIREKIPERLYPQHNLNSL	60
Dy	85	TIEMGTFIDINSRRGGCGGNANACASNAKSAALNLSKRAELIIRKKLPDPFYHNLNSL	144
Dy	63	DRI-----FDKTPR	69
Dy	145	DRIAPLEVPFCPTASSDFOVE	169
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RESULT	13		
OY2084	PRELIMINARY:	PRT:	190 AA.
AC	092084		
AC	092084:		
DT	01-MAY-1999	(TRMBJREL	10, Created)
DT	01-MAY-1999	(TRMBJREL	10, Last sequence update)
DT	01-JUN-2001	(TRMBJREL	17, Last annotation update)
DE	C1 AND C4 GENES, CLONE YOKOHAMA-2, PARTIAL AND COMPLETE CDS		
DE	(FRAGMENT).		
OS	tobacco leaf curl virus,		
OC	Viruses; ssDNA viruses; Geminitviridae; Begomovirus.		
OX	NBI Taxid=67762;		
RX	[1]		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=YOKOHAMA-2		
RA	NO. R. IN THE SEQUENCE	Ishi T., Yahara T.	
RL	%Plant phylogeny of geminiviruses infecting wild plants in Japan.*;		
RL	J Plant Res. 110: 247-257(1997).		
DR	EMBL: AB001318; BAA34039.1;		
DR	Interpro: IPRO01191; Gemini1.ALL.		
DR	Fam: PF00799; Gemini_1A1.1.		
DR	PRINTS: PR00227; GEMCOATALL.		
DR	Prodom: P000736; Gemini1.ALL; 1.		
FT	NON_TER	190	
SQ	SEQUENCE	190 AA:	AAC1C243E3E01AD CRC64;
<hr/>			
OY	Query Match	72.9%	Score 264; DB 12; Length 190;
OY	Best Local Similarity	61.2%;	Pred. No. 1,4e-21;
OY	Matches	52; Conservative	9; Mismatches 9; Indels 16; Gaps 1;
Dy	1	TIVMGEPVAGSRARSGCCGTSDAAALNALNSKEEALQIIREKIPERLYPQHNLNSL	60
Dy	85	TIEMGTFIDINSRRGGCGGNANACASNAKSAALNLSKRAELIIRKKLPDPFYHNLNSL	144
Dy	61	DRI-----FDKTPR	69
Dy	145	DRIAPLEVPFCPTASSDFOVE	169
<hr/>			
RESULT	14		
OY2087	PRELIMINARY:	PRT:	190 AA.
AC	09W827		
AC	09W827:		
DT	01-NOV-1999	(TRMBJREL	12, Created)
DT	01-NOV-1999	(TRMBJREL	12, Last sequence update)
DT	01-JUN-2001	(TRMBJREL	17, Last annotation update)
DE	C1 PROTEIN (FRAGMENT).		
GN	C1.		
OS	tobacco leaf curl virus.		
OC	Viruses; ssDNA viruses; Geminitviridae; Begomovirus.		

Fri Jan 4 09:40:17 2002

us-09-289-346a-9.rpt

Page 6

Job time: 1122 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.
OM protein - protein search, using sw model

Run on: January 3, 2002, 15:38:51 ; Search time 65.28 seconds
(without alignments)
24,130 Million cell updates/sec

Title: US-09-289-346a-9

Perfect score: 362
Sequence: 1 TLVWGEFVQVGRSARGCQQT.....FQFHLMNSNLDRIEDTPEP 70

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Displaying first 45 summaries

Database : Issued Patents, AA.*

1: /cgn2.6/p/ctdata/2/1aa/5A.COMB.pep.*
2: /cgn2.6/p/ctdata/2/1aa/5B.COMB.pep.*
3: /cgn2.6/p/ctdata/2/1aa/6A.COMB.pep.*
4: /cgn2.6/p/ctdata/2/1aa/6B.COMB.pep.*
5: /cgn2.6/p/ctdata/2/1aa/PCUTS.COMB.pep.*
6: /cgn2.6/p/ctdata/2/1aa/bocktest1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	222	61.3	353	4	US-08-838-151A-44
2	222	61.3	353	4	US-08-838-151A-46
3	222	61.3	353	4	US-08-838-151A-49
4	222	61.3	353	4	US-08-838-151A-52
5	222	61.3	353	4	US-08-838-151A-55
6	222	61.3	359	4	US-08-809-103B-2
7	222	61.3	359	4	US-08-809-103B-4
8	222	61.3	359	4	US-08-809-103B-8
9	222	61.3	359	4	US-08-809-103B-8
10	220	60.8	361	4	US-08-838-151A-2
11	220	60.8	361	4	US-08-838-151A-4
12	220	60.8	361	4	US-08-838-151A-6
13	220	60.8	361	4	US-08-838-151A-9
14	207	57.2	357	4	US-08-838-151A-24
15	207	57.2	357	4	US-08-838-151A-30
16	207	57.2	357	4	US-08-838-151A-20
17	199	55.0	357	4	US-08-838-151A-20
18	167	1713	3	US-08-600-982-24	
19	60.5	16.7	1713	5	PCT-US94-10261A-24
20	60	16.6	446	4	US-08-672-812D-11
21	60	16.6	446	4	US-08-672-812D-11
22	58	16.0	844	3	US-09-023-267-20
23	55	15.5	454	3	US-08-446-100-31
24	55	15.5	602	2	US-08-419-652-6
25	55	15.5	771	1	US-07-923-976-6
26	56	15.5	783	6	5422248-2
27	56	15.5	836	1	US-07-923-976-4

28	56	15.5	863	1	US-07-923-976-8	Sequence 8, Appl
29	56	15.5	2161	1	US-07-743-206A-2	Sequence 2, Appl
30	56	15.5	2161	1	US-08-455-543A-19	Sequence 49, Appl
31	56	15.5	2161	1	US-08-455-543A-51	Sequence 51, Appl
32	56	15.5	2161	2	US-08-323-105C-51	Sequence 51, Appl
33	56	15.5	2161	2	US-08-111-163-2	Sequence 27, Appl
34	56	15.5	2161	2	US-08-928-442-3	Sequence 3, Appl
35	55	15.2	384	4	US-08-946-100-30	Sequence 30, Appl
36	55	14.9	454	3	US-08-446-100-27	Sequence 6, Appl
37	53.5	14.8	81	4	US-08-959-159-6	Sequence 27, Appl
38	53.5	14.8	91	4	US-09-042-165A-27	Sequence 2, Appl
39	53.5	14.8	312	4	US-08-114-625-2	Sequence 2, Appl
40	53.5	14.8	312	4	US-08-114-625-2	Sequence 40, Appl
41	53	14.6	286	6	US-07-857-224B-40	Sequence 26, Appl
42	53	14.6	454	3	US-08-446-100-27	Sequence 27, Appl
43	53	14.6	454	3	US-08-446-100-27	Sequence 28, Appl
44	53	14.6	454	3	US-08-446-100-28	Sequence 29, Appl
45	53	14.6	454	3	US-08-446-100-29	

ALIGNMENTS

RESULT 1
US-08-838-151A-44
: Sequence 44, Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: John T
: APPLICANT: Louis Hong T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: NUMBER OF SEQUENCES: 63
: CORRESPONDING ADDRESS:
: ADDRESS: Rockefeller University
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIL: 60601
: COMPUTER GENERATED FROM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838,151A
: FILING DATE: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5460
: TELEPHONE: 312-616-5400
: IMPUTED SOURCE: 44:
: SEQUENCE CHARACTERISTICS: 44:
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-838-151A-44
Query Match 61.3%; Score 222; DB 4; Length 353;
Best Local Similarity 60.0%; Pred. No. 96-21;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
CY 1 TLVWGEFVQVGRSARGCQTSNDAAEALNASSKEPALQIIRKIPKYLQFQFHLMNSNLDRIEDTPEP

DB 110 110TENGPOVGRSANGCQGSNDYAKALNADSIJESALITLKEQPDYVLOJHHIISNL 169

OY 61 DRIFDTEP 70

DB 170 ERIVKVEP 179

RESULT 2

US-08-838-151A-46
 : Sequence 46, Application US/08838151A
 : Patent No. 6291743
 : GENERAL INFORMATION:
 : APPLICANT: Stout, John T
 : APPLICANT: Maxwell, Douglas
 : APPLICANT: Ahlquist, Paul
 : APPLICANT: Hanson, Steve
 : TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 : NUMBER OF SEQUENCES: 63
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 : STREET: Two Prudential Plaza, Suite 4700
 : CITY: Chicago
 : STATE: Illinois
 : COUNTRY: U.S.A.
 : ZIP: 60601
 : TELEPHONE: 312-616-5460
 : TELEFAX: 312-616-5460
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : FILING DATE: 05/08/83B, 151A
 : CLASSIFICATION: 800
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Mueller, Lisa V
 : REGISTRATION NUMBER: 38,978
 : REFERENCE/DOCKET NUMBER: SVS3801P0260
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 312-616-5460
 : TELEFAX: 312-616-5460
 : INFORMATION FOR SEQ ID NO: 46:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 353 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-838-151A-46

Query Match 61.3%; Score 222; DB 4; Length 353;

Best Local Similarity 60.0%; Pred. No. 9e-21;

Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

OY 1 110TENGPOVGRSANGCQGSNDYAKALNADSIJESALITLKEQPDYVLOJHHIISNL 60

DB 110 110TENGPOVGRSANGCQGSNDYAKALNADSIJESALITLKEQPDYVLOJHHIISNL 169

OY 61 DRIFDTEP 70

DB 170 ERIVKVEP 179

RESULT 3

US-08-838-151A-49
 : Sequence 49, Application US/08838151A
 : Patent No. 6291743
 : GENERAL INFORMATION:
 : APPLICANT: Stout, John T
 : APPLICANT: Ewu, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Ahlquist, Paul

APPLICANT: Hanson, Steve

TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Rocky, Milnamow & Katz

STREET: Two Prudential Plaza, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60601

TELEPHONE: 312-616-5460

TELEFAX: 312-616-5460

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: 05/08/83B, 151A

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V

REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: SVS3801P0260

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5460

TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 353 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-838-151A-49

Query Match 61.3%; Score 222; DB 4; Length 353;

Best Local Similarity 60.0%; Pred. No. 9e-21;

Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

OY 1 110TENGPOVGRSANGCQGSNDYAKALNADSIJESALITLKEQPDYVLOJHHIISNL 60

DB 110 110TENGPOVGRSANGCQGSNDYAKALNADSIJESALITLKEQPDYVLOJHHIISNL 169

OY 61 DRIFDTEP 70

DB 170 ERIVKVEP 179

RESULT 4

US-08-838-151A-52
 : Sequence 52, Application US/08838151A
 : Patent No. 6291743
 : GENERAL INFORMATION:
 : APPLICANT: Stout, John T
 : APPLICANT: Ewu, Hang T
 : APPLICANT: Maxwell, Douglas
 : APPLICANT: Ahlquist, Paul
 : APPLICANT: Hanson, Steve
 : TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 : NUMBER OF SEQUENCES: 63
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 : STREET: Two Prudential Plaza, Suite 4700
 : CITY: Chicago
 : STATE: Illinois
 : COUNTRY: U.S.A.
 : ZIP: 60601
 : TELEPHONE: 312-616-5460
 : TELEFAX: 312-616-5460
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk


```

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  PATENTIN RELEASE #1.0, Version #1.30
  FILING DATE: 05/08/93B.151A
  CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
  NAME: Mueller, Lisa V
  REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS801P0260
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 312-616-5400
  TELEFAX: 312-616-5400
  INFORMATION FOR SEQ ID NO: 52:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 353 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
      MOLECULE TYPE: protein
US-08-838-151A-52

Query Match
Best Local Similarity 61.3%; Score 222; DB 4; Length 353;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

1 TLVGEFVAGSARGGCQTSNDAAALNASSKEBALQIREKIPKTLPOFHLNSML 60
110 TLVGEFVAGSARGGCQTSNDAAALNASSKEBALQIREKIPKTLPOFHLNSML 169
DB 110 TLVGEFVAGSARGGCQTSNDAAALNASSKEBALQIREKIPKTLPOFHLNSML 169
OY 61 DRIDKTEP 70
DB 170 ERIFVAVPEP 179

```

```

SEQUENCE CHARACTERISTICS:
  LENGTH: 353 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  MOLECULE TYPE: protein
US-08-838-151A-55

Query Match
Best Local Similarity 61.3%; Score 222; DB 4; Length 353;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

1 TLVGEFVAGSARGGCQTSNDAAALNASSKEBALQIREKIPKTLPOFHLNSML 60
110 TLVGEFVAGSARGGCQTSNDAAALNASSKEBALQIREKIPKTLPOFHLNSML 169
DB 110 TLVGEFVAGSARGGCQTSNDAAALNASSKEBALQIREKIPKTLPOFHLNSML 169
OY 61 DRIDKTEP 70
DB 170 ERIFVAVPEP 179

```



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? ZIP: 22202
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/809,1038
? FILING DATE: 17-MAR-1997
? CLASSIFICATION: 800
? PRIOR APPLICATION NUMBER: FR 94,11040
? FILING DATE: 15-SEP-1994
? PENDING APPLICATION DATA: NO PCT/FR95/01192
? APPLICATION NUMBER:
? FILING DATE: 15-SEP-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: PATCH, Andrew J.
? REGISTRATION NUMBER: 32,925
? REFERENCE/DOCKET NUMBER: US94AL CNR TOM
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 665-0527
? TELEFAX: (703) 665-0523
? TELEX: 248425 EMBON
? INFORMATION FOR SEQ ID NO: 8:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 359 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-809-1038-8

```

```

Query Match 61.3%; Score 222; DB 4; Length 359;
Best Local Similarity 58.0%; Pred. No. 9,2e-21;
Matches 40; Conservative 11; Mismatches 16; Indels 0; Gaps 0:
OY 2 1WMEQVAGSRAGCGCTGNDAARALNASKREALQIIRKIPKYLQFPHNLSMD 61
DB 111 LEMGTQIDGRSARGGQOTANDYAKAKINAGSKSQLDIKELRDYLHFHNINSMD 170
OY 62 RIEFKTPEP 70
DB 171 KFYQYPAEP 179

```

```

RESULT 10
US-08-838-151A-2
? Sequence 2, Application US/08838151A
? Patent No. 6291743
? GENERAL INFORMATION: John T
? APPLICANT: Louis, Hans T
? APPLICANT: Maxwell, Douglas
? APPLICANT: Ahlquist, Paul
? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing Geminiiviruses
? NUMBER OF SEQUENCES: 63
? ADDRESSER: Dressler, Rocky, Milnamow & Katz
? STREET: Two Prudential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A

```

```

? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: SVS3801P0260
? REFERENCE/DOCKET NUMBER: US94AL CNR TOM
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 361 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-838-151A-2

```

```

Query Match 60.8%; Score 220; DB 4; Length 361;
Best Local Similarity 57.1%; Pred. No. 1,7e-20;
Matches 40; Conservative 16; Mismatches 14; Indels 0; Gaps 0:
OY 1 1TWGCEVQVAGSRAGCGCTGNDAARALNASKREALQIIRKIPKYLQFPHNLSMD 60
DB 110 LEMGTQIDGRSARGGQOTANDYAKAKINAGSKSQLDIKELRDYLHFHNINSMD 169
OY 61 RIEFKTPEP 70
DB 170 KFYQYPAEP 179

```

```

RESULT 11
US-08-838-151A-4
? Sequence 4, Application US/08838151A
? Patent No. 6291743
? GENERAL INFORMATION: John T
? APPLICANT: Louis, Hans T
? APPLICANT: Maxwell, Douglas
? APPLICANT: Ahlquist, Paul
? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing Geminiiviruses
? NUMBER OF SEQUENCES: 63
? ADDRESSER: Dressler, Rocky, Milnamow & Katz
? STREET: Two Prudential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE: 17-MAR-1997
? CLASSIFICATION: 800
? PRIOR APPLICATION NUMBER: FR 94,11040
? PENDING APPLICATION DATA: NO PCT/FR95/01192
? APPLICATION NUMBER:
? FILING DATE: 15-SEP-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 361 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein

```

US-08-838-151A-4

Query Match 60.8%, Score 220; DB 4; Length 361;
 Sequence Similarity 57.1%; Pred. NO. 1.7e-20;
 Matches 40; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

OY 1 TLWGEFVQAGSANGCOTSNDAAEALMASSKEAQLIRKIPKYLFOFHNLNSU 60
 DB 110 TLEMGDPJDRSANGQGSANSYAKMALSSVGSALAVIREQPDVYLNHNINSU 169
 OY 61 DRIEDKTPP 70
 DB 170 ERTFAKAP 179

RESULT 12

US-08-838-151A-6
 Sequence 6; Application US/08838151A

GENERAL INFORMATION:
 APPLICANT: Stout, John T
 APPLICANT: Liu, Hang T
 APPLICANT: Maxwell, Douglas
 APPLICANT: Ahlquist, Paul
 APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 NUMBER OF INVENTION: 63
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Rocky, Milanow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 05/08/838.151A

CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 361 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-838-151A-6

Query Match 60.8%, Score 220; DB 4; Length 361;
 Best Local Similarity 57.1%; Pred. NO. 1.7e-20;
 Matches 40; Conservative 16; Mismatches 14; Indels 0; Gaps 0;
 OY 1 TLWGEFVQAGSANGCOTSNDAAEALMASSKEAQLIRKIPKYLFOFHNLNSU 60
 DB 110 TLEMGDPJDRSANGQGSANSYAKMALSSVGSALAVIREQPDVYLNHNINSU 169
 OY 61 DRIEDKTPP 70
 DB 170 ERTFAKAP 179

RESULT 13

US-08-838-151A-8
 Sequence 8; Application US/08838151A

GENERAL INFORMATION:
 APPLICANT: Stout, John T
 APPLICANT: Liu, Hang T
 APPLICANT: Maxwell, Douglas
 APPLICANT: Ahlquist, Paul
 APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 NUMBER OF INVENTION: 63
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Rocky, Milanow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 05/08/838.151A

CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 361 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-838-151A-8

Query Match 60.8%, Score 220; DB 4; Length 361;
 Best Local Similarity 57.1%; Pred. NO. 1.7e-20;
 Matches 40; Conservative 16; Mismatches 14; Indels 0; Gaps 0;
 OY 1 TLWGEFVQAGSANGCOTSNDAAEALMASSKEAQLIRKIPKYLFOFHNLNSU 60
 DB 110 TLEMGDPJDRSANGQGSANSYAKMALSSVGSALAVIREQPDVYLNHNINSU 169
 OY 61 DRIEDKTPP 70
 DB 170 ERTFAKAP 179

RESULT 14

US-08-838-151A-24
 Sequence 24; Application US/08838151A

PATENT NO. 6291743
 GENERAL INFORMATION:
 APPLICANT: Stout, John T
 APPLICANT: Liu, Hang T
 APPLICANT: Maxwell, Douglas
 APPLICANT: Ahlquist, Paul
 APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 NUMBER OF INVENTION: 63
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Rocky, M11namow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838,151A
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5600
 TELEFAX: 312-616-5600
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 357 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-838-151A-24

Query Match 57.2% Score 207; DB 4; Length 357;
 Best Local Similarity 65.6%; Pred. No. 7.9e-19;

Matches 40; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 4 MEEFYVAGRSAGCGCOTSDAAAEALNASSKEEALQIIRKTEPKYLPQFINLNSNDRI 63

DB 111 FVSGIDGRSHRGGQGDNDVAYAFALNASSKEEALNILEKNAKQYILDQFINLNSNDRI 170

QY 64 F 64

DB 171 F 171

RESUME 15
 US-08-838-151A-27
 Sequence 27, Application US/08838151A
 Patent No. 6291743
 GENERAL INFORMATION:
 APPLICANT: Stoult, John T
 APPLICANT: Ewu, Hang T
 APPLICANT: Maxwell, Douglas
 APPLICANT: Margulies, Paul
 APPLICANT: Hwang, Isidor
 TITLE OF INVENTION: Transgenic Plants Expressing Geminitovirus
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Rocky, M11namow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838,151A
 FILING DATE:
 CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5600
 TELEFAX: 312-616-5600
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 357 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-838-151A-27

Query Match 57.2% Score 207; DB 4; Length 357;
 Best Local Similarity 65.6%; Pred. No. 7.9e-19;

Matches 40; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 4 MEEFYVAGRSAGCGCOTSDAAAEALNASSKEEALQIIRKTEPKYLPQFINLNSNDRI 63

DB 111 FVSGIDGRSHRGGQGDNDVAYAFALNASSKEEALNILEKNAKQYILDQFINLNSNDRI 170

QY 64 F 64

DB 171 F 171

Search completed: January 3, 2002, 15:38:51
 Job time: 228 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 3, 2002, 15:37.38 ; Search time 144.17 Seconds
(without alignments)
35.965 Million cell updates/sec

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Title:      US-09-289-346A-10
Perfect score: 364
Sequence:   1 TLVAGEQYVDGSAAGGCGT.....FGFINLNSLDRIPDKTPPEP 70
Scoring table:
BLOSUM62

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Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%

Database :

1:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1980.DAT*</i>
2:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1981.DAT*</i>
3:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1982.DAT*</i>
4:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1983.DAT*</i>
5:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1984.DAT*</i>
6:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1985.DAT*</i>
7:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1986.DAT*</i>
8:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1987.DAT*</i>
9:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1988.DAT*</i>
10:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1989.DAT*</i>
11:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1990.DAT*</i>
12:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1991.DAT*</i>
13:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1992.DAT*</i>
14:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1993.DAT*</i>
15:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1994.DAT*</i>
16:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1995.DAT*</i>
17:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1997.DAT*</i>
18:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1999.DAT*</i>
19:	<i>S1D58/sgcdat4/geneseq/geneseq/AA1999.DAT*</i>
20:	<i>S1D58/sgcdat4/geneseq/geneseq/AA2000.DAT*</i>
21:	<i>S1D58/sgcdat4/geneseq/geneseq/AA2000.DAT*</i>
22:	<i>S1D58/sgcdat4/geneseq/geneseq/AA2001.DAT*</i>

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	364	100	70	AA116566	Protein
2	349	95.9	70	AA116577	Peptide
3	340	95.9	356	AA116587	Amino acid sequenc
4	341	93.7	70	AA116583	Mutant peptide des
5	338	92.9	70	AA116588	Mutant peptide des
6	336	92.6	70	AA116592	Mutant peptide des
7	336	92.6	70	AA116592	Mutant peptide des
8	335	92.0	70	AA116590	Mutant peptide des
9	334	91.8	70	AA116578	Mutant peptide des
10	333	91.5	70	AA116589	Mutant peptide des
11	331	90.9	70	AA116580	Mutant peptide des

[illegible]

ALIGNMENTS

RESULT

ID AAE18686 standard; peptide; 70 AA

AC AAB18686;

DT 22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.

KW GemIn1 virus; replication protein; Rep protein; ALL; transgenic plant;

emphatic
XX
XX
XX

XX Tomato golden mosaic virus

FT	Misc-difference	24
en	key	location/

FT	Misc-difference	25	7/1000	with type

FT	Misc-difference	26

XX

XX

[illegible]

XX

PR 09-APR-1999; 99US-0289346

PA (UYNC-) UNIV-NORTH CAROLINA STATE

comprise a nucleic acid construct containing a nucleic acid sequence
encoding a mutant A11 protein with a mutation in the Rb binding region

Disclosure: Page 47-48; 73pp; English.

The present sequence represents a geminivirus replication (Rep)
protein, which is also known as A11. A11 binds double-stranded DNA,
catalyzes cleavage and ligation of single-stranded DNA, and interacts
with other viral and host proteins. Mutants of the A11 protein are used
to produce transgenic plants. The mutation in A11 is present in a
ribosome binding region, and expression of mutant A11 protein imparts
increased resistance to geminivirus infection in the plant. Mutant A11
proteins are used to produce transgenic plants. The mutation in A11 is
present in a ribosome binding region, and expression of mutant A11
protein imparts increased resistance to geminivirus infection in the
plant. Mutant A11 proteins are used to produce transgenic plants. The
mutation in A11 is present in a ribosome binding region, and expression
of mutant A11 protein imparts increased resistance to geminivirus
infection in the plant. Mutant A11 proteins are used to produce
transgenic plants. The mutation in A11 is present in a ribosome binding
region, and expression of mutant A11 protein imparts increased
resistance to geminivirus infection in the plant. Mutant A11 proteins
are used to produce transgenic plants. The mutation in A11 is present
in a ribosome binding region, and expression of mutant A11 protein
imparts increased resistance to geminivirus infection in the plant.
Mutant A11 proteins are used to produce transgenic plants. The
mutation in A11 is present in a ribosome binding region, and
expression of mutant A11 protein imparts increased resistance to
geminivirus infection in the plant. Mutant A11 proteins are used to
produce transgenic plants. The mutation in A11 is present in a
ribosome binding region, and expression of mutant A11 protein
imparts increased resistance to geminivirus infection in the plant.

Sequence 356 AA:

Query Match 95.9%; Score 349; DB 21; Length 356;
Best Local Similarity 95.7%; Pred. No. 4, 9e-36;
Matches 67; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 TLWGPFGVDRSANGCGTNSDILLPLANSSKPEALDIIIRKXIPKXYIROPFNINSN 60
|||||
DB 110 TLWGEIQRVGRARAGCGTNSDILANSSKEALIIIRKXIPKXYIROPFNINSN 169

OY 61 DRIEFGKTPRP 70
|||||
DB 170 dritakrpep 179

RESULT 4

AAB18685
ID AAB18685 standard; peptide: 70 AA.

XX AAB18685:

XX 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.

XX Geminivirus; replication protein; Rep protein; A11; transgenic plant;
ribosome binding region; resistance; geminivirus infection.

XX Synthetic;
XX tomato golden mosaic virus.

XX Key Location/Qualifiers

XX MISC-difference 10 /note="Wild type residue replaced with Ala"

XX MO200054573-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000MO-0806759.

XX 18-MAR-1999; 990US-0125004.

XX 09-APR-1999; 990US-0289346.

XX (UNNC-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.
XX Transgenic plants with increased resistance to geminivirus infection

comprise a nucleic acid construct containing a nucleic acid sequence
encoding a mutant A11 protein with a mutation in the Rb binding region

Claim 53; Page 46; 73pp; English.

The present sequence represents a mutant peptide, derived from a
geminivirus replication (Rep) protein, also known as A11. A11 binds
double-stranded DNA, catalyzes cleavage and ligation of single-stranded
DNA, and interacts with other viral and host proteins. Mutants of the A11
protein are used to produce transgenic plants. The mutation in A11 is
present in a ribosome binding region, and expression of mutant A11
protein imparts increased resistance to geminivirus infection in the
plant. Mutant A11 proteins are used to produce transgenic plants. The
mutation in A11 is present in a ribosome binding region, and expression
of mutant A11 protein imparts increased resistance to geminivirus
infection in the plant. Mutant A11 proteins are used to produce
transgenic plants. The mutation in A11 is present in a ribosome binding
region, and expression of mutant A11 protein imparts increased
resistance to geminivirus infection in the plant. Mutant A11 proteins
are used to produce transgenic plants. The mutation in A11 is present
in a ribosome binding region, and expression of mutant A11 protein
imparts increased resistance to geminivirus infection in the plant.
Mutant A11 proteins are used to produce transgenic plants. The
mutation in A11 is present in a ribosome binding region, and
expression of mutant A11 protein imparts increased resistance to
geminivirus infection in the plant. Mutant A11 proteins are used to
produce transgenic plants. The mutation in A11 is present in a
ribosome binding region, and expression of mutant A11 protein
imparts increased resistance to geminivirus infection in the plant.

Sequence 70 AA:

Query Match 93.7%; Score 341; DB 21; Length 70;
Best Local Similarity 94.3%; Pred. No. 6, 5e-36;
Matches 66; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TLWGPFGVDRSANGCGTNSDILLPLANSSKPEALDIIIRKXIPKXYIROPFNINSN 60
|||||
DB 1 TLWGEIQRVGRARAGCGTNSDILANSSKEALIIIRKXIPKXYIROPFNINSN 169

OY 61 DRIEFGKTPRP 70
|||||
DB 61 dritakrpep 70

RESULT 5

AAB18688
ID AAB18688 standard; peptide: 70 AA.

XX AAB18688:

XX 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.

XX Geminivirus; replication protein; Rep protein; A11; transgenic plant;
ribosome binding region; resistance; geminivirus infection.

XX Synthetic;
XX tomato golden mosaic virus.

XX Key Location/Qualifiers

XX MISC-difference 19 /note="Wild type residue replaced with Ala"

XX MISC-difference 20 /note="Wild type residue replaced with Ala"

XX MO200054573-A1.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000MO-0806759.

XX 18-MAR-1999; 990US-0125004.

XX 09-APR-1999; 990US-0289346.

XX (UNNC-) UNIV NORTH CAROLINA STATE.

XX Hanley-Bowdoin L, Orozco BM, Kong L;

XX WPI; 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 encoding a mutant A11 protein with a mutation in the Rb binding region
 XX
 XX
 PS Disclosure: Page 48: 73pp: English.

XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as A11. A11 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the A11
 CC protein are used to produce transgenic plants. The mutation in A11
 CC present in a ribosome binding region, and expression of mutant A11
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant A11 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to geminiviruses such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 CC
 XX Sequence 70 AA:

Query Match 92.9% Score 388; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 5e-35;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TLVWGEFQVDSRSKRGCGTSDLLLEALNASSKEEALQIRKIPKRYLFGPHNLSNL 60
 DB 1 FLVWGEIqydgtrsgygcusdaaeealnasskeeeqlirfkipekylfgthmnsnl 60
 OY 61 DRIFFKPTPEP 70
 DB 61 drrffakcpap 70

RESULT 6
 AAB18692 standard; peptide: 70 AA.
 AAB18692:

22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
 XX Geminivirus: replication protein; Rep protein; A11; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 OS Synthetic.
 XX Tomato golden mosaic virus.

XX Key Location/Qualifiers
 FT MISC-difference 66 /note= "Wild type residue replaced with Ala"
 FT MISC-difference 69 /note= "Wild type residue replaced with Ala"
 FT MISC-difference 69 /note= "Wild type residue replaced with Ala"
 PN WO200054573-A1.
 PD 21-SEP-2000.
 XX 15-MAR-2000: 2000MO-US06759.
 XX 18-MAR-1999: 99US-0125004.
 PR 09-APR-1999: 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA Hanley-Bowdoin L, Orozco BM, Kong L,

XX WPI: 2000-618851/59.
 DR
 XX Transgenic plants with increased resistance to geminivirus infection
 PT comprise a nucleic acid construct containing a nucleic acid sequence
 encoding a mutant A11 protein with a mutation in the Rb binding region
 XX
 XX
 PS Disclosure: Page 50: 73pp: English.

XX The present sequence represents a mutant peptide, derived from a
 CC geminivirus replication (Rep) protein, also known as A11. A11 binds
 CC double-stranded DNA, catalyzes cleavage and ligation of single-stranded
 CC DNA, and interacts with other viral and host proteins. Mutants of the A11
 CC protein are used to produce transgenic plants. The mutation in A11
 CC present in a ribosome binding region, and expression of mutant A11
 CC protein imparts increased resistance to geminivirus infection in the
 CC plant. Mutant A11 proteins are useful for producing plants having
 CC increased resistance or reduced sensitivity to geminiviruses such as
 CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
 CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian
 CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
 CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
 CC virus, cotton leaf curl virus or beet curly top virus.
 CC
 XX Sequence 70 AA:

Query Match 92.6% Score 317; DB 21; Length 70;
 Best Local Similarity 92.9%; Pred. No. 2.1e-35;
 Matches 65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TLVWGEFQVDSRSKRGCGTSDLLLEALNASSKEEALQIRKIPKRYLFGPHNLSNL 60
 DB 1 FLVWGEIqydgtrsgygcusdaaeealnasskeeeqlirfkipekylfgthmnsnl 60
 OY 61 DRIFFKPTPEP 70
 DB 61 drrffakcpap 70

RESULT 7
 AAB18684 standard; peptide: 70 AA.
 AAB18684:

22-JAN-2001 (first entry)

DE Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.
 XX Geminivirus: replication protein; Rep protein; A11; transgenic plant;
 XX ribosome binding region; resistance; geminivirus infection.
 OS Synthetic.
 XX Tomato golden mosaic virus.

XX Key Location/Qualifiers
 FT MISC-difference 7 /note= "Wild type residue replaced with Ala"
 FT MISC-difference 8 /note= "Wild type residue replaced with Ala"
 FT MISC-difference 8 /note= "Wild type residue replaced with Ala"
 PN WO200054573-A1.
 PD 21-SEP-2000.
 XX 15-MAR-2000: 2000MO-US06759.
 XX 18-MAR-1999: 99US-0125004.
 PR 09-APR-1999: 99US-0289346.
 XX (UYNC-) UNIV NORTH CAROLINA STATE.
 PA Hanley-Bowdoin L, Orozco BM, Kong L,

XX	(UYN-C-) UNIV NORTH CAROLINA STATE.
PA	
PI	Hanley-Bowdoin L., Orozco BM, Kong L;
DR	WPI; 2000-61851/59.
XX	
PT	Transgenic plants with increased resistance to geminivirus infection
PT	comprise a nucleic acid construct containing a nucleic acid sequence
PT	encoding a mutant AII protein with a mutation in the Rd binding region
XX	
XX	Disclosure: Page 49; 73pp: English.
CC	The present sequence represents a mutant peptide, derived from a
CC	geminivirus replication (Rep) protein, also known as AII. AII binds
CC	double-stranded DNA, catalyses cleavage and ligation of single-stranded
CC	DNA, and interacts with other viral and host proteins. Mutants of the AII
CC	protein are used to produce transgenic plants. The mutation in AII is
CC	present in a ribosome binding region, and expression of mutant AII is
CC	pleiotropic, imparts increased resistance to geminiviruses having the
CC	same or similar regions as the AII protein. Transgenic plants having the
CC	AII mutation exhibit increased resistance to geminiviruses such as
CC	tomato yellow mosaic virus, tomato mottle virus, tomato yellow leaf curl
CC	virus, tomato leaf curl virus, African cassava mosaic virus, Indian
CC	cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
CC	virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper
CC	virus, cotton leaf curl virus or beet curly top virus.
XX	
XX	Sequence 70 AA:
SQ	
Query Match	92.0% Score 335; DB 21; Length 70;
Best Local Similarity	92.9%; Pred.No. 3; Be-35;
Matches	65; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY	1 TLVSGEVDNGSRAGGCGTSMNLTLEALMASSKEPALDITREKIPKPYFOEFNNLSNL 60
DB	1 TLLVGGGQVGSSTVGSGSDANAAAAAIAASAKSGLATREKPKNYIGDFNNML 60
OY	61 DLLEPKRPPR 70
DB	61 DLIETLKCPPEP 70
Db	61 dltetlkcppep 70
RESULT 9	
ID	AAI18678 standard; peptide: 70 AA.
AB18678	
AC	AAI18678:
DT	22-JAN-2001 (first entry)
XX	
KM	Mutant peptide derived from amino acids 110-179 of Rep (AII) protein.
KM	Ribosome virus; replication protein; Rep protein; AII; transgenic plant;
KM	ribosome binding region; resistance; geminivirus infection.
OS	Synthetic.
OS	Tomato golden mosaic virus.
XX	
FT	Key Location/Qualifiers
FT	Misc-difference 12 /note= "wild type residue replaced with Ala"
FT	Misc-difference 13 /note= "wild type residue replaced with Ala"
FT	Misc-difference 15 /note= "wild type residue replaced with Ala"
XX	
XX	MO2000054573-A1.
XD	21-SEP-2000.

FT XX /note= "wild type residue replaced with Ala"

FN W0200054573-A1.

FR 21-SEP-2000.

DP 15-MAR-2000: 2000MO-US06759.

XX 18-MAR-1999: 9905-0126004.

PR 09-APR-1999: 9905-0289346.

XX (UNC-) UNIV NORTH CAROLINA STATE.

PA Hanley-Bowdoin L, Orozco BM, Kong L;

DR WPI: 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence

PP encoding a mutant A11 protein with a mutation in the Rb binding region

XX

PS Claim 52, Page 43-44; 73pp: English.

CC The present sequence represents a mutant peptide, derived from a

CC geminivirus replication (Rep) protein, also known as A11. A11 binds

CC double-stranded DNA, catalyses cleavage and ligation of single-stranded

CC DNA, and interacts with other viral and host proteins. Mutants of the A11

CC protein are used to produce transgenic plants. The mutation in A11 is

CC present in a ribosome binding region, and expression of mutant A11

CC protein imparts increased resistance to geminivirus infection in the

CC plant. Mutant A11 proteins are useful for producing plants having

CC increased resistance or reduced sensitivity to a geminivirus such as

CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl

CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian

CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic

CC virus, cotton leaf curl virus or beet curly top virus.

CC virus, cotton leaf curl virus or beet curly top virus.

XX

SO Sequence 70 AA;

Query Match 80.9%, Score 331; DB 21; Length 70;

Best Local Similarity 91.4%; Pred. No. 1,2e-34;

Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 TLVGEFQVDRGARGCCGTSNDLLLEPLANSSKEPAQLIRKXIPKTLTGFPHNLSN; 60

DB 1 TLVGEFQVDRGARGCCGTSNDLLLEPLANSSKEPAQLIRKXIPKTLTGFPHNLSN; 60

OY 61 DRIPKTPPEP 70

DB 61 dritdtkp 70

DB 61 dritdtkp 70

RESULT 12

AAB18691

ID AAB18691 standard; peptide: 70 AA.

AC AAB18691:

XX 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.

XX Geminivirus; replication protein; Rep protein; A11; Transgenic plant;

XX ribosome binding region; resistance; geminivirus infection.

XX Synthetic.

OS Tomato golden mosaic virus.

XX

FN Key

MI Misc-difference 34

FT XX /note= "wild type residue replaced with Ala"

FN Misc-difference 35

FT /note= "wild type residue replaced with Ala"

FT Misc-difference 36

FT /note= "wild type residue replaced with Ala"

FN W0200054573-A1.

FR 21-SEP-2000.

DP 15-MAR-2000: 2000MO-US06759.

XX 18-MAR-1999: 9905-0126004.

PR 09-APR-1999: 9905-0289346.

XX (UNC-) UNIV NORTH CAROLINA STATE.

PA Hanley-Bowdoin L, Orozco BM, Kong L;

DR WPI: 2000-618851/59.

XX Transgenic plants with increased resistance to geminivirus infection

PT comprise a nucleic acid construct containing a nucleic acid sequence

PP encoding a mutant A11 protein with a mutation in the Rb binding region

XX

PS Disclosure: Page 49; 73pp: English.

CC The present sequence represents a mutant peptide, derived from a

CC geminivirus replication (Rep) protein, also known as A11. A11 binds

CC double-stranded DNA, catalyses cleavage and ligation of single-stranded

CC DNA, and interacts with other viral and host proteins. Mutants of the A11

CC protein are used to produce transgenic plants. The mutation in A11 is

CC present in a ribosome binding region, and expression of mutant A11

CC protein imparts increased resistance to geminivirus infection in the

CC plant. Mutant A11 proteins are useful for producing plants having

CC increased resistance or reduced sensitivity to a geminivirus such as

CC tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl

CC virus, tomato leaf curl virus, African cassava mosaic virus, Indian

CC cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic

CC virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper

CC virus, cotton leaf curl virus or beet curly top virus.

XX

SO Sequence 70 AA;

Query Match 90.9%, Score 331; DB 21; Length 70;

Best Local Similarity 91.4%; Pred. No. 1,2e-34;

Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 TLVGEFQVDRGARGCCGTSNDLLLEPLANSSKEPAQLIRKXIPKTLTGFPHNLSN; 60

DB 1 TLVGEFQVDRGARGCCGTSNDLLLEPLANSSKEPAQLIRKXIPKTLTGFPHNLSN; 60

OY 61 DRIPKTPPEP 70

DB 61 dritdtkp 70

DB 61 dritdtkp 70

RESULT 13

AAB18681

ID AAB18681 standard; peptide: 70 AA.

AC AAB18681:

XX 22-JAN-2001 (first entry)

XX Mutant peptide derived from amino acids 110-179 of Rep (A11) protein.

XX Geminivirus; replication protein; Rep protein; A11; Transgenic plant;

XX ribosome binding region; resistance; geminivirus infection.

XX Synthetic.

OS

KM	Geminivirus; replication protein; Rep protein; ALI; Transgenic plant;
KL	Ribosome binding region; resistance; geminivirus infection.
OS	Synthetic.
XX	Tomato golden mosaic virus.
FT	Key Location/Qualifiers
FT	Misc-difference 59 /note= "wild type residue replaced with Ala"
FT	Misc-difference 61 /note= "wild type residue replaced with Ala"
FT	Misc-difference 62 /note= "wild type residue replaced with Ala"
PN	MO200054573.AL.
PD	21-SEP-2000.
PF	15-MAR-2000: 2000MO-US06759.
XP	18-MAR-1999: 980US-0125004.
PR	05-MAR-1999: 990US-0269346.
PA	(UYNC-) UNIV NORTH CAROLINA STATE.
PI	Hanley-Bowdoin L., Orozco BW, Kong L:
DR	WPI: 2000-618651/59.
CC	Transgenic plants with increased resistance to geminivirus infection comprise a new class of transgenic plants. A mutation in the Rb protein encoding a mutant ALI protein with a mutation in the Rb binding region
PT	xx
PT	xx
PS	Claim 53: Page 45: 73pp: English.
XX	The present sequence represents a mutant peptide, derived from a geminivirus replication (Rep) protein, also known as ALI. ALI binds to the Rb protein of geminiviruses. The amino acid residues of the Rb DNA, and interacts with other viral and host proteins within the ALI protein are used to produce transgenic plants. The mutation in ALI is present in a ribosome binding region, and expression of mutant ALI protein imparts increased resistance to geminivirus infection in the plant. Mutant ALI proteins are useful for producing plants having increased resistance or reduced sensitivity to a geminivirus such as tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic virus, bean dwarf mosaic virus, squash leaf curl virus, Texas pepper virus, cotton leaf curl virus or beet curly top virus.
CC	virus, cotton leaf curl virus or beet curly top virus.
CC	xx
CC	Sequence 70 AA:
QY	Query Match: 88 88. Score 327. DB 21: Length 70: Best local similarity 91.48. Pfam No. 3, 9e-34. Matches 64: Conservative 0: Mismatches 6: Indels 0: Gaps 0
QY	1 TLVMSRFDVGSMKRCGGCSDNLLLEALNMSKKEALITREKTPERYLPFGFINNSLT 60 Db 1 TLVAGFVDGVSIRSGCGTINDAAEAALNASSKEELGLIREKIPKYLTFGINNAEL 60 QY 61 DREFKKPEP 70 Db 61 AAILDKPEP 70 _
RESULT 15	
AAAB18682	
ID	AAAB18682 standard; peptide: 70 AA.
XX	
XX	AAAB18682.

Job time: 155 sec

```

DN 22-JAN-2001 (first entry)
XX
DE Mutant peptide derived from amino acids 110-179 of Rep (AL1) protein.
XX
KM Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
XX Ribosome binding region; resistance; geminivirus infection.
XX Synthetic.
OS Tomato golden mosaic virus.
XX
FH Key Location/Qualifiers
FH Misc-difference 52
FH Misc-difference /note= "wild type residue replaced with Ala"
FH Misc-difference /note= "wild type residue replaced with Ala"
FH Misc-difference 55
FH Misc-difference /note= "wild type residue replaced with Ala"
XX
PN MO200054573-AL.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000: 2000MO-0806759.
XX
XX 18-MAR-1999: 9905-0125004.
XX 09-APR-1999: 9905-0289346.
XX
XX (UYNC-) ONLY NORTH CAROLINA STATE.
XX
XX Hanley-Bowdoin L, Orozco BM, Kong LT.
XX WPI: 2000-618851/59.
XX
XX Transgenic plants with increased resistance to geminivirus infection
XX comprise a nucleic acid construct containing a nucleic acid sequence
XX encoding a mutant AL1 protein with a mutation in the Rb binding region
XX
XX
XX Claim 53; Page 44-45; 73pp: English.
XX
XX The present sequence represents a mutant peptide, derived from a
XX geminivirus replication (Rep) protein, also known as AL1. AL1 binds
XX double-stranded DNA, catalyses cleavage and ligation of single-stranded
XX DNA, and interacts with other viral and host proteins. Mutants of the AL1
XX protein have been identified that are resistant to geminivirus infection.
XX present in a ribosome binding region and expression of mutant AL1
XX protein imparts increased resistance to geminivirus infection in the
XX plant. Mutant AL1 proteins are useful for producing plants having
XX increased resistance or reduced sensitivity to a geminivirus such as
XX tomato golden mosaic virus, tomato mottle virus, tomato yellow leaf curl
XX virus, tomato leaf curl virus, African cassava mosaic virus, Indian
XX cassava mosaic virus, potato yellow mosaic virus, bean golden mosaic
XX virus, bean yellow mosaic virus, bean yellow vein virus, Texas pepper
XX virus, cotton leaf curl virus or beet curly top virus.
XX
XX Sequence 70 AA:

```

```

Query Match 89.3%; Score 325; DB 21; Length 70;
Best Local Similarity 91.4%; Pred. NO. 76-34;
Matches 64; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY 1 TLVGEFQDQSGANGCQTSNDLLLEALNASKKEALQITREKTPKRYDQPHNINSL 60
DB 1 TLVGEFQDQSGANGCQTSNDLLLEALNASKKEALQITREKTPKRYDQPHNINSL 60
OY 61 DRIEDKTPPEP 70
DB 61 DRIEDKTPPEP 70

```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 3, 2002, 15:40:12 : Search time 72.79 seconds
(without alignments)
73.255 Million cell updates/sec

Title: US-09-289-346A-10

Sequence: 1 TWYGEFVDNSRARGCQCT.....RQPINNSNLDRIETKPEP 70

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	349	95.9	352.1	OOCCV1
2	249	68.4	361.1	AAI protein - toma
3	242	66.5	358.2	AAI protein - toma
4	235	64.6	362.1	hypothetical prote
5	228	62.6	349.2	AAI protein - toma
6	228	62.6	349.2	AAI protein - toma
7	228	62.6	349.2	AAI protein - toma
8	221	60.7	359.2	AAI protein - toma
9	220	60.4	355.1	AAI protein - toma
10	218	59.9	351.2	AAI protein - toma
11	217	59.6	358.1	AAI protein - toma
12	217	59.6	358.1	AAI protein - toma
13	215	57.1	365.2	AAI protein - toma
14	213	56.6	357.1	AAI protein - toma
15	206	56.6	357.1	AAI protein - toma
16	206	56.6	357.1	AAI protein - toma
17	125	34.3	347.1	AAI protein - toma
18	64	17.6	587.1	AAI protein - toma
19	63.5	17.4	1229.1	AAI protein - toma
20	63	17.3	343.2	AAI protein - toma
21	62	17.0	343.2	AAI protein - toma
22	62	17.0	343.2	AAI protein - toma
23	62	17.0	343.2	AAI protein - toma
24	62	17.0	343.2	AAI protein - toma
25	61.5	16.9	333.2	AAI protein - toma
26	61.5	16.9	333.2	AAI protein - toma
27	61.5	16.9	333.2	AAI protein - toma
28	61	16.8	333.2	AAI protein - toma
29	61	16.8	333.2	AAI protein - toma

30	61	16.8	763.2	JH0329
31	61	16.8	863.2	CJ8252
32	60.5	16.6	447.2	T12544
33	60.5	16.6	1792.2	T13939
34	60	16.5	247.2	H86844
35	60	16.5	719.2	T13939
36	60	16.5	759.2	T46889
37	60	16.5	1117.2	T14891
38	60	16.5	1265.2	T02131
39	59.5	16.3	79.1	A58656
40	59.5	16.3	210.2	T05021
41	59.5	16.3	388.2	C69196
42	59.5	16.3	388.2	C69196
43	59.5	16.3	388.2	C69196
44	59	16.2	215.2	G85710
45	59	16.2	373.2	A71690

ALIGNMENTS

RESULT 1
OOCCV1
AAI protein - tomato golden mosaic virus
C:Species: Tomato golden mosaic virus
A:Note: host Nicotiana sp. (tobacco)
C:Date: 28-Aug-1985 #sequence revision 28-Aug-1985 #text change 08-Apr-1994
C:Accession: A04170
E:111 TWYGEFVDNSRARGCQCTSDMAAEALNASKSEKALQIETKPEKLYFOHNLNSL 170
F:111 TWYGEFVDNSRARGCQCTSDMAAEALNASKSEKALQIETKPEKLYFOHNLNSL 170
P:111 TWYGEFVDNSRARGCQCTSDMAAEALNASKSEKALQIETKPEKLYFOHNLNSL 170
A:Title: Complete nucleotide sequence of the infectious cloned DNA components of tomato golden mosaic virus
A:Reference number: A04153
A:Accession: A04170
A:Molecule type: DNA
A:Residues: 1-352 <HAM>
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A and DNA B.
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus AAI protein

Query Match
Best Local Similarity 95.9%, Score 349, DB 1, Length 352:
Matches 0/7, Conservative 0/7, Mismatches 3/7, Indels 0/7, Gaps 0/7

0/ 1 TWYGEFVDNSRARGCQCTSDMAAEALNASKSEKALQIETKPEKLYFOHNLNSL 60
DB 111 TWYGEFVDNSRARGCQCTSDMAAEALNASKSEKALQIETKPEKLYFOHNLNSL 170

0/ 61 DRIETKPEP 70
DB 171 DRIETKPEP 180

RESULT 2
OOCCV1
AAI protein - potato yellow mosaic virus (isolate Venezuela)
C:Species: Potato yellow mosaic virus
C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 16-Jun-2000
C:Accession: J00361
R:Goulet, R.H.A.; Coffin, R.S.; Roberts, E.J.F.; Hamilton, W.D.O.
J:Gen. Virol. 72, 1515-1520, 1991
A:Title: The nucleotide sequence of the infectious cloned DNA components of potato yellow mosaic virus
A:Reference number: J00362; NCBI:J0311403
A:Accession: J00361
A:Map position: not shown
A:Molecule type: DNA
A:Residues: 1-361 <COU>
C:Cross-references: GB:J000940; NID:9222458; PIDN:BA00782.1; PID:9222459
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus AAI protein

```

Query Match      68.4%; Score 249; DB 1; Length 361;
Best Local Similarity 68.7%; Pred. No. 3.1e-20;
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

OY 1 T1WNGEFOVDRSARGCQTSNDLLLEALNASSKEEAOLIIREKIPKYLQFPHNLSNTL 60
    11:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 110 T1EMGCLFOIDRSARGCQOTVDMAAEALNMSQTEKAMKIIKEKLEFQVHNLSCNTL 169
    11:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 DRIEDKTPP 69
DB 170 DRIEMKAP 178

RESULT 3
507594
Hypothetical protein, 40.4k - cassava latent virus (Migerian isolate)
C:Species: cassava latent virus
C:Accession: J02300
C:Description: "Sequence, revision 07-Sep-1990 *text_change 20-Sep-1999
R:Morris, B.; Coates, L.; Lowe, S.; Richardson, K.; Eddy, P.
Nucleic Acids Res. 18, 197-198, 1990
A:Title: Nucleotide sequence of the infectious cloned DNA components of African cassava
A:Reference number: S07590; M01D:90174930
A:Accession: S07594
A:Status: translation not shown
A:Molecule type: DNA
A:Host: cassava
A:Cross-references: EMBL:X17095; NID:959371; P1DN:CA434953.1; P1D:959376
C:Genetics:
A:Map position: segment DN1
C:Superfamily: tomato golden mosaic virus A1 protein

Query Match      66.5%; Score 242; DB 2; Length 358;
Best Local Similarity 61.4%; Pred. No. 1.9e-19;
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

OY 1 T1WNGEFOVDRSARGCQTSNDLLLEALNASSKEEAOLIIREKIPKYLQFPHNLSNTL 60
    11:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 109 T1EMGCLFOIDRSARGCQOSANDVAKALNASSKSEALNLTRELVADVLOFPHNLSNTL 168
    11:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 DRIEDKTPP 70
DB 169 DRIEDKTPP 178

RESULT 4
501887
A1 protein - tomato yellow leaf curl virus (strain Australia)
N:Alternate names: Cf protein
C:Species: tomato yellow leaf curl virus
C:Date: 17-Feb-1994 *sequence_revision 17-Feb-1994 *text_change 07-May-1999
C:Accession: J01887
R:Day, I.B.; Ridgen, J.E.; Krake, L.R.; Mullineaux, P.M.; Bezanin, M.A.
J. Gen. Virol. 74, 147-151, 1993
A:Title: Nucleotide sequence and genome organization of tomato leaf curl geminivirus.
A:Accession: J01887
A:Reference number: S01885; M01D:9315778
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-362 <DRY>
A:Cross-references: GB:S53251
C:Superfamily: tomato golden mosaic virus A1 protein

Query Match      64.6%; Score 235; DB 1; Length 362;
Best Local Similarity 54.1%; Pred. No. 1.1e-18;
Matches 46; Conservative 9; Mismatches 14; Indels 16; Gaps 1;

OY 1 T1WNGEFOVDRSARGCQTSNDLLLEALNASSKEEAOLIIREKIPKYLQFPHNLSNTL 60
    11:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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DB 110 T1EMGCLFOIDRSARGCQOSANDVAKALNASSKSEALNLTRELVADVLOFPHNLSNTL 169
OY 61 DRI-----FDKTPP 69
    11:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 170 DRIETPPELVYSPFLSSFDVAP 194

RESULT 5
J02300
replicase - pepper huasteco virus (component A)
N:Alternate names: ORF A1 protein
C:Species: pepper huasteco virus
C:Accession: J02300
C:Description: "Sequence, revision 14-Jul-1994 *text_change 20-Sep-1999
R:Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Herrera-Estrella, L.; Rivera-Bustamante,
J. Gen. Virol. 74, 2225-2231, 1993
A:Title: Complete nucleotide of pepper huasteco virus: Analysis and comparison with b
A:Reference number: J02299; M01D:94015007
A:Accession: J02300
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364
A:Cross-references: GB:X70418; NID:961023; P1DN:CA449856.1; P1D:961025
C:Superfamily: tomato golden mosaic virus A1 protein

Query Match      62.6%; Score 228; DB 2; Length 349;
Best Local Similarity 60.0%; Pred. No. 6.7e-18;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

OY 1 T1WNGEFOVDRSARGCQTSNDLLLEALNASSKEEAOLIIREKIPKYLQFPHNLSNTL 60
    11:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 110 T1EMGCLFOIDRSARGCQOSANDVAKALNASSAEBAOLIIKEEOPHFFLOPHNVSNA 169
    11:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 DRIEDKTPP 70
DB 170 NRIIDQTPPP 179

RESULT 6
S31875
A1 protein - pepper rizado amarillo virus
C:Species: pepper rizado amarillo virus
C:Accession: J03187
C:Description: "Sequence, revision 26-May-1995 *text_change 20-Sep-1999
R:Torres-Pacheco, I.; Garzon-Tiznado, J.A.; Jimenez, B.; Herrera-Estrella, L.; Rivera
submitted to the EMU Data Library, February 1993
A:Description: Complete nucleotide sequence of pepper huasteco virus: analysis and co
A:Reference number: S31872
A:Accession: S31875
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349
A:Cross-references: EMBL:X70418; NID:961023; P1DN:CA449856.1; P1D:961025
A:Note: the source is designated as pepper huasteco virus
C:Superfamily: tomato golden mosaic virus A1 protein

Query Match      62.6%; Score 228; DB 2; Length 349;
Best Local Similarity 60.0%; Pred. No. 6.7e-18;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

OY 1 T1WNGEFOVDRSARGCQTSNDLLLEALNASSKEEAOLIIREKIPKYLQFPHNLSNTL 60
    11:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 110 T1EMGCLFOIDRSARGCQOSANDVAKALNASSAEBAOLIIKEEOPHFFLOPHNVSNA 169
    11:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 DRIEDKTPP 70
DB 170 NRIIDQTPPP 179

RESULT 7
539211
gene Cf protein - tomato yellow leaf curl virus

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C:Species: tomato yellow leaf curl virus
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
 C:Accession: S39211
 R:Morris, E.; Roldán, R.; Acotto, G.; Moriones, E.
 A:Description: Tomato yellow leaf curl virus isolate from the
 A:Reference number: S39209
 A:Accession: S39211
 A>Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-359 <NCOR>
 A:Cross-references: EMBL:Z25751; NID:9433655; PIDN:CA81026.1; PID:9433658
 C:Superfamily: tomato golden mosaic virus A11 protein

Query Match 62.6%; Score 228; DB 2; Length 359;
 Best Local Similarity 59.4%; Pred. No. 6,9e-18;
 Matches 41; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

2 LAMGPDGNSARSGCCTSDLLLEAMSSKEEALQIREKIPKYLEFQFINLSND 61
 DB 111 LEMGPDGNSARSGCCTSDNDAVAKAINSGSEALDVIKELAPROYLIHNNISND 170

QY 62 RIFKPTPE 70
 DB 171 RYKVPPEP 179

RESULT 8
 S22593
 Hypothetical protein C4 - tomato yellow leaf curl virus
 C:Species: tomato yellow leaf curl virus
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Sep-1999
 C:Accession: S22593
 R:Morris, E.; Roldán, R.; Acotto, G.; Moriones, E.
 A:Description: Tomato yellow leaf curl virus isolate from the
 A:Reference number: S22588; MUID:92107660
 A:Accession: S22593
 A>Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-359 <NCOR>
 A:Cross-references: EMBL:X61153; NID:963211; PIDN:CA41466.1; PID:963217
 A:Superfamily: tomato golden mosaic virus A11 protein

Query Match 60.7%; Score 221; DB 2; Length 359;
 Best Local Similarity 56.5%; Pred. No. 4,2e-17;
 Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

2 LAMGPDGNSARSGCCTSDLLLEAMSSKEEALQIREKIPKYLEFQFINLSND 61
 DB 111 LEMGPDGNSARSGCCTSDNDAVAKAINSGSEALDVIKELAPROYLIHNNISND 170

QY 62 RIFKPTPE 70
 DB 171 RYKVPPEP 179

RESULT 9
 OOCVMI
 AV1 protein - abutilon mosaic virus (isolate West India)
 C:Species: abutilon mosaic virus
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 08-Apr-1994
 C:Accession: A36214
 R:Jensen, H.
 A:Description: The nucleotide sequence of the abutilon mosaic virus reveals prototypic
 A:Reference number: A36214; MUID:91020984
 A:Accession: A36214
 A:Molecule type: DNA
 A:Residues: 1-355 <FRI>

A:Cross-references: EMBL:X15983
 C:Genetics:
 A:Map position: segment A
 C:Superfamily: tomato golden mosaic virus A11 protein

Query Match 60.4%; Score 220; DB 1; Length 355;
 Best Local Similarity 58.6%; Pred. No. 5,4e-17;
 Matches 41; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

1 TLWGPVDSARSGCCTSDLLLEAMSSKEEALQIREKIPKYLEFQFINLSND 60
 DB 110 TLWGPVDSARSGCCTSDNDAVAKAINSGSEALDVIKELAPROYLIHNNISND 169

QY 61 DRIPKPTPE 70
 DB 170 ERIFKAPPEP 179

RESULT 10
 S20327
 A11 protein - Indian cassava mosaic virus
 N:Alternate names: replication-associated protein
 C:Species: Indian cassava mosaic virus
 C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 20-Sep-1999
 C:Accession: J03227; S35883
 R:Hong, Y.G.; Robinson, D.J.; Harrison, B.D.
 J:Gen. Virol. 74, 2437-2443, 1993
 A:Description: The nucleotide sequence for the occurrence of three distinct whitefly-t
 A:Reference number: J03226; MUID:94065670
 A:Accession: J03227
 A:Molecule type: DNA
 A:Residues: 1-351 <NON>
 A:Cross-references: EMBL:Z24758; NID:9395351; PIDN:CA80891.1; PID:9584046
 C:Superfamily: tomato golden mosaic virus A11 protein

Query Match 59.9%; Score 218; DB 2; Length 351;
 Best Local Similarity 61.2%; Pred. No. 8,9e-17;
 Matches 41; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

4 WEPVDSARSGCCTSDLLLEAMSSKEEALQIREKIPKYLEFQFINLSND 63
 DB 113 WGPVDSARSGCCTSDNDAVAKAINSGSEALQIREKIPKYLEFQFINLSND 172

QY 64 FPKPTPE 70
 DB 173 FTKPTPEP 179

RESULT 11
 S20327
 A11 protein - tomato mottle virus (isolate Florida)
 C:Species: tomato mottle virus
 C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 07-May-1999
 C:Accession: J01870
 R:Abouzaid, A.M.; Polston, J.E.; Hiebert, E.
 J:Gen. Virol. 73, 3225-3229, 1992
 A:Description: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated f
 A:Reference number: J01869; MUID:93107858
 A:Accession: J01870
 A>Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-358 <ABO>
 A:Cross-references: GB:114460
 C:Genetics:
 A:Map position: segment A
 C:Superfamily: tomato golden mosaic virus A11 protein

Query Match 59.6%; Score 217; DB 1; Length 358;
 Best Local Similarity 55.7%; Pred. No. 1,2e-16;
 Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

OY 1 TLWGEFQVDSRSGCGQTSNDLLLEALNASSKEBALQIREKIPKYLQFPHNLNSL 60
 Db 107 TLWGEFQVDSRSGCGQTSNDLLLEALNASSKEBALQIREKIPKYLQFPHNLNSL 166
 OY 61 DRIEFPKPP 70
 Db 167 ERIEFAKPEP 176

RESULT 12

A2: protein - beet curly top virus
 A1: protein - beet curly top virus
 C.Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 20-Sep-1999
 C.Accession: S58360
 R.Stanley, J.; Martham, P.G.; Callis, R.J.; Pinner, M.S.
 EMBL J. 5, 1761-1767, 1986
 A.Title: The nucleotide sequence of an infectious clone of the geminivirus beet curly top
 A.Reference number: S58360
 A.Description: Nucleotide sequence of an infectious clone of the geminivirus beet curly top
 A.Molecule type: DNA
 A.Status: preliminary
 A.Cross-references: GB:M42597; EMBL:X04144; NID:9210678; PID:AAA42751.1; PID:9210679
 C.Superfamily: tomato golden mosaic virus A1 protein

Query Match 59.6%; Score 217; DB 2; Length 385;
 Best Local Similarity 55.7%; Pred. No. 1,3e-16;
 Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

OY 1 TLWGEFQVDSRSGCGQTSNDLLLEALNASSKEBALQIREKIPKYLQFPHNLNSL 60
 Db 137 TLWGEFQVDSRSGCGQTSNDLLLEALNASSKEBALQIREKIPKYLQFPHNLNSL 196
 OY 61 DRIEFPKPP 70
 Db 197 OKIFORPPP 206

RESULT 13

A2: protein - tomato yellow leaf curl virus
 A1: protein - tomato yellow leaf curl virus
 C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
 C.Accession: S59235
 R.Crepel, S.; Norris, E.; Valira, A.; Bosco, D.; Accotto, G.
 Submitted to the EMBL Data Library, December 1993
 A.Description: A cloned DNA from a TILCV isolate from Sicily showing low infectivity.
 A.Reference number: S59235
 A.Description: A cloned DNA from a TILCV isolate from Sicily showing low infectivity.
 A.Molecule type: DNA
 A.Status: preliminary
 A.Cross-references: EMBL:Z28390; NID:91041671; PID:91334964
 C.Superfamily: tomato golden mosaic virus A1 protein

Query Match 59.1%; Score 215; DB 2; Length 359;
 Best Local Similarity 55.1%; Pred. No. 2e-16;
 Matches 38; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

OY 2 LWGEFQVDSRSGCGQTSNDLLLEALNASSKEBALQIREKIPKYLQFPHNLNSL 61
 Db 111 LWGEFQVDSRSGCGQTSNDLLLEALNASSKEBALQIREKIPKYLQFPHNLNSL 170
 OY 62 RIFDKTPEP 70
 Db 171 KFEQVPPAP 179

RESULT 14

S5985
 replication-associated protein C1 - tomato yellow leaf curl virus
 C.Species: tomato yellow leaf curl virus
 C.Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 20-Sep-1999
 C.Accession: S59850
 R.D. submitted to the EMBL Data Library, February 1995
 A.Description: Nucleotide sequences from tomato leaf curl viruses from different countries
 A.Reference number: S58346
 A.Accession: S59850
 A.Status: preliminary
 A.Molecule type: DNA
 A.Cross-references: EMBL:Z48182; NID:9944838; PID:CAA88229.1; PID:974211
 C.Superfamily: tomato golden mosaic virus A1 protein

Query Match 57.1%; Score 208; DB 2; Length 360;
 Best Local Similarity 51.1%; Pred. No. 1,2e-15;
 Matches 39; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

OY 4 WGEFQVDSRSGCGQTSNDLLLEALNASSKEBALQIREKIPKYLQFPHNLNSL 63
 Db 113 WGEFQVDSRSGCGQTSNDLLLEALNASSKEBALQIREKIPKYLQFPHNLNSL 172
 OY 64 FDKTPEP 69
 Db 173 FTSKPE 178

RESULT 15

A2: protein - tomato yellow leaf curl virus
 A1: protein - tomato yellow leaf curl virus
 C.Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
 C.Accession: D40779
 R.Navot, N.; Pichersky, E.; Zeidan, M.; Zamir, D.; Czosnek, H.
 A.Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a single
 A.Reference number: D40779
 A.Description: A cloned DNA from a TYLCV isolate from Israel showing low infectivity.
 A.Molecule type: DNA
 A.Status: preliminary
 A.Cross-references: GB:X15656; NID:962204; PID:CAA33688.1; PID:962207
 C.Superfamily: tomato golden mosaic virus A1 protein

Query Match 56.6%; Score 206; DB 1; Length 357;
 Best Local Similarity 61.9%; Pred. No. 2e-15;
 Matches 39; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

OY 4 WGEFQVDSRSGCGQTSNDLLLEALNASSKEBALQIREKIPKYLQFPHNLNSL 63
 Db 111 WGEFQVDSRSGCGQTSNDLLLEALNASSKEBALQIREKIPKYLQFPHNLNSL 170
 OY 64 F 64
 Db 171 F 171

Search completed: January 3, 2002, 15:40:12
 Job time: 308 sec

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RESULT 2
VAL1 PYMY

RESULT	2
VALL_PYMV	

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ID VAL1.PYMW STANDARD; PRT: 361 AA.
AC E27256;
DT 01-AUG-1992 (rel. 23, Created)
DE 01-AUG-1992 (rel. 23, Last annotation update)
AL1 PROTEIN
OC Potato yellow mosaic virus (Isolate Venezuela).
OS Viruses; ssDNA viruses; geminiviridae; Begomovirus.
OX NCBI_TaxID=10828;
RN 11;
RS SOURCE FROM N.A.
RX MEDLINE=9111403; PubMed=1856690;
RA "Coates R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.:
RT "The nucleotide sequence of the infectious cloned DNA components of
RT potato yellow mosaic virus."
RL J. Gen. Virol. 72:1515-1520(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC
CC EMBL: J00340; GOCVPT.
DR PIR: J00344; GOCVPT.
DR InterPro: IPR001191; Gemin1_AL1.
DR Pfam: PF00799; Gemin1_AL1; 1.
DR PRINTS: PR00227; GEMCONVAL1.
DR PRODOM: P000736; Gemin1_AL1; 1.
DR MEDLINE=9114930; PubMed=2216433;
NP_BIND: 222 229 AAP (POTENTIAL).
SEQUENCE 361 AA: 40850 MW: 5627433BP1264383 CRC64;

Query Match 66.4%; Score 249; DB 1; Length 361;
Best Local Similarity 66.7%; Pred. No. 2e-20;
Matches 46; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

OY 1 TLWGEFQVDSRSGRCGTSNDDLLFMANSSKRPGLQIRREKIPKRYQPPHNSN 60
DB 110 TLWGEFQVDSRSGRCGTSNDDLLFMANSSKRPGLQIRREKIPKRYQPPHNSN 169
OY 61 DRIEFTKTP 69
DB 170 DRIEFTKTP 178

RESULT 3
VAL1.CLV
ID VAL1.CLV STANDARD; PRT: 358 AA.
AC E14982;
DT 01-APR-1990 (rel. 14, Created)
DE 01-APR-1990 (rel. 14, Last sequence update)
AL1 PROTEIN
OC Cassava latent virus (strain West Kenya 844).
OS Viruses; ssDNA viruses; geminiviridae; Begomovirus.
OX NCBI_TaxID=10818;
RN 11;
RS SOURCE FROM N.A.
RX MEDLINE=9105403; PubMed=1856690;
RA "Coates R.H.A., Coffin R.S., Roberts E.J.F., Hamilton W.D.O.:
RT "The nucleotide sequence of the infectious cloned DNA components of
RT cassava latent virus."
RL J. Gen. Virol. 72:1515-1520(1991).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC
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CC
CC EMBL: J00340; GOCVPT.
DR PIR: J00344; GOCVPT.
DR InterPro: IPR001191; Gemin1_AL1.
DR Pfam: PF00799; Gemin1_AL1; 1.
DR PRINTS: PR00227; GEMCONVAL1.
DR PRODOM: P000736; Gemin1_AL1; 1.
DR MEDLINE=9114930; PubMed=2216433;
NP_BIND: 222 227 AAP (POTENTIAL).
SEQUENCE 358 AA: 40850 MW: 5627433BP1264383 CRC64;

Query Match 66.5%; Score 242; DB 1; Length 358;
Best Local Similarity 61.4%; Pred. No. 1.2e-19;
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

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CC
CC EMBL: J00340; GOCVPT.
DR PIR: J00344; GOCVPT.
DR InterPro: IPR001191; Gemin1_AL1.
DR Pfam: PF00799; Gemin1_AL1; 1.
DR PRINTS: PR00227; GEMCONVAL1.
DR PRODOM: P000736; Gemin1_AL1; 1.
DR MEDLINE=9114930; PubMed=2216433;
NP_BIND: 220 227 AAP (POTENTIAL).
SEQUENCE 358 AA: 40346 MW: 561738733BP25069 CRC64;

Query Match 66.5%; Score 242; DB 1; Length 358;
Best Local Similarity 61.4%; Pred. No. 1.2e-19;
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

OY 1 TLWGEFQVDSRSGRCGTSNDDLLFMANSSKRPGLQIRREKIPKRYQPPHNSN 60
DB 109 TLWGEFQVDSRSGRCGTSNDDLLFMANSSKRPGLQIRREKIPKRYQPPHNSN 168
OY 61 DRIEFTKTP 70
DB 169 DRIEFTKTP 178

RESULT 4
VAL1.CLV
ID VAL1.CLV STANDARD; PRT: 358 AA.
AC E14972;
DT 01-APR-1990 (rel. 14, Created)
DE 01-APR-1990 (rel. 14, Last sequence update)
AL1 PROTEIN
OC Cassava latent virus (strain Nigerian).
OS Viruses; ssDNA viruses; geminiviridae; Begomovirus.
OX NCBI_TaxID=10819;
RN 11;
RS SOURCE FROM N.A.
RX MEDLINE=90114930; PubMed=22108831;
RA "Mortimer B., Coates R., Lowe S., Richardson K., Eddy P.:
RT "Nucleotide sequence of the infectious cloned DNA components of
RT African cassava mosaic virus (Nigerian strain)."
RL Nucleic Acids Res. 18:197-198(1990).
CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
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CC
CC EMBL: X17095; CA343953.1.
DR PIR: S07594; S07594.
DR InterPro: IPR001191; Gemin1_AL1.
DR Pfam: PF00799; Gemin1_AL1; 1.
DR PRINTS: PR00227; GEMCONVAL1.
DR PRODOM: P000736; Gemin1_AL1; 1.
DR MEDLINE=9114930; PubMed=2216433;
NP_BIND: 220 227 AAP (POTENTIAL).
SEQUENCE 358 AA: 40435 MW: 10816580CB285DE2C CRC64;

Query Match 66.5%; Score 242; DB 1; Length 358;
Best Local Similarity 61.4%; Pred. No. 1.2e-19;
Matches 43; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

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OY 1 TWGGEFVDGSRGANGCQTSNDLLLEALMASSKEEALQIIREKIPKYLDFPHNLSN. 60
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 109 TWGCFOTIDGSRGANGSQSANRVAKALNSGKSEALNIRELPDPIQDFPHNLSN. 168
OY 61 DRITDQTPPEP 70
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 169 DRITDQTPPEP 178

RESULT 5
VAL1_TYICU STANDARD: PRT: 362 AA.
ID VAL1_TYICU
DR 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE AL1 PROTEIN (C1 PROTEIN).
CN C1.
CS Tomato yellow leaf curl virus (strain Australia) (TYLCV).
OC Viruses: SSRNA viruses; Geminiviridae; Begomovirus.
KW NCBI_TaxID=36447;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93139778; PubMed-8423446;
RA Dry I. B., Rigden J. E., Krake L. R., Mullineaux P. M., Rezaian M. A.;
RT Nucleotide sequence and genome organization of tomato leaf curl
    geminivirus. J. Virol. 67: 74:147-151(1993).
CF C1.
CF -1. SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
DR InterPro: IPR001191; Gemin1_AL1.
DR Pfam: PF00799; Gemin1_AL1.
DR PRINTS: PR00227; GEMCOATC1V1.
DR PRODOM: PD000736; Gemin1_AL1.
DR App-Binding: 221
NP BIND
SQ SEQUENCE 362 AA: 41197 MW: 343678484704098 CMC64;

Query Match 64.6%; Score 235; DB 1; Length 362;
Best Local Similarity 54.1%; Pred. No. 7, 2e-19;
Matches 46; Conservative 9; Mismatches 14; Indels 16; Gaps 1;

OY 1 TWGGEFVDGSRGANGCQTSNDLLLEALMASSKEEALQIIREKIPKYLDFPHNLSN. 60
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TWGCFOTIDGSRGANGSQSANRVAKALNSGKSEALNIRELPDPIQDFPHNLSN. 169
OY 61 DRI-----PDRPE 69
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 170 DRIPTPELEVYVPSFLSSSDRPE 194

RESULT 6
VAL1_PHVU STANDARD: PRT: 349 AA.
ID VAL1_PHVU
AC 006923;
DR 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 01-JUN-1994 (Rel. 29, Last annotation update)
DE AL1 PROTEIN.
CN AL1.
CS Pepper huasteco virus (PHV).
OC Viruses: ssRNA viruses; Geminiviridae; Begomovirus.
KW NCBI_TaxID=28349;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-94015007; PubMed-840944;
RA Torres-Pacheco I. F., Garzon-Tiznado J. A., Herrera-Estrella L.,
    Ryleva-Bustamante I. F.;
    Complete nucleotide sequence of pepper huasteco virus: analysis and
    comparison with bipartite geminiviruses. J.

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RL J. Gen. Virol. 74:2225-2231(1993).
CC -1. SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC CC
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    or send an email to license@isb-sib.ch).
CC CC
DR EMBL: X70416; CA49856.1;
DR PIR: S31875; S31875.
DR PIR: J02300; J02300.
DR Pfam: PF00799; Gemin1_AL1.
DR PRINTS: PR00227; GEMCOATC1V1.
DR PRODOM: PD000736; Gemin1_AL1.
DR App-Binding: 221
NP BIND
SQ SEQUENCE 349 AA: 39722 MW: 534676CD6370F4 CMC64;

Query Match 62.6%; Score 228; DB 1; Length 349;
Best Local Similarity 60.0%; Pred. No. 4, 2e-18;
Matches 42; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

OY 1 TWGGEFVDGSRGANGCQTSNDLLLEALMASSKEEALQIIREKIPKYLDFPHNLSN. 60
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 TWGCFOTIDGSRGANGSQSANRVAKALNSGKSEALNIRELPDPIQDFPHNLSN. 169
OY 61 DRITDQTPPEP 70
    1:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 170 NRITQTPPEP 179

RESULT 7
VAL1_TYICU STANDARD: PRT: 359 AA.
ID VAL1_TYICU
AC P38609;
DR 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 01-OCT-1994 (Rel. 30, Last annotation update)
DE AL1 PROTEIN (C1 PROTEIN).
CN C1.
CS Tomato yellow leaf curl virus (strain Murcia) (TYLCV).
OC Viruses: ssRNA viruses; Geminiviridae; Begomovirus.
KW NCBI_TaxID=37139;
RN [1]
RX MEDLINE-9425636; PubMed-8198442; Mortenow E.;
    High similarity among the tomato yellow leaf curl virus isolates
    from the west Mediterranean basin: the nucleotide sequence of an
    infectious clone from Spain. J.
    Arch. Virol. 135:165-170(1994).
CF -1. SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.
CC CC
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    or send an email to license@isb-sib.ch).
CC CC
DR EMBL: Z25751; CA81026.1;
DR PIR: S39211; S39211.
DR InterPro: IPR001191; Gemin1_AL1.
DR Pfam: PF00799; Gemin1_AL1.
DR PRINTS: PR00227; GEMCOATC1V1.

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ID      VAL1_TYLCM      STANDARD:      PRT:      359 AA.
CC      P27260.0
DT      01-AUG-1992 (Rel. 23, Created)
DT      01-AUG-1992 (Rel. 19, Last sequence update)
DT      01-AUG-1994 (Rel. 20, Last annotation update)
DE      A11 PROTEIN (CI, PROTEIN) .
GN      Cl.
OS      Tomato yellow leaf curl virus (strain Mornande) (TYLCV) .
OC      viruses; ssDNA viruses; Geminitviridae; Begomovirus.
NCBI_TaxID=10833.
CC      -1- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC      This ssDNA protein is responsible for inducing the collation
CC      between the Swiss Institute of Bioinformatics and the Publications
CC      of the European Bioinformatics Institute. There are no restrictions on
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      MDL: 359; 14666.1; -
CC      PRT: 32583; 52583
CC      InterPro: IPRO01191; Gemin1.A1
CC      Pfam: PF00799; Gemin1.A1.1
CC      PRINTS: PRO0227; GEMCONAT.A1.
CC      PRINTS: PRO0228; GEMCONAT.C1.V1.
CC      Prodom: PD00736; Gemin1.A1; 1.
CC      ARP-binding 320
CC      ARP-binding 320
CC      SPOUNCE 359 AA; 4.0733 MW; 97178407C33E87 CRC64;
SO      protein
Query Match 60.7%; Score 221; DB 1; Length 359;
Best Local Similarity 56.5%; Pred.No. 2,6e-17;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;
OY      2 TWCEPDGDSRANCCOTSTGDUULLKELAKSGKGLIHKYIKPKYDPQHWNSLD 61
DB      111 LKQGTFOIDRSRANGOOTANDVAKAKIMKSSQALDIYKELAPROYVIAFHINSLD 170
OY      62 RIEPKTEP 70
DB      171 KRYQVHPAP 179
RESULT 10
ID      VAL1_ABYW      STANDARD:      PRT:      355 AA.
CC      P21947.0
DT      01-AUG-1991 (Rel. 19, Created)
DT      01-AUG-1991 (Rel. 19, Last sequence update)
DT      01-JUN-1994 (Rel. 29, Last annotation update)
DE      A11 PROTEIN.
GN      AC1
OS      Abolition mosaic virus (Isolate West India) .
OC      viruses; ssDNA viruses; Geminitviridae; Begomovirus.
NCBI_TaxID=10816;
CC      -1- SIMILARITY: BELONGS TO GEMINIVIRUSES A11 PROTEIN FAMILY.
CC      This ssDNA protein is responsible for inducing the collation
CC      between the Swiss Institute of Bioinformatics and the Publications
CC      of the European Bioinformatics Institute. There are no restrictions on
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb.ch/announce/)
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      MDL: 355; 14666.1; -
CC      PRT: 32583; 52583
CC      InterPro: IPRO01191; Gemin1.A1
CC      Pfam: PF00799; Gemin1.A1.1
CC      PRINTS: PRO0227; GEMCONAT.A1.
CC      PRINTS: PRO0228; GEMCONAT.C1.V1.
CC      Prodom: PD00736; Gemin1.A1; 1.
CC      ARP-binding 320
CC      ARP-binding 320
CC      SPOUNCE 359 AA; 4.0733 MW; 97178407C33E87 CRC64;
SO      protein
Query Match 60.7%; Score 221; DB 1; Length 359;
Best Local Similarity 56.5%; Pred.No. 2,6e-17;
Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;
OY      2 TWCEPDGDSRANCCOTSTGDUULLKELAKSGKGLIHKYIKPKYDPQHWNSLD 61
DB      111 LKQGTFOIDRSRANGOOTANDVAKAKIMKSSQALDIYKELAPROYVIAFHINSLD 170
OY      62 RIEPKTEP 70
DB      171 KRYQVHPAP 179

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DR EMBL; X15983; -; NOT_ANNOTATED.CDS.
DR PIR; A36214; OOCV1.
DR InterPro; IPR001191; Gemin1_AL1.
DR Pfam; PF00759; Gemin1_AL1.
DR PRINTS; PR00227; GEMCOATL1.
DR PRINTS; PR00228; GEMCOATL1.
DR PRODOM; P000736; Gemin1_AL1.
KW ATP-binding.
KW NP_BIND.
SQ SEQUENCE 355 AA; 40257 MW; 16ACACAB63251E95 CRC64;

Query Match Best Local Similarity 60.4%; Score 220; DB 1; Length 355;
Matches 41; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

OY 1 TLWGEFVDGRSARGCCTNSDILLEFLVASSSEPALQIIRKIPKYLFOFHMLNSL 60
DB 110 TLKMEQFQIDGRSARGCCTNSDYNASVAKALNAGDVQSLMLKLEQPKDFVLOHNNHNSL 169
OY 61 DRIPTKPEP 70
DB 170 ERIFAKAP 179

RESULT 11
ID VAL1.TMOV STANDARD; PRT; 358 AA.
AC 006657;

DR 01-APR-1990 (Rel. 14, Created)
DR 01-APR-1990 (Rel. 14, Last sequence update)
DR 01-AUG-1992 (Rel. 23, Last annotation update)
DB AL1 PROTEIN (40.8 KDA PROTEIN).
CC bect curly top virus (BCTV).
CC OS viruses; ssDNA viruses; geminiviridae; Curtovirus.
CC NCBI_TaxID:10840;

RA Stanley J., Marham P.G., Callis R.J., Pinner M.S.;
RP "The nucleotide sequence of an infectious clone of the geminivirus
RP bect curly top virus."
RL EMBL J. 5:1761-1767(1986).
CC - SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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DR EMBL; X04144; -; NOT_ANNOTATED.CDS.
DR InterPro; IPR001191; Gemin1_AL1.
DR Pfam; PF00759; Gemin1_AL1.
DR PRINTS; PR00227; GEMCOATL1.
DR PRINTS; PR00228; GEMCOATL1.
DR PRODOM; P000736; Gemin1_AL1.
KW ATP-binding.
KW NP_BIND.
SQ SEQUENCE 358 AA; 40889 MW; 39A45FECC0B9C33 CRC64;

Query Match 59.6%; Score 217; DB 1; Length 358;

Best Local Similarity 55.7%; Pred. No. 7.2e-17;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

OY 1 TLWGEFVDGRSARGCCTNSDILLEFLVASSSEPALQIIRKIPKYLFOFHMLNSL 60
DB 110 TLKMEQFQIDGRSARGCCTNSDYNASVAKALNAGDVQSLMLKLEQPKDFVLOHNNHNSL 169
OY 61 DRIPTKPEP 70
DB 170 ERIFAKAP 179

RESULT 12
ID VAL1.TMOV STANDARD; PRT; 361 AA.
AC 006657;

DR 01-JUN-1994 (Rel. 29, Created)
DR 01-JUN-1994 (Rel. 29, Last sequence update)
DR 01-JUN-1994 (Rel. 29, Last annotation update)
DB AL1 PROTEIN.
CC OS Tomato mottle virus (Isolate Florida) (TMV).
CC NCBI_TaxID:36449;

RA SEQUENCE FROM N.A.
RA MEDLIN:93107858; PubMed:1469361;
RA Accurid A.M., Polston J.E., Hiebert E.;
RP "Isolation and characterization of a new geminivirus
RP isolated from tobacco plants infected with tobacco etch virus."
RL J. gen. Virol. 73:3225-3229(1992).
CC - SIMILARITY: BELONGS TO GEMINIVIRUSES AL1 PROTEIN FAMILY.

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DR EMBL; U14460; AAC32414.1;
DR PIR; J01870; J01870.
DR InterPro; IPR001191; Gemin1_AL1.
DR Pfam; PF00759; Gemin1_AL1.
DR PRINTS; PR00227; GEMCOATL1.
DR PRINTS; PR00228; GEMCOATL1.
DR PRODOM; P000736; Gemin1_AL1.
KW ATP-binding.
KW NP_BIND.
SQ SEQUENCE 361 AA; 40516 MW; 813B865CECE9590 CRC64;

Query Match Best Local Similarity 59.6%; Score 217; DB 1; Length 361;
Matches 39; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

OY 1 TLWGEFVDGRSARGCCTNSDILLEFLVASSSEPALQIIRKIPKYLFOFHMLNSL 60
DB 110 TLKMEQFQIDGRSARGCCTNSDYNASVAKALNAGDVQSLMLKLEQPKDFVLOHNNHNSL 169
OY 61 DRIPTKPEP 70
DB 170 ERIFAKAP 179

RESULT 13
ID VAL1.TYLCY STANDARD; PRT; 357 AA.
AC P27259;

DR 01-AUG-1992 (Rel. 23, Created)
DR 01-AUG-1992 (Rel. 23, Last sequence update)
DR 01-JUN-1994 (Rel. 29, Last annotation update)


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CC -----
DR EMBL: U14003; AAA97267.1; -.
DR EMBL: AE000507; AAC7724.1; -.
DR EMBL: E31220.6; famc. Mfase.
DR EMBL: U13900.2; famc. Mfase.
DR InterPro: IPR000051; SAM bind.
DR PROSITE: PS00092; N6_MTFASF; UNKNOWN 1.
KW rRNA processing; Transferase; Methyltransferase; Magnesium;
KW Complete proteome.
FT INIT_MET 0
FT SEQUENCE 342 AA; 37493 MW; C7A18155700302D CRC64;
OY 4 MEEFQVDGRS-----ARGSCQTSNDLLEALNASSKEALDI 40
DB 158 MOEISVDGIHYKTLPGVFSNDLDVGSOLLSTLPHTKGVLDV 202

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Search completed: January 3, 2002, 15:57:18
 Job time: 1104 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 15:56:26 ; Search time 131.66" Seconds

(without alignments) 77.751 Million cell updates/sec

Title: US-09-289-346a-10

Sequence: 1 TLWGEFYQDNRSGANGCCT.....FGHNLNSNLDRIFGKTPPEP 70

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 473505 seqs, 146273239 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP plant:*
7: SP mic.*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	298	81.9	352	12	09E000 tomato rugo
2	281	77.2	226	12	009727 leonurus mlo
3	281	77.2	226	12	09M165 tomato mild
4	279	76.6	225	12	09D284 bean golden
5	279	76.6	225	12	09D284 bean golden
6	277	76.1	314	12	09B178 Ogelis sweet potato
7	277	76.1	314	12	09B178 Ogelis sweet potato
8	274	75.3	185	12	09B693 sida golden
9	266	73.1	149	12	09B975 sida golden
10	266	73.1	149	12	09B975 sida golden
11	261	71.7	190	12	09Z088 tobacco lea
12	261	71.7	190	12	09Z088 tobacco lea
13	260	71.4	190	12	09M827 tobacco lea
14	260	71.4	208	12	09Z0C4 tobacco lea
15	260	71.4	234	12	093180 potato yell
16	258	70.9	208	12	09Z0C0 tobacco lea
17	258	70.9	208	12	09Z0C0 tobacco lea
18	256	70.3	208	12	09Z0B6 tobacco lea
19	256	70.3	208	12	09Z0B6 tobacco lea
20	255	70.1	203	12	09Z0B3 tobacco lea

20	251	69.0	363	12	073577 cotton leaf
21	250	68.7	363	12	072705 cotton leaf
22	250	68.7	363	12	072715 cotton leaf
23	249	68.4	359	12	09B886 tomato psu
24	249	68.4	359	12	09B886 tomato psu
25	247	67.9	190	12	09Z0B6 tobacco lea
26	247	67.9	208	12	09Z0C6 tobacco lea
27	247	67.9	359	12	09Z0V4 tobacco yell
28	247	67.9	359	12	09Z0V4 tobacco yell
29	247	67.9	359	12	09Y0X7 tomato yell
30	247	67.9	359	12	09Y0X7 tomato yell
31	246	67.6	359	12	09B942 tomato yell
32	246	67.6	359	12	09B942 tomato yell
33	245	67.3	362	12	091M48 tobacco lea
34	245	67.3	362	12	091M48 tobacco lea
35	244	67.0	307	12	091R77 cotton leaf
36	243	66.8	190	12	09Z0A7 tobacco lea
37	243	66.8	190	12	09Z0A7 tobacco lea
38	242	66.5	354	12	091M42 south afric
39	242	66.5	354	12	091M42 south afric
40	242	66.5	354	12	09B616 chayaote mos
41	240	65.9	353	12	072692 beet curly
42	240	65.9	354	12	065438 beet curly
43	239	65.7	153	12	041475 sida golden
44	238	65.4	360	12	09Y0M5 althea rose
45	238	65.4	362	12	09Y0Y7 althea rose

ALIGNMENTS

RESULT 1

AC 09E000; PRELIMINARY; PRT; 352 AA.
AC 09E000; 01-MAR-2001 (TRENEMREL, 15, Created)
DP 01-MAR-2001 (TRENEMREL, 16, Last sequence update)
DP 01-JUN-2001 (TRENEMREL, 17, Last annotation update)
DE REPLICATION-ASSOCIATED PROTEIN.
GN AC1.
OS Tomato rugose mosaic virus.
OC Viruses; ssDNA viruses; Gemlinviridae; Begomovirus.
NCBI_TaxID=134599;
NP 352 (1)
RP SEQUENCE FROM N.A.
RA Fernandes J.J., Fontes E.P.B., Brommonschenkel S.H., Carvalho M.G.,
F Zambolim E.M., Zerbini F.M.;
FM "Molecular Cloning and Characterization of Tomato rugose mosaic virus
(TRMV), a Begomovirus isolated from tomatoes at Triangulo Mineiro,
Minas Gerais, Brazil."
RT Submitted (03-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL:AF231055; Genbank:AF231055; DDBJ:AF231055.
DR InterPro: IPR001931; Gemlinv.AL1.
DR Pfam: PF00799; Gemlinv.AL1.
DR PRINTS: PD00227; Gemlinv.AL1.
DR ProDom: PD000736; Gemlinv.AL1.
SO SEQUENCE 352 AA; 40012 MW; 47CD5838E24D613 CRC64;

Query Match 81.9%; Score 298; DB 12; Length 352;
Best local similarity 78.6%; Pred. No. 1.8e-24;
Matches 55; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 1 TLWGEFYQDNRSGANGCCTNDLLEEMASSFEEDAOIIRKIPKYLTFPHNLNSN 60
DB 111 TLWGEFYQDNRSGANGCCTNDLLEEMASSFEEDAOIIRKIPKYLTFPHNLNSN 170
OY 61 DRIFDKTPPEP 70
DB 171 DRIFDKTPPEP 180
RESULT 2

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009727 ID 009727 PRELIMINARY: PRT: 226 AA.
AC AC
DT 01-JUL-1997 (TRENKLEL: 04, Created)
DT 01-JUL-1997 (TRENKLEL: 14, Last sequence update)
DT 01-JUN-2001 (TRENKLEL: 17, Last annotation update)
DE REP PROTEIN (FRAGMENT).
GN REP.
OS Leonurus mosaic virus.
OC Viruses; ssDNA viruses; Gemnivirusidae; Begomovirus.
NCBI_TaxID=58177;
RA RA
RM SOURCE FROM N.A.
RC STRAIN=LEWY-BRASIL 1;
RL Faria J.C., Maxwell D.P.;
RL Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: 092332; AB5157.1;
DR InterPro: IPR001191; Gemnivirusidae.
DR Pfam: PF00799; Gemnivirusidae.
DR PRINTS: PD00736; GEMNIVIR.
DR NON_TER 226
FT FT
SQ SEQUENCE 226 AA: 25617 MW: 730DB5676083FC5 CRC64:

Query Match 77.2%; Score 281; DB 12; Length 226;
Best Local Similarity 77.1%; Pred. No. 7.7e-23;
Matches 54; Conservative 4; Mismatches 12; Indels 0; Gaps 0:

OY 1 TLVNGEFOVDRSGAGCGQTNDLLALNASSKEPALDIIRKIPKXIFQFINHNSNL 60
DB 111 TVMGCEFOVDRSGAGCGQTNDLLALNASSKEPALDIIRKIPKXIFQFINHNSNL 170
DB 171 DRIFFKTPPEP 70
DB 171 DRIFFKTPPEP 180

RESULT 3
OYMHF6 ID OYMHF6 PRELIMINARY: PRT: 226 AA.
AC AC
DT 01-NOV-1999 (TRENKLEL: 12, Created)
DT 01-NOV-1999 (TRENKLEL: 17, Last sequence update)
DT 01-JUN-2001 (TRENKLEL: 17, Last annotation update)
DE REPLICATION-ASSOCIATED PROTEIN (FRAGMENT).
GN REP.
OS Lomato mild mottle geminivirus.
OC Viruses; ssDNA viruses; Gemnivirusidae; Unclassified Gemnivirusidae.
NCBI_TaxID=92943;
RA RA
RM SOURCE FROM N.A.
RC STRAIN=HNS6-HSKW;
RA Makhlis M.K., Mejia L., Ramirez P., Karkashian J.P., Doyle M.M.,
RA Maxwell D.P.;
RA "Molecular characterization and DNA-based detection methods for
RA vegetable-infecting geminiviruses in Central America.";
RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF131072; AB034471.1;
DR GenBank: F00729; GEMNIVIR.
DR Pfam: PF00799; Gemnivirusidae.
DR PRINTS: PD00227; GEMNIVIR.
DR PRODOM: PD000736; Gemnivirusidae.
DR NON_TER 226
FT FT
SQ SEQUENCE 226 AA: 25941 MW: 25M116712871A23 CRC64:

Query Match 77.2%; Score 281; DB 12; Length 226;
Best Local Similarity 77.9%; Pred. No. 7.7e-23;
Matches 51; Conservative 12; Mismatches 7; Indels 0; Gaps 0:

OY 1 TLVNGEFOVDRSGAGCGQTNDLLALNASSKEPALDIIRKIPKXIFQFINHNSNL 60

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DB 111 TVMGCEFOVDRSGAGCGQTNDLLALNASSKEPALDIIRKIPKXIFQFINHNSNL 170
OY 61 DRIFFKTPPEP 70
DB 171 DRIFFKTPPEP 180

RESULT 4
OYMHF6 ID OYMHF6 PRELIMINARY: PRT: 361 AA.
AC AC
DT 01-NOV-1996 (TRENKLEL: 01, Created)
DT 01-NOV-1996 (TRENKLEL: 17, Last sequence update)
DT 01-JUN-2001 (TRENKLEL: 17, Last annotation update)
DE PUTATIVE REPLICATIVE PROTEIN.
GN ALI.
OS Bean golden mosaic virus.
OC Viruses; ssDNA viruses; Gemnivirusidae; Begomovirus.
NCBI_TaxID=10839;
RA RA
RM SOURCE FROM N.A.
RC STRAIN=R.L.; Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RL Phytopathology 81:980-985(1991).
RN 121
RP SEQUENCE FROM N.A.
RA Gilchriston R.L., Hidayat S.H., Martinez R.T., Leong S.A., Faria J.C.,
RA Morales F.J., Maxwell D.P.;
RN 131
RP Submitted (MAY-1992) to the EMBL/Genbank/DBJ databases.
RA EMBL: M88686; AAA6312.1;
RL InterPro: IPR001191; Gemnivirusidae.
DR Pfam: PF00799; Gemnivirusidae.
DR PRINTS: PD00736; GEMNIVIR.
DR PRODOM: PD000736; Gemnivirusidae.
SQ SEQUENCE 361 AA: 41041 MW: 0094C7ACAF06B788 CRC64:

Query Match 77.2%; Score 281; DB 12; Length 361;
Best Local Similarity 77.6%; Pred. No. 1.3e-22;
Matches 52; Conservative 6; Mismatches 7; Indels 0; Gaps 0:

OY 4 WEPVNGSARAGCGQTNDLLALNASSKEPALDIIRKIPKXIFQFINHNSNDRI 63
DB 113 WGPVNGSARAGCGQTNDLLALNASSKEPALDIIRKIPKXIFQFINHNSNDRI 172
OY 64 FDKTPPEP 70
DB 173 FDKTPPEP 179

RESULT 5
OYQDB1 ID OYQDB1 PRELIMINARY: PRT: 225 AA.
AC AC
DT 01-MAY-2000 (TRENKLEL: 13, Created)
DT 01-MAY-2000 (TRENKLEL: 17, Last sequence update)
DT 01-JUN-2001 (TRENKLEL: 17, Last annotation update)
DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
GN REP.
OS Cowpea golden mosaic geminivirus.
OC Viruses; ssDNA viruses; Gemnivirusidae; Begomovirus.
NCBI_TaxID=69263;
RA RA
RM SOURCE FROM N.A.
RC STRAIN=CGW-BR;
RA Faria J.C.;
RA "Partial nucleotide sequence of cowpea golden mosaic geminivirus from
RA Brazil.";
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.

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DR EMBL: AF188708; AAP06318.1; -.
DR InterPro: IPR001191; Gemini.AL1.
DR Pfam: PF00799; Gemini.AL1.1.
DR PRINTS: PR00227; GEMCONFALI.
DR Prodom: PD00736; Gemini.AL1.1.
DR NON_TER 225
FT SEQUENCE 225 AA; 25766 MW; 1089C6BDD015B5D CRC64;
SQ

Query Match
Best Local Similarity 76.6%; Score 277; DB 12; Length 225;
Matches 52; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 4 TLMGEFVQDNRSGCGTNDLLLEALMASSKEEALQITREKIPKRYLQFPHNINSNT 63
DB 113 MGHFDIGNRSGCGQTINDASALMASSKEEMQIKETLKEFIFQYINLSNDR 172
DB 64 FKPTPEP 70
DB 173 FKPTPEP 179

RESULT 6
OYETL8 PRELIMINARY: PRT; 314 AA.
AC 09ETL8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DR 01-FEB-2001 (TREMBLrel. 17, Last annotation update)
DE REPLICATION ASSOCIATION PROTEIN.
GN ACL.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OK NCBI_TaxID=100755;
RN SEQUENCE FROM N.A.
RA Sumter, R., Valverde R.A., Clark C.A., Sim J., De la Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RN States.";
RL Plant Dis. 82:1253-1257(1998).
[2]
RN SEQUENCE FROM N.A.
RA Lorekul P., Valverde R.A.;
RT Sumter, R., Valverde R.A., Clark C.A., Sim J., De la Torre R.;
RN InterPro: IPR001191; Gemini.AL1.
DR Pfam: PF00799; Gemini.AL1.1.
DR PRINTS: PR00227; GEMCONFALI.
DR Prodom: PD00736; Gemini.AL1.1.
DR SEQUENCE 314 AA; 35153 MW; 6B6220613046943F CRC64;
SQ

Query Match
Best Local Similarity 76.1%; Score 277; DB 12; Length 314;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

OY 1 TLMGEFVQDNRSGCGTNDLLLEALMASSKEEALQITREKIPKRYLQFPHNINSNT 60
DB 110 TLMGEFVQDNRSGCGQTANDMAALMASSKEEALQITREKIPKRYLQFPHNINSNT 169
OY 61 DRIPKTP 68
DB 170 DRIPKTP 177

RESULT 7
OYETL8 PRELIMINARY: PRT; 364 AA.
AC 09OES55;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE REPLICATION INITIATION PROTEIN ACL.

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GN ACL.
OS Sweet potato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OK NCBI_TaxID=100755;
RN SEQUENCE FROM N.A.
RA Sumter, R., Valverde R.A., Clark C.A., Sim J., De la Torre R.;
RT "Detection of a geminivirus infecting sweet potato in the United
RN States.";
RL Plant Dis. 82:1253-1257(1998).
DR EMBL: AF104036; AAD47173.1; -.
DR InterPro: IPR001191; Gemini.AL1.
DR Pfam: PF00799; Gemini.AL1.1.
DR PRINTS: PR00227; GEMCONFALI.
DR Prodom: PD00736; Gemini.AL1.1.
DR SEQUENCE 364 AA; 40680 MW; 5F7972A31A09D6E CRC64;
SQ

Query Match
Best Local Similarity 76.1%; Score 277; DB 12; Length 364;
Matches 54; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

OY 1 TLMGEFVQDNRSGCGTNDLLLEALMASSKEEALQITREKIPKRYLQFPHNINSNT 60
DB 110 TLMGEFVQDNRSGCGQTANDMAALMASSKEEALQITREKIPKRYLQFPHNINSNT 169
OY 61 DRIPKTP 68
DB 170 DRIPKTP 177

RESULT 8
OYETL8 PRELIMINARY: PRT; 185 AA.
AC 09B693;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-FEB-2001 (TREMBLrel. 17, Last annotation update)
DE REP PROTEIN (FRAGMENT).
GN ACL.
OS sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OK NCBI_TaxID=51034;
RN SEQUENCE FROM N.A.
RA STRAIN=LAMATCH.
RA Roye M.E., McLaughlin M.A., Nakhia N.K., Maxwell D.P.;
RL Plant Dis. 81:1251-1258(1997).
DR EMBL: U67926; AAB97865.1; -.
DR InterPro: IPR001191; Gemini.AL1.
DR Pfam: PF00799; Gemini.AL1.1.
DR PRINTS: PR00227; GEMCONFALI.
DR Prodom: PD00736; Gemini.AL1.1.
DR NON_TER 185
FT SEQUENCE 185 AA; 20975 MW; 3918950A025A5E1 CRC64;
SQ

Query Match
Best Local Similarity 75.3%; Score 274; DB 12; Length 185;
Matches 49; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 1 TLMGEFVQDNRSGCGTNDLLLEALMASSKEEALQITREKIPKRYLQFPHNINSNT 60
DB 89 TLMGEFVQDNRSGCGQTANDMAALMASSKEEALQITREKIPKRYLQFPHNINSNT 148
OY 61 DRIPKTP 70
DB 149 DRIPKTP 158

RESULT 9
P88975

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ID P88975 PRELIMINARY: PRT: 149 AA.
AC P88975
DT 01-MAY-1997 (TREMURREL 03, Created)
DD 01-MAY-1997 (TREMURREL 03, Last sequence update)
DE 01-JUN-2001 (TREMURREL 17, Last annotation update)
DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
GN ACL
OC Macroplasma golden mosaic geminivirus.
OS VIRUSES; ssDNA viruses; geminiviridae; Begomovirus.
NCBI_TaxID=51676;
RN 111
RP SEQUENCE FROM N.A.
RA ROYE M.E.;
RL Thesis (1996). Biochemistry, University of the West Indies, Jamaica.
DR EMBL: U75278; AAB36919.1;
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1;
DR PRINTS: PR00227; GEMCON1AL1.
DR PROSITE: PS00036; Gemini_AL1;
DR NON_TER 149
FT 149
SQ
SEQUENCE 149 AA: EACFSEPCAC9CDD508 CAC64;

Query Match 73.1%; Score 266; DB 12; Length 149;
Best Local Similarity 68.6%; Pred. No. 2,1e-21;
Matches 48; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

OY 1 TLVNGEYVDGRSANGCCTSDLLLEALNASSKEALQIIRKIPKYLQFPHNINSNL 60
DB 52 TLVNGEYVDGRSANGCCTSDLLLEALNASSKEALQIIRKIPKYLQFPHNINSNL 111
OY 61 DRIEKPTEP 70
DB 112 DRIEKPTEP 121

RESULT 10
OY144 PRELIMINARY: PRT: 233 AA.
AC OY144
DT 01-MAY-1999 (TREMURREL 10, Created)
DD 01-MAY-1999 (TREMURREL 10, Last sequence update)
DE 01-JUN-2001 (TREMURREL 17, Last annotation update)
DE REPLICATION ASSOCIATED PROTEIN (FRAGMENT).
GN REP
OC Macroplasma golden mosaic geminivirus.
OS VIRUSES; ssDNA viruses; geminiviridae; Begomovirus.
NCBI_TaxID=51676;
RN 111
RP SEQUENCE FROM N.A.
RA ROYE M.E.;
RL Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica. (12) to the EMBL/Gembank/DBJ databases.
DD Submitted (OCT-1998) to the EMBL/Gembank/DBJ databases.
RT latipoloids from Jamaica.*
RA Molecular characterization of two distinct geminiviruses infecting M.
RL EMBL: AK039903; J021780.1;
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1;
DR PRINTS: PR00227; GEMCON1AL1.
DR PROSITE: PS00036; Gemini_AL1;
DR NON_TER 233
SQ
SEQUENCE 233 AA: AA490AF4D2156A02 CAC64;

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Query Match 73.1%; Score 266; DB 12; Length 233;
Best Local Similarity 68.6%; Pred. No. 3.4e-21;
Matches 48; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

OY 1 TLVNGEYVDGRSANGCCTSDLLLEALNASSKEALQIIRKIPKYLQFPHNINSNL 60
DB 110 TLVNGEYVDGRSANGCCTSDLLLEALNASSKEALQIIRKIPKYLQFPHNINSNL 169
OY 61 DRIEKPTEP 70
DB 170 DRIEKPTEP 179

RESULT 11
OY2089 PRELIMINARY: PRT: 190 AA.
AC OY2089
DT 01-MAY-1999 (TREMURREL 10, Created)
DD 01-MAY-1999 (TREMURREL 10, Last sequence update)
DE 01-JUN-2001 (TREMURREL 17, Last annotation update)
DE CLONING GENES; CLONE YOKOHAMA5-1, PARTIAL AND COMPLETE CDS (FRAGMENT).
GN C1.
OS Tobacco leaf curl virus.
OS VIRUSES; ssDNA viruses; geminiviridae; Begomovirus.
NCBI_TaxID=67762;
RN 111
RP SEQUENCE FROM N.A.
RA OOI K.; Ohshtita S.; Ishii I.; Yahara T.;
RL "Molecular phylogeny of geminiviruses infecting wild plants in Japan.*"
J. Plant Res. 110:247-257(1997).
DR EMBL: AB001315; BAA34033.1;
DR InterPro: IPR001191; Gemini_AL1.
DR Pfam: PF00799; Gemini_AL1;
DR PRINTS: PR00227; GEMCON1AL1.
DR PROSITE: PS00036; Gemini_AL1;
DR NON_TER 190
FT 190
SQ
SEQUENCE 190 AA: AAC093DD1610FAD CAC64;

Query Match 71.7%; Score 261; DB 12; Length 190;
Best Local Similarity 60.0%; Pred. No. 9.4e-21;
Matches 51; Conservative 8; Mismatches 10; Indels 16; Gaps 1;

OY 1 TLVNGEYVDGRSANGCCTSDLLLEALNASSKEALQIIRKIPKYLQFPHNINSNL 60
DB 85 TLVNGEYVDGRSANGCCTSDLLLEALNASSKEALQIIRKIPKYLQFPHNINSNL 144
OY 61 DRIEKPTEP 69
DB 145 DRIEKPTEP 169

RESULT 12
OY2084 PRELIMINARY: PRT: 190 AA.
AC OY2084
DT 01-MAY-1999 (TREMURREL 10, Created)
DD 01-MAY-1999 (TREMURREL 10, Last sequence update)
DE 01-JUN-2001 (TREMURREL 17, Last annotation update)
DE C1 AND C4 GENES; CLONE YOKOHAMA5-2, PARTIAL AND COMPLETE CDS (FRAGMENT).
GN C1.
OS Tobacco leaf curl virus.
OS VIRUSES; ssDNA viruses; geminiviridae; Begomovirus.
NCBI_TaxID=67762;
RN 111
RP SEQUENCE FROM N.A.
RA OOI K.; Ohshtita S.; Ishii I.; Yahara T.;
RL "Molecular phylogeny of geminiviruses infecting wild plants in Japan.*"

```

RL J. Plant Res. 110:247-257(1997).
 DR EMBL: AB001318; BA334039.1; -
 DR InterPro: IPR001191; Gemini_AL1.
 DR Plant: P00059; Gemini_AL1.1.
 DR RefSeq: NC002727; GEMINIAAL1.
 DR Prodom: P0000736; Gemini_AL1.1.
 FT NON_TER 1 190
 FT NON_TER 190 190
 SO SEQUENCE 190 AA: 21444 MW: 44629.333701AD CRC64:

Query Match 71.4% Score 260; DB 12; Length 190;
 Best Local Similarity 60.0%; Pred. No. 1, 3e-20;
 Matches 51; Conservative 8; Mismatches 10; Indels 16; Gaps 1;

OY 1 TLWGEFVQDGRSARGCGCTSDNLLLEALNASSKEPALQIIRKXIPKXYLPQPHNLSNL 60
 DB 85 TLEMGTFQIDGRSARGCGCTSDNLLLEALNASSKEPALQIIRKXIPKXYLPQPHNLSNL 144
 OY 61 DRI-----PKTPPE 69
 DB 145 DRIAPPLIEVPCPSNSRDQVPE 169

RESULT 13
 OY98827 PRELIMINARY; PRT; 190 AA.
 ID 098827
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE C1 PROTEIN (FRAGMENT).

OS Tobacco leaf curl virus.
 GN Tobacco leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 NC NCB1_TaxID=67762;
 RP SEQUENCE FROM N.A.
 RC STRAIN-CORAL;
 RA Ooi K., Ohshima S., Ishii I., Yahara T.;
 RL "Molecular phylogeny of geminiviruses infecting wild plants in Japan."
 J. Plant Res. 110:247-257(1997).
 DR EMBL: AB001318; BA334010.1; -
 DR RefSeq: NC002727; GEMINIAAL1.
 DR Prodom: P000736; Gemini_AL1.1.
 DR PRINTS: PR00227; Gemini_AL1.1.
 DR Prodom: P000736; Gemini_AL1.1.
 FT NON_TER 1 190
 FT NON_TER 190 190
 SO SEQUENCE 190 AA: 21444 MW: 933742488DB7EB CRC64:

Query Match 71.4% Score 260; DB 12; Length 190;
 Best Local Similarity 60.0%; Pred. No. 1, 3e-20;
 Matches 51; Conservative 8; Mismatches 10; Indels 16; Gaps 1;

OY 1 TLWGEFVQDGRSARGCGCTSDNLLLEALNASSKEPALQIIRKXIPKXYLPQPHNLSNL 60
 DB 85 TLEMGTFQIDGRSARGCGCTSDNLLLEALNASSKEPALQIIRKXIPKXYLPQPHNLSNL 144
 OY 61 DRI-----PKTPPE 69
 DB 145 DRIAPPLIEVPCPSNSRDQVPE 169

RESULT 14
 OY98827 PRELIMINARY; PRT; 208 AA.
 ID 098827
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE C1 AND C4 GENES, CLONE ABRA3-1, PARTIAL AND COMPLETE CDS (FRAGMENT).

GN C1.
 OS Tobacco leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 NC NCB1_TaxID=67762;
 RP SEQUENCE FROM N.A.
 RC STRAIN-ABRA3;
 RA Ooi K., Ohshima S., Ishii I., Yahara T.;
 RL "Molecular phylogeny of geminiviruses infecting wild plants in Japan."
 J. Plant Res. 110:247-257(1997).
 DR EMBL: AB001294; BA33992.1; -
 DR InterPro: IPR001191; Gemini_AL1.
 DR Plant: P00059; Gemini_AL1.1.
 DR RefSeq: NC002727; GEMINIAAL1.
 DR Prodom: P0000736; Gemini_AL1.1.
 FT NON_TER 1 208
 FT NON_TER 208 208
 SO SEQUENCE 208 AA: 23526 MW: 249CC31B8729C72D CRC64:

Query Match 71.4% Score 260; DB 12; Length 208;
 Best Local Similarity 60.0%; Pred. No. 1, 3e-20;
 Matches 51; Conservative 8; Mismatches 10; Indels 16; Gaps 1;

OY 1 TLWGEFVQDGRSARGCGCTSDNLLLEALNASSKEPALQIIRKXIPKXYLPQPHNLSNL 60
 DB 102 TLEMGTFQIDGRSARGCGCTSDNLLLEALNASSKEPALQIIRKXIPKXYLPQPHNLSNL 161
 OY 61 DRI-----PKTPPE 69
 DB 162 DRIAPPLIEVPCPSNSRDQVPE 186

RESULT 15
 OY98180 PRELIMINARY; PRT; 234 AA.
 ID 098180
 DT 01-JUN-1998 (TREMblrel. 05, Created)
 DT 01-JUN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE REPLICATION-ASSOCIATED PROTEIN (FRAGMENT).
 OS Potato yellow mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 GN NCB1_TaxID=10627;
 RP SEQUENCE FROM N.A.
 RC STRAIN-TOMATO STRAIN;
 RA Guzman P., Arredondo C.R., Emmatty D., Portillo R.J., Gilbertson R.L.;
 RL Plant Dis. 81:312-312(1997).
 DR EMBL: AF026553; AB87605.1; -
 DR InterPro: IPR001191; Gemini_AL1.
 DR Plant: P00059; Gemini_AL1.1.
 DR RefSeq: NC00227; GEMINIAAL1.
 DR Prodom: P0000736; Gemini_AL1.1.
 FT NON_TER 234 234
 SO SEQUENCE 234 AA: 26486 MW: 98B8F0697105CD19 CRC64:

Query Match 71.4% Score 260; DB 12; Length 234;
 Best Local Similarity 67.1%; Pred. No. 1, 5e-20;
 Matches 47; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

OY 1 TLWGEFVQDGRSARGCGCTSDNLLLEALNASSKEPALQIIRKXIPKXYLPQPHNLSNL 60
 DB 110 TLEMGTFQIDGRSARGCGCTSDNLLLEALNASSKEPALQIIRKXIPKXYLPQPHNLSNL 169
 OY 61 DRIEKPTEP 70
 DB 170 DRIEKPTEP 179

Search completed: January 3, 2002, 15:56:26

Job time: 1122 sec

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: January 3, 2002, 15:38:51 ; Search time 65.28 Seconds
(without alignments) 24.130 Million cell updates/sec

Title: US-09-289-346A-10

Accession: 1 T1WNGEFOVGRSARGCOT.....EPHININSNDITPEKTPPP 70

Sequence:

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503295 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing list: 45 summaries

Database: Issued Patents AA:*

1: /cgn2-6/plocata/2/1aa/5A.COMB.pep:*

2: /cgn2-6/plocata/2/1aa/5B.COMB.pep:*

3: /cgn2-6/plocata/2/1aa/6A.COMB.pep:*

4: /cgn2-6/plocata/2/1aa/6B.COMB.pep:*

5: /cgn2-6/plocata/2/1aa/6C.COMB.pep:*

6: /cgn2-6/plocata/2/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	223	61.3	353	4	US-08-838-151A-44
2	223	61.3	353	4	US-08-838-151A-46
3	223	61.3	353	4	US-08-838-151A-49
4	223	61.3	353	4	US-08-838-151A-52
5	223	61.3	353	4	US-08-838-151A-55
6	223	61.3	353	4	US-08-838-151A-57
7	223	61.3	353	4	US-08-838-151A-60
8	223	61.3	353	4	US-08-838-151A-63
9	223	61.3	353	4	US-08-838-151A-66
10	223	61.3	353	4	US-08-838-151A-69
11	223	61.3	353	4	US-08-838-151A-72
12	223	61.3	353	4	US-08-838-151A-75
13	223	61.3	353	4	US-08-838-151A-78
14	223	61.3	353	4	US-08-838-151A-81
15	223	61.3	353	4	US-08-838-151A-84
16	223	61.3	353	4	US-08-838-151A-87
17	223	61.3	353	4	US-08-838-151A-90
18	223	61.3	353	4	US-08-838-151A-93
19	223	61.3	353	4	US-08-838-151A-96
20	223	61.3	353	4	US-08-838-151A-99
21	223	61.3	353	4	US-08-838-151A-102
22	223	61.3	353	4	US-08-838-151A-105
23	223	61.3	353	4	US-08-838-151A-108
24	223	61.3	353	4	US-08-838-151A-111
25	223	61.3	353	4	US-08-838-151A-114
26	223	61.3	353	4	US-08-838-151A-117
27	223	61.3	353	4	US-08-838-151A-120

28	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 51, Appl
29	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 2, Appl
30	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 7, Appl
31	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 20, Appl
32	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 24, Appl
33	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 24, Appl
34	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 24, Appl
35	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 24, Appl
36	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 24, Appl
37	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 24, Appl
38	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 24, Appl
39	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 24, Appl
40	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 24, Appl
41	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 24, Appl
42	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 24, Appl
43	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 24, Appl
44	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 24, Appl
45	58.5	16.1	2161	2	US-08-223-305C-51	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-08-838-151A-44
Sequence 44, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
INVENTOR: John T.
APPLICANT: Maxell, Douglas
APPLICANT: Ahlquist, Paul
TITLE OF INVENTION: Transgenic Plants Expressing GeminiViruses
NUMBER OF SEQUENCES: 63
ADDRESS: Dressler, Rocky, Milnrow & Katz
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838, 151A
FILING DATE: 800
CLASSIFICATION: 800
ATTORNEY INFORMATION:
NAME: Meller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INSTRUMENT FOR SEQ ID NO: 44:
SEQUENCE LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-44
Query Match 61.3%, Score 223, DB 4, Length 353.
Best Local Similarity 60.0%, Pred. No. 1.5e-21;
Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;
Query 1 T1WNGEFOVGRSARGCOTSNDILEALNASKREAOLIIKERIPKYLPPHINNSND, 60

DB 110 TIMGQFOVDRSARNGCQSDSLLEAKMANSKEALDITREKPKDYVQHNNISRL 169
 QY 61 DRIEFPKPEP 70
 DB 110 ERIFKVPPEP 179

RESULT 2

US-08-838-151A-46
 Sequence 46, Application US/08838151A
 Patent No. 6291743
 INVENTION INFORMATION:
 APPLICANT: Stout, John T
 APPLICANT: Lou, Haog T
 APPLICANT: Maxwell, Douglas
 APPLICANT: Ahlquist, Paul
 APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/838,151A
 FILING DATE:
 CLASSIFICATION: B00
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 353 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-838-151A-46

Query Match

Best Local Similarity 61.3%; Score 223; DB 4; Length 353;
 Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 TIVGCFQVDRSARNGCQSDSLLEAKMANSKEALDITREKPKDYVQHNNISRL 60
 DB 110 TIMGQFOVDRSARNGCQSDSLLEAKMANSKEALDITREKPKDYVQHNNISRL 169
 QY 61 DRIEFPKPEP 70
 DB 110 ERIFKVPPEP 179

RESULT 3

US-08-838-151A-45
 Sequence 49, Application US/08838151A
 Patent No. 6291743
 GENERAL INFORMATION:
 APPLICANT: Stout, John T
 APPLICANT: Lou, Haog T

APPLICANT: Maxwell, Douglas
 APPLICANT: Ahlquist, Paul
 APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/838,151A
 FILING DATE:
 CLASSIFICATION: B00
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 353 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-838-151A-45

Query Match

Best Local Similarity 61.3%; Score 223; DB 4; Length 353;
 Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 TIVGCFQVDRSARNGCQSDSLLEAKMANSKEALDITREKPKDYVQHNNISRL 60
 DB 110 TIMGQFOVDRSARNGCQSDSLLEAKMANSKEALDITREKPKDYVQHNNISRL 169
 QY 61 DRIEFPKPEP 70
 DB 110 ERIFKVPPEP 179

RESULT 4

US-08-838-151A-52
 Sequence 52, Application US/08838151A
 Patent No. 6291743
 GENERAL INFORMATION:
 APPLICANT: Stout, John T
 APPLICANT: Lou, Haog T
 APPLICANT: Maxwell, Douglas
 APPLICANT: Ahlquist, Paul
 APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838,151A
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SYS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 52:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 353 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULAR TYPE: protein
 US-08-838-151A-52

Query Match 61.3%; Score 223; DB 4; Length 353;
 Best Local Similarity 60.0%; Pred. No. 1,5e-21;
 Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

OY 1 TVWGVGVGSGAGCGGCGNDLLLEKASSKEPAQITREKTPKTFQPHMNSH, 60
 DB 110 TTEMCGFQVDSGANGQGSANQSAKAMADISFALTLEKQPDVYVQHHNINSN, 169
 OY 61 DRIFDTPPEP 70
 DB 170 ERIEIVPVEP 179

RESULT 5
 US-08-838-151A-55
 Sequence 55, Application US/0838151A
 Patent No. 6291743
 GENERAL INFORMATION:
 APPLICANT: Stout, John T
 APPLICANT: Liu, Hang T
 APPLICANT: Maxwell, Douglas
 APPLICANT: Abshire, Paul
 APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing Geminiavirus
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Rocky, Mlunmow & Katz
 ADDRESS: 2000 Presidential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838,151A
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SYS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 55:

SEQUENCE CHARACTERISTICS:
 LENGTH: 353 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULAR TYPE: protein
 US-08-838-151A-55

Query Match 61.3%; Score 223; DB 4; Length 353;
 Best Local Similarity 60.0%; Pred. No. 1,5e-21;
 Matches 42; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

OY 1 TVWGVGVGSGAGCGGCGNDLLLEKASSKEPAQITREKTPKTFQPHMNSH, 60
 DB 110 TTEMCGFQVDSGANGQGSANQSAKAMADISFALTLEKQPDVYVQHHNINSN, 169
 OY 61 DRIFDTPPEP 70
 DB 170 ERIEIVPVEP 179

RESULT 6
 US-08-809-1038-2
 Sequence 2, Application US/088091038
 Patent No. 613305
 GENERAL INFORMATION:
 APPLICANT: GONENBORN, Bruno
 TITLE OF INVENTION: PHOTOTROGENIC DNA VIRUS RESISTANT
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: YOUNG & THOMPSON
 STREET: 745 South 23rd Street
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/809,1038
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 94,11040
 FILING DATE: 15-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/FR95/01192
 ATTORNEY/AGENT INFORMATION:
 NAME: PATCH, Andrew J
 REGISTRATION NUMBER: 32,925
 REFERENCE/DOCKET NUMBER: US94AL CNR TOM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 521-2297
 TELEFAX: (703) 665-0573
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 359 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULAR TYPE: protein
 US-08-809-1038-2

Query Match 60.7%; Score 221; DB 4; Length 359;
 Best Local Similarity 56.5%; Pred. No. 2,8e-21;
 Matches 39; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 2 LWAGEFOVDSARGGCGTSDNLLLEALNASSKEPALQIREKIPKYLFOFHNLNSMD 61
 DB 111 LEMGFPOIDGSRAGGCGQTANDAYAKAINGSKSALDVIKELAPROYLHFNHNSMD 170
 QY 62 RIFDKTPEP 70
 DB 171 KVFQVPPAP 179

RESULT 7
 US-08-809-103b-4
 : Sequence 4, Application US/08809103b
 : Patent No. 6133505
 : GENERAL INFORMATION:
 : APPLICANT: GROENENBORN, Bruno
 : TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 : TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
 : NUMBER OF SEQUENCES: 17
 : CORRESPONDENCE ADDRESS: THOMPSON
 : STREET: 745 South 23rd Street
 : CITY: Arlington
 : STATE: Virginia
 : COUNTRY: U.S.A.
 : ZIP: 22202
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: IBM PC compatible
 : SOFTWARE: Patentln Release #1.0, Version #1.30
 : APPLICATION NUMBER: US/08/809,103b
 : FILING DATE: 17-MAR-1997
 : CLASSIFICATION: B00
 : PRIOR APPLICATION DATA: FR 94,11040
 : FILING DATE: 15-SEP-1994
 : APPLICATION NUMBER: WO PCT/FR95/01192
 : FILING DATE: 15-SEP-1995
 : ATTORNEY/AGENT INFORMATION:
 : NAME: PATCH, Andrew J. 2, 925
 : REGISTRATION NUMBER: 32,925
 : REFERENCE/DOCKET NUMBER: US94AL CNR TOM
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (703) 521-2297
 : TELEFAX: 248425 EMBON
 : TELEX: 248425 EMBON
 : INFORMATION FOR SEQ ID NO: 4:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 359 amino acids
 : TYPE: amino acid
 : TOPOLOGY: 1 linear
 : MOLECULE TYPE: protein
 : US-08-809-103b-4

Query Match 60.7%, Score 221, DB 4, Length 359;
 Best Local Similarity 56.5%, Pred. No. 2,8e-21;
 Matches 39, Conservative 11, Mismatches 19, Indels 0, Gaps 0;
 QY 2 LWAGEFOVDSARGGCGTSDNLLLEALNASSKEPALQIREKIPKYLFOFHNLNSMD 61
 DB 111 LEMGFPOIDGSRAGGCGQTANDAYAKAINGSKSALDVIKELAPROYLHFNHNSMD 170
 QY 62 RIFDKTPEP 70
 DB 171 KVFQVPPAP 179

: Patent No. 6133505
 : GENERAL INFORMATION:
 : APPLICANT: GROENENBORN, Bruno
 : TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 : TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
 : NUMBER OF SEQUENCES: 17
 : CORRESPONDENCE ADDRESS: THOMPSON
 : STREET: 745 South 23rd Street
 : CITY: Arlington
 : STATE: Virginia
 : COUNTRY: U.S.A.
 : ZIP: 22202
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: IBM PC compatible
 : SOFTWARE: Patentln Release #1.0, Version #1.30
 : APPLICATION NUMBER: US/08/809,103b
 : FILING DATE: 17-MAR-1997
 : CLASSIFICATION: B00
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: FR 94,11040
 : FILING DATE: 15-SEP-1994
 : APPLICATION NUMBER: WO PCT/FR95/01192
 : FILING DATE: 15-SEP-1995
 : ATTORNEY/AGENT INFORMATION:
 : NAME: PATCH, Andrew J. 2, 925
 : REGISTRATION NUMBER: 32,925
 : REFERENCE/DOCKET NUMBER: US94AL CNR TOM
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (703) 521-2297
 : TELEFAX: 248425 EMBON
 : TELEX: 248425 EMBON
 : INFORMATION FOR SEQ ID NO: 6:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 359 amino acids
 : TYPE: amino acid
 : TOPOLOGY: 1 linear
 : MOLECULE TYPE: protein
 : US-08-809-103b-6

Query Match 60.7%, Score 221, DB 4, Length 359;
 Best Local Similarity 56.5%, Pred. No. 2,8e-21;
 Matches 39, Conservative 11, Mismatches 19, Indels 0, Gaps 0;
 QY 2 LWAGEFOVDSARGGCGTSDNLLLEALNASSKEPALQIREKIPKYLFOFHNLNSMD 61
 DB 111 LEMGFPOIDGSRAGGCGQTANDAYAKAINGSKSALDVIKELAPROYLHFNHNSMD 170
 QY 62 RIFDKTPEP 70
 DB 171 KVFQVPPAP 179


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1      FILING DATE:
2      CLASSIFICATION: 800
3      ATTORNEY/AGENT INFORMATION:
4      NAME: Mueller, Lisa V
5      REGISTRATION NUMBER: 39, 978
6      REFERENCE/DOCID NUMBER: S538010260
7      TELEPHONE NUMBER: 312-616-5400
8      TELEFAX: 312-616-5460
9      INFORMATION FOR SEQ ID NO: 2:
10     SEQUENCE CHARACTERISTICS:
11     LENGTH: 361 amino acids
12     TYPE: amino acid
13     TOPOLOGY: linear
14     MOLECULE TYPE: protein
15     OS-08-938-151A-2
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US-08-838-151A-4

Query Match 60.7%; Score 221; DB 4; Length 361;
 Best Local Similarity 57.1%; Pred. No. 2, 8e-21;
 Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

OY 1 TLWGEFVDGRSANGGCTNSDILLEALNASSKEPALQIRKIPKYLPGPHNINSN 60
 DB 110 TLEMDPDIDRSANGGOSANDSVKALNASSVQSALVAREOPKDPVLOHNINSN 169

OY 61 DRIFPKTPEP 70
 DB 170 ERIFAKAPEP 179

RESULT 12
 US-08-838-151A-6

; Sequence 6, Application US/08838151A
 ; Patent No. 6291743
 ; GENERAL INFORMATION:
 ; APPLICANT: Scout, John T
 ; APPLICANT: Lau, Hang T
 ; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlquist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Rocky, Milwaukee & Katz
 ; STREET: Two Prudential Plaza, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; TELEPHONE: 312-616-5400
 ; TELECOMMUNICATION INFORMATION:
 ; COMPUTER: IBM PC compatible
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/838,151A
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mueller, Lisa V
 ; REGISTRATION NUMBER: 38,978
 ; REFERENCE/DOCKET NUMBER: SVS3801P0260
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-616-5400
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 361 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-838-151A-6

Query Match 60.7%; Score 221; DB 4; Length 361;
 Best Local Similarity 57.1%; Pred. No. 2, 8e-21;
 Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

OY 1 TLWGEFVDGRSANGGCTNSDILLEALNASSKEPALQIRKIPKYLPGPHNINSN 60
 DB 110 TLEMDPDIDRSANGGOSANDSVKALNASSVQSALVAREOPKDPVLOHNINSN 169

OY 61 DRIFPKTPEP 70
 DB 170 ERIFAKAPEP 179

RESULT 13
 US-08-838-151A-8

; Sequence 8, Application US/08838151A
 ; Patent No. 6291743
 ; GENERAL INFORMATION:
 ; APPLICANT: Scout, John T
 ; APPLICANT: Lau, Hang T
 ; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlquist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Rocky, Milwaukee & Katz
 ; STREET: Two Prudential Plaza, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; TELEPHONE: 312-616-5400
 ; TELECOMMUNICATION INFORMATION:
 ; COMPUTER: IBM PC compatible
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/838,151A
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mueller, Lisa V
 ; REGISTRATION NUMBER: 38,978
 ; REFERENCE/DOCKET NUMBER: SVS3801P0260
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-616-5400
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 361 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-838-151A-8

Query Match 60.7%; Score 221; DB 4; Length 361;
 Best Local Similarity 57.1%; Pred. No. 2, 8e-21;
 Matches 40; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

OY 1 TLWGEFVDGRSANGGCTNSDILLEALNASSKEPALQIRKIPKYLPGPHNINSN 60
 DB 110 TLEMDPDIDRSANGGOSANDSVKALNASSVQSALVAREOPKDPVLOHNINSN 169

OY 61 DRIFPKTPEP 70
 DB 170 ERIFAKAPEP 179

RESULT 14
 US-08-838-151A-24

; Sequence 24, Application US/08838151A
 ; Patent No. 6291743
 ; GENERAL INFORMATION:
 ; APPLICANT: Scout, John T
 ; APPLICANT: Lau, Hang T
 ; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlquist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:

```

ADDRESSER: Dressler, Rocky, Milamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 09/08/83B, 151A
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-24

Query Match 56.6%; Score 206; DB 4; Length 357;
Best Local Similarity 63.9%; Pred. No. 2.7e-19;
Matches 39; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

OY 4 WGEYDNGSRAGCGCGTNSNLLDLAINSKREALOITREIKYIROPFNINSNDRI 63
DB 111 FGVSQIDGRSAGCGQANDAVAAALNAGSKSEALNLEKRAKDYILOPFNINSNDRI 170

OY 64 F 64
DB 171 F 171

RESULT 15
US-08-838-151A-27
Sequence 27, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Liu, Hong T
APPLICANT: Hanson, Steve
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSER: Dressler, Rocky, Milamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 09/08/83B, 151A
CLASSIFICATION: 800

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ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-27

Query Match 56.6%; Score 206; DB 4; Length 357;
Best Local Similarity 63.9%; Pred. No. 2.7e-19;
Matches 39; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

OY 4 WGEYDNGSRAGCGCGTNSNLLDLAINSKREALOITREIKYIROPFNINSNDRI 63
DB 111 FGVSQIDGRSAGCGQANDAVAAALNAGSKSEALNLEKRAKDYILOPFNINSNDRI 170

OY 64 F 64
DB 171 F 171

Search completed: January 3, 2002, 15:38:52
Job time: 229 sec

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34 ysglucuaialaenclnlelleatrglnlyslleproglutystyleu 50
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2171 AAGACAGACCCGCGACATATTCAGAGAAATCCCGAAATATTTA 2122
Phleboflavivirusleuanserserfatleaparg1lephasaplysth 67
|||||
51 TTTCACTTCGCAATCAATTAATAGCAATTTAGTAGATATTGATTAAGAC 2072
|||||
67 rProgluPro 70
|||||
2071 TCTCGAGCCA 2062
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seq_name: gb_v1:AY029750
seq_documentation_block: 2598 bp DNA circular VRL 08-MAY-2001
LOCUS AY029750
DEFINITION Tomato severe rugose virus DNA-A, complete sequence.
VERSION AY029750.1 GI:14009278
KEYWORDS
SOURCE
ORGANISM Tomato severe rugose virus.
Virus: SSbNA viruses; Gemnilyviridae; Begomovirus.
REFERENCE
1 (bases 1 to 2588)
Rezende,M.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
Tomato-infecting Begomovirus, Tomato severe rugose virus, in Brazil
JOURNAL Unpublished
2 (bases 1 to 2588)
Rezende,M.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
Submitted (03-APR-2001) Instituto de Genetica e Biogenetica,
Universidade Federal de Uberlândia, Av. Amazonas s/n, Bloco 2E,
Sala 241, Campus Umuarama, Uberlândia, Minas Gerais 38.400-000,
Brazil
FEATURES
source
1. 2588
/organism="Tomato severe rugose virus"
/strain="Minas Gerais"
/db_xref="taxon:158463"
/notice="Brazil"
/notice="segment: DNA-A"
305..1060
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/codon_start=1
/product="coat protein"
/translation="MPKKDAPVRIAMGRSVSRNSANTSPRAGYGRKYNAAWBNBP
YKRPPIRTLGGDVPKRCGCGKVSERNDVSGYSCVYGRNGGITHRYCK
RRCVYSILYKGMWDESILKLNHTSVMENLVRREPGCTPMDDGGVNNMDEPST
ATYKNDLRDFOVMHPEYAAVGVGGYASNEQALAKRPMKVNANNVNHDEAGKEMHT
ENALLLYMACHTSNPEYATKRITIFYDSITN"
complement(1057..1455)
complement(1057..1455)
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/product="enhancer protein"
/protein_id="AAK50358.1"
/db_xref="GI:14009280"
/translation="MDSRTGGLTARQAENGYIWEISNLPYKRNVEDRWTTTSRV
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NNVITANRARSQVYNNRNNKRNITAFET
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/codon_start=1
/product="TIRAP"

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/translation="NRSSSLTPSTIKVQRAARKKQIRRRIDIECGCSLYWHICK
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/gene="AC1"
complement(1533..2588)
/gene="AC1"
/codon_start=1
/product="rep protein"
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/translation="MPSATKRPOLKAKKVEFLYKGSLSKREALSQALKATPTNPKK
IKVCELEHNEPHFLYLQEGNGCTONORFPLVSPRTSFRFRPIORAKSSPVK
SYVKDQGDITLMEGEFOIDKSGAGCGGTAAADAAEALNAPKVALQITIRKLPKPL
FOENHLSLDRIFARAPBEMVATPPPLSTFVWRBQDNADYDTCGAAAPRERIST
IIEGDSKTRKMAFARAHYISGLDFPMPVYSHNVEYVTDIAPYATKIKHKE
LIGAKRWKSGSKCTKRPVQIKGCPTELCNGECSKVPYERHKNASLNNTKIINA
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/codon_start=1
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/translation="MKKGSILSTCFNSKATYAKKINOSNPSRQGGUJISIRPREL
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BASE COUNT 660 a 525 c 598 g 805 t
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Ratio: 300.00 Length: 70
Percent Similarity: 91.429 Percent Identity: 78.571
alignment_block:
US-09-289-346a-2 x AY029750/rev ..
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YCGGCTGphsersasasasasasasasasasasasasasasasasasas 34
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2208 TTTCGACACAGCTACGATCGCTCGGACAGACGCTTGACACGACCTTCA 2159
|||||
34 ysglucuaialaenclnlelleatrglnlyslleproglutystyleu 50
|||||
2158 AAGACGTCGCTTCGAGAAATCCGAGACGTCGAGAAATATTTTA 2109
|||||
51 Phleboflavivirusleuanserserfatleaparg1lephasaplysth 67
|||||
2108 TTTCACTTCGCAATCAATTAATAGCAATTTAGTAGATATTGATTAAGAC 2059
|||||
67 rProgluPro 70
|||||
2058 TCTCGAGCCA 2049
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seq_name: gb_v1:AF291705
seq_documentation_block: 2622 bp DNA circular VRL 25-SEP-2000
LOCUS AF291705
DEFINITION Tomato rugose mosaic virus DNA-A, complete sequence.
ACCESSION AF291705
VERSION AF291705.1 GI:10281644

```



```

JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 1193)
AUTHORS     Faria,J.C. and Maxwell,D.P.
TITLE        Direct Submission
SOURCE       GenBank (Sep-1997), Plant Pathology, University of Wisconsin,
              1630 Linden Dr., Madison, WI 53706-1598, USA
FEATURES
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                1..1193
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                    /strain="LMV- Brazil 1"
                    /db_xref="taxon:58177"
                    complement(1)..(678)
                    complete_length<1..(678)
                    /gene="rep"
                    /note="ACI: replication associated protein"
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                    /protein_id="AA53157.1"
                    /db_xref="GI:1916345"
                    /translation="MTGKPKYAKNITFLTYGCTIKREPLDQGLAQIQSPNKE
                    IKICREREDCGIPHLDELILKKRKOITNNHLDLYLSTSEAFIRPNDCASSSDWY
                    SYTDDCDVDVEGVGGSGGGGTIVNDAAALANPKRTALDIIRKLEDEXTI
                    FORHMLNSIDRIFAPEDEWPPEPSFTFNPDENMDATRGSSSAAPLPMS
                    LIVEGSR"
                    rep_origin
                        676..797
                            /note="Origin of replication; common region"
                    gene
                        103..1193
                        1039..>1193
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                        /gene="AV1"
                        /note="CP"
                        /codon_start=1
                        /product="coat protein"
                        /protein_id="AA53158.1"
                        /translation="MKRQDSRPFMWGTSKISHTSNFRRGIGRKTNASBWRKP
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    Query: 281.00      Length: 70
    Subject: 4.532      Gaps: 0
Percent Similarity: 88.571 Percent Identity: 77.143
alignment_block:
US-09-289-346A-2 x LMU92532/rev ..
Align seg 1/1 to reverse of: LMU92532 from: 1 to: 1193
1   TTTLeuValTPpLgphGcIGaaTsPGcIyVALaLaALaLaAGlSYl 17
    |||||.....|||||.....|.....|.....|.....|.....|
348 ACAGCTGAATGCCGCCTGAATTCCAGGTCGCCAGCGGAGAATTCTTAAGAGAG 299
17 ycyScInThrSezaanSpAlaLaALaAguaLaLaanaSaIsaSerI 34
    I |||||.....|.....|.....|.....|.....|.....|.....|
298 CCAGAACAGACTTAAATGACGCTGACGCTGAGGCGCTTAATACCTCCAGATA 249
34 yaqJuuGLaLaLaandIdIleLaagSiLUlySLepFGGluysLySLau 50
    |||||.....|.....|.....|.....|.....|.....|.....|.....|
248 AACGACGGCTCTCCAATTAATTAAGAGGAATTCGCCGAGAAAATATCT 199
51 pHeqLiPhetHaIsaLuauaNsErSaLnLeuaPaPyLIePhaapLySt 67
    |||||.....|.....|.....|.....|.....|.....|.....|.....|
198 TTTCATATTCATATTAATTAATTCATATTCATAGCATTTTCCACAAAGCC 149
67 rProGUUpRo 70 ..|||
148 TCccGAGAcCa 139 .....
seq_name: gb_v1:AF131071

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seq_documentation_block:		VRL	17-JUN-1999
LOCUS	AF131071 1345 bp DNA		
DEFINITION	Tomato mild mottle geminivirus segment A replicon; associated protein (rep) and coat protein (cp) genes, partial cds.		
ACCESSION	AF131071.1	GI:4928223	
VERSION			
KEYWORDS			
SOURCE	Tomato mild mottle geminivirus. Tomato mild mottle geminivirus.		
ORGANISM	Yluses; ssDNA viruses; Geminiviridae; Unclassified Geminiviridae.		
REFERENCE	1 (bases 1 to 1345)		
AUTHORS	Maxwell,D.P., Ramirez,P., Karkashian,J.P., Doyle,M.M. and Nakhla M.K., Wejda,L.,		
JOURNAL	2 (bases 1 to 1345)		
AUTHORS	Nakhla M.K., Weiland,G., Kamal,S. and Maxwell,D.P.		
TITLE	Direct Submission		
JOURNAL	Submitted (25-FEB-1999) Plant pathology, University of Wisconsin-Madison, 1630 Linden Dr., Madison, WI 53706-1598, USA		
FEATURES	Location: Openly 1. openintron="Tomato mild mottle geminivirus" /isolate="HN96-H5Kv" /specimen_voucher="H5" /db_xref="taxon:92943" /chromosome="segment_A" /clone="BHMH54Kv" /country="Honolulu: Comayagua Valley" note="Obtained from a tomato plant collected in Dec. 1996 from a field at the station of the University of Hawaii." complement(<1..678) /gene="rep" /note="aol" complement(<1..678) /gene="cp" /note="rep protein" /codon_start=1 product="replication-associated protein" product_keywords="replication-associated protein" /db_xref="c1:492824" /translati... SYNDONDIOTEMERGIDIGASRGGCQTANDMAALNASSKEEAMGIIKSKLPKEPFI FOVHAHSLSMLRIFAAPEFPIPELSTFTVDENOMDTDYGGAARPERPIS IIEEDSR"		
CDS	676..932 1001..1345 /gene="cp" /note="aol" 1001..>1345 /gene="cp" /note="aol" 1001..>1345 /gene="cp" /note="capsid protein" /codon_start=1 product="coat protein" product_keywords="coat protein" /db_xref="c1:492825" /translati... YRPPIFYAVSDAENMKRHDAWPKRMATIPVRSRSSNYVPDGSGRKFDKSAMANNRP YRPPIFYAVSDAENMKRHDAWPKRMATIPVRSRSSNYVPDGSGRKFDKSAMANNRP RCVSAYITLKAY"		
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gene	1001..1345		
CDS	1001..>1345		
BASE COUNT	329 a 289 c 313 g 414 t		
ORIGIN			
alignment_scores:			
Quality:	281.00	length:	70
Ratio:	4.333	caps:	0
Percent similarity:	92.857	Percent identity:	72.857
alignment_block:			


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          /note="replication-associated protein"
          /codon_start=1
          /product="ACI"
          /protein_id="AA082605.1"
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          /translation="MPKRSFSIRAKNYFITTPGCSISREDAISLQNTITPVKKPT
          YVNRNMESEPHATPLDLEKNGCTNNMLTDLSTYSHIRTOASASSWS
          YKRNKSNKSNKSNKSNKSNKSNKSNKSNKSNKSNKSNKSNKSNKSNKSNKSNK
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BASE COUNT      350 a      264 c      256 g      295 t
ORIGIN
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    Query: 260.00 Length: 70
    Ratio: 4.002 Gaps: 0
Percent Similarity: 91.429 Percent Identity: 67.143
alignment_block:
US-09-289-346A-2 x AF026553 ..
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791 ACCATCGAATGGGCAATGGTCGCAGATTGACGGAGAAGATCGCTCCAGGTGG 840
17 ycgsglnrthseraanmpaspaiaaiaaiaagiualaiauausaiaaseel 34
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
841 CCACAGACCACCAAACGCCACGCGAGGGCATTTAAACCTCTGGACA 950
34 ysglmglaiaandhlleilaesglilylylleipactgtysrytleu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
891 AGCAAGAACCCCAATAATCATAAAGAGAAATGGCGCAAACTTTCTT 940
51 pheicnphenlsasluansrsersanleuaspaaytylepheaspysyth 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
941 TTTCAGATCATCATCAATCAATGACGTCGTGATGAGATTTTCAATGAAGCC 950
67 prgplugat 70
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991 TCCAAATCCG 1000
seq_name: gb_vl:AB001315
doc documentation_block:
Accession: AB001315 13-FEB-1998
Definition: tobacco leaf curl virus CI and CA genes, clone YOKOHAMA3-1, partial
accession version keywords
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
DIRECT SUBMISSION
Submitted (19-FEB-1997) to the DDBJ/EMBL/Genbank databases.
Kazuyuki Ooi, Kyushu University, Department of Biology; 6-10-1
Shokakuji, Minamiku, Fukuoka 812, Japan
E-mail: koo@shokakuji.kyushu-u.ac.jp, Tel:+81-92-642-2624,
Fax:+81-92-642-2645
2. (bases 1 to 560)
Ooi,K., Ohnishi,S., Ishii,I., and Yahara,T.
Molecular phylogeny of geminiviruses infecting wild plants in Japan

```

```

JOURNAL      3 Plant Res. 110, 247-257 (1997)
FEATURES
    source     1..570 bp=richness leaf curl virus"
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               /clone="YOKOHAMA3-1"
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               complement(<1..5570)
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               ASSFQVPEELSEWASBEWASBWRBPM"
               complement(231..488)
    gene       /gene="C4"
               /cdo_start=1
               /protein_10="BA3403.1"
               /db_xref="GI:3198715"
               /translation="MBAISMCFSSKANKNTKTSSTWYPPQPDHISITPRELINF
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    ORIGIN     141 a 121 c 126 g 102 t
               BPS COUNT

alignment_scores:
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    ratio: 4.145        gaps: 1
    percent similarity: 72.941 percent identity: 58.824

alignment block:
US-09-289-346A-2 x AB001315/rev ...

Align seg 1/1 to reverse of: AB001315 from: 1 to: 570

1  ThrtlevaltrpClyglubheglinvalaspGyalalalalaglycl 17
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   |||||
318 AGCGTCGAATGGGACATCTCGATCGATACGAGAGAGATCGAGAGAG 269
   |||||
17  Ycysglntlrserasnpalalalaglylalnlsuansaserl 34
   |||||
   |||||
268 CTGCCGAATCTCAACGACGAGTCGACGAGCCCTTAAAGCAGATTGCA 219
   |||||
34  Ysglucnlalalendllletlratrglulyslleptroglyultrytleu 50
   |||||
   |||||
218 AGCGACACACATTCAGCATATAGGACAAAGCTCCCTCAAAAGATTATA 169
   |||||
   |||||
51  Pheglapbhehslaslnlsuanserasesluenapaylle 63
   |||||
   |||||
168 TTTCATATATCATATTAAATAGCTAATTAGATAGATTTTGCGCTCC 119
   |||||
   |||||
64  .....Pheasplythrpp 68
   |||||
   |||||
118 GTTGGAGGTTTTTGTTGGTCCCTTCACAGCCCTCATCTTGAATGAC 69
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   |||||
68  roglu 69
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68  CAGAA 64

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FT misc_feature 429..459
FT /tag- e
FT /note= "Ribozyme R3 target sequence"
FT misc_feature 442..444
FT /tag- d
FT /note= "Ribozyme R3 cleavage site"
XX
XX M09503404-A.
XX
XX 02-FEB-1995.
XX
XX 22-JUL-1993. 93MO-EP01946.
XX
XX 22-JUL-1993. 93AU-0047014.
XX 22-JUL-1993. 93MO-EP01946.
XX
XX (BIOC) BIOCEN SA.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Baudino S, Comeau D, Dry IB, Gruber V, Lence P,
XX Mason J, Rezalan MA, Rigney JE, Rezalan MA.
XX WPI: 1995-075232/10.
XX
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX and/or assembly of viruses by cleaving target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX
XX Example 10: Fig 11c: 90pp; English.
XX
XX The sequence is a tomato leaf curl virus target sequence for
XX polyribozyme-P, which hybridizes to and cleaves the sequence and
XX thereby reduces replication, infection and/or assembly of the virus
XX substantially. The ribozyme may be expressed in a transgenic plant,
XX e.g. tomato, to confer virus disease-resistance.
XX
XX Sequence 479 BP: 145 A; 95 C; 97 G; 142 T; 0 other:

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alignment_scores:
Quality: 229.00 length: 85
Ratio: 3.754 Gaps: 1
Percent Similarity: 71.765 Percent Identity: 52.941

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alignment_block:

US-09-289-346a-2 x A084372 ..

Align seq 1/1 to: A084372 from: 1 to: 479

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1 Thrluvaltrpglygluphginvalapjyalaialaialaaglygl 17
||||| ||||||| ||||||| ||||||| |||||||
140 ACCCTCGAATGGGAGAGATTTCAGATTCACGACATCGCAAGAGGGG 189
17 YCysgltrhserasnspalialaialaialaialaialaiala 34
||||| ||||||| ||||||| ||||||| |||||||
190 ACAACATCAGCAGCATGACGCTTACGCCACGCCCTTACATCGAAGTA 239
34 ysglglualaleuglnlileargllyslleprogluytyrleu 50
||||| ||||||| ||||||| ||||||| |||||||
240 AGCTAGAGGCTTTACAGCTTCAGAGCATTCACCCCTTACAGATTCGT 289
51 Phcglrpheliasenleuasnserasnleuasnarglle..... 63
||||| ||||||| ||||||| ||||||| |||||||
290 TTTCANITTCATTAATTTAAATNGATTAATTAATGATTTTACACCC 339
64 ..... Phaspltyrtp 68
340 GTTCAGAGCTTATGCTTCCTTTTATGCTTCCTTCCTTCATGAGATTC 389
68 roglu 69
|||||
390 CAGAA 394

```

```

seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT:A084375
seq_documentation_block:
ID A084375 standard: DNA: 550 BP.
XX
XX A084375;
XX
XX 19-AUG-1995 (first entry)
XX
XX Tomato leaf curl virus Australian strain DNA sequence.
XX
XX Tomato leaf curl virus: Australia strain; plant disease: ds.
XX
XX Tomato leaf curl virus (Australia).
XX
XX M09503404-A.
XX
XX 02-FEB-1995.
XX
XX 22-JUL-1993. 93MO-EP01946.
XX
XX 22-JUL-1993. 93AU-0047014.
XX 22-JUL-1993. 93MO-EP01946.
XX
XX (BIOC) BIOCEN SA.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Baudino S, Comeau D, Dry IB, Gruber V, Lence P,
XX Mason J, Rezalan MA, Rigney JE, Rezalan MA.
XX WPI: 1995-075232/10.
XX
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX and/or assembly of viruses by cleaving target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX
XX Disclosure: Fig 1: 90pp; English.
XX
XX The sequence represents the complementary sense DNA strand of an
XX Australian strain of tomato leaf curl virus. Ribozymes specific
XX for this sequence may be used in generation of transgenic plants
XX with disease-resistance.
XX
XX Sequence 550 BP: 149 A; 120 C; 134 G; 142 T; 6 other:

```

```

alignment_scores:
Quality: 228.50 length: 86
Ratio: 3.746 Gaps: 1
Percent Similarity: 70.930 Percent Identity: 52.326

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alignment_block:

US-09-289-346a-2 x A084375 ..

Align seq 1/1 to: A084375 from: 1 to: 550

```

1 Thrluvaltrpglygluphginvalapjyalaialaialaaglygl 17
||||| ||||||| ||||||| ||||||| |||||||
201 ACCCTCGAATGGGAGAGATTTCAGATTCACGACATCGCAAGAGGGG 250
17 YCysgltrhserasnspalialaialaialaialaialaiala 34
||||| ||||||| ||||||| ||||||| |||||||
251 ACAACATCAGCAGCATGACGCTTACGCCACGCCCTTACATCGAAGTA 300
34 ysglglualaleuglnlileargllyslleprogluytyrleu 50
||||| ||||||| ||||||| ||||||| |||||||
301 AGCTAGAGGCTTTACAGCTTCAGAGCATTCACCCCTTACAGATTCGT 350
51 Phcglrpheliasenleuasnserasnleuasnarglle..... 63
||||| ||||||| ||||||| ||||||| |||||||
351 TTTCANITTCATTAATTTAAATNGATTAATTAATGATTTTNNATCAC 400
64 ..... Phaspltyrtp 67

```



```

1  ThleuValTrpGlyGlnPheGlnValAspGlyValAlaAlaAlaIactGyl 17
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
328  ACATCGACATCGGACACATTCACAGTCGACGCGACGATTCACAGAGG 377
17  YCYSGInThrSerAsnAspAlaAlaIactGylValAlaAlaAlaIactGyl 34
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
378  TCAGCAGTCGCCACGACCTCATTCGACAGCATTTAAAGCGCATTCACA 427
34  YSGInGluAlaLeuGlnIleIleIleArgGlyIuysIleProGlyuysTYleu 50
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
428  TTGACATCTGCTCCACACATTCGACGACGACGATTCGATTCAGTC 477
51  PheGlnPheIleAsnLeuAsnSerAsnLeuAsnAspArgIlePheAsnPluysTh 67
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
478  CTTCCACATCCACACATTCGCTTCATATTCGACAGCATTCCTGTCAAAGT 527
67  rProGluPro 70
|||||  |||||||  |||
528  GCCGGAACCA 537

seq.name: /cgnl_B/gcgdata/geneseq/geneseq/NA1997.DAT:AA793292
seq.documentatation_block:
ID  AA793292 standard; DNA; 1062 BP.
XX
XX
AA793292:
XX
XX
27-APR-1998 (first entry)
XX
DE  Bean golden mosaic geminivirus CI mutant ORF BGAC228.
XX
KW  Geminivirus; BGWV; CI gene; transdominant mutation;
transgenic plant; disease resistance; ss; cyclic; circular.
XX
OS  Bean golden mosaic virus type II isolate Guatemala.
XX
XX
MO9739110-A1.
XX
XX
23-OCT-1997.
XX
XX
15-APR-1997: 97MO-US06300.
XX
XX
16-APR-1996: 960US-0015517.
XX
XX
(SEMT-) SEMINIS VEGETABLE SEEDS INC.
XX
PA  (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX
Abiquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT:
WPI: 1997-526447/48.
P-PSDB: AAM34354.
XX
XX
Transgenic plants expressing geminivirus ACI and CI wild-type and
mutant genes - have increased resistance to geminivirus infection
e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
golden mosaic geminivirus
XX
XX
Claim 13: Page 111-112; 132pp; English.
XX
XX
This DNA sequence comprises construct BGAC228 that codes for a
transdominant lethal mutant (see AAM34334) of the CI protein (see
AAM34338) of bean golden mosaic virus (BGWV). It was obtained by
Ruhel mutagenesis of the wild-type CI gene (see AA793314). CI is
required for replication. The invention involves production of
transgenic plants containing DNA comprising geminivirus CI or ACI
wild type or mutant sequences that negatively interfere in trans
geminivirus replication. The invention also involves transgenic
plants are resistant to viral infection. The ACI/CI genes are
especially from BGWV, tomato mottle virus or tomato yellow leaf
curl virus (see AA793282-93) and encode polypeptides (see AAM34324-35)
that have mutations in the highly conserved DNA-nicking and/or the
NTP-binding domains.

```

```

XX
SQ  Sequence 1062 BP; 338 A; 247 C; 218 G; 259 T; 0 other;
alignment_scores:
Quality: 215.00 Length: 70
Ratio: 3.644 Gaps: 0
Percent similarity: 84.286 Percent identity: 57.143
alignment_block:
US-09-289-346a-2 x AA793292
Align seg 1/1 to: AA793292 from: 1 to: 1062
1  ThleuValTrpGlyGlnPheGlnValAspGlyValAlaAlaAlaIactGyl 17
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
328  ACATCGACATCGGACACATTCACAGTCGACGCGACGATTCACAGAGG 377
17  YCYSGInThrSerAsnAspAlaAlaIactGylValAlaAlaAlaIactGyl 34
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
378  TCAGCAGTCGCCACGACCTCATTCGACAGCATTTAAAGCGCATTCACA 427
34  YSGInGluAlaLeuGlnIleIleIleArgGlyIuysIleProGlyuysTYleu 50
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
428  TTGACATCTGCTCCACACATTCGACGACGACGATTCGATTCAGTC 477
51  PheGlnPheIleAsnLeuAsnSerAsnLeuAsnAspArgIlePheAsnPluysTh 67
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
478  CTTCCACATCCACACATTCGCTTCATATTCGACAGCATTCCTGTCAAAGT 527
67  rProGluPro 70
|||||  |||||||  |||
528  GCCGGAACCA 537

seq.name: /cgnl_B/gcgdata/geneseq/geneseq/NA1997.DAT:AA793293
seq.documentatation_block:
ID  AA793293 standard; DNA; 1062 BP.
XX
XX
AA793293:
XX
XX
27-APR-1998 (first entry)
XX
DE  Bean golden mosaic geminivirus CI mutant ORF BGAC262.
XX
XX
KW  Geminivirus; BGWV; CI gene; transdominant mutation;
transgenic plant; disease resistance; ss; cyclic; circular.
XX
XX
OS  Bean golden mosaic virus type II isolate Guatemala.
XX
XX
MO9739110-A1.
XX
XX
23-OCT-1997.
XX
XX
15-APR-1997: 97MO-US06300.
XX
XX
16-APR-1996: 960US-0015517.
XX
XX
(SEMT-) SEMINIS VEGETABLE SEEDS INC.
XX
PA  (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX
Abiquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT:
WPI: 1997-526447/48.
P-PSDB: AAM34355.
XX
XX
Transgenic plants expressing geminivirus ACI and CI wild-type and
mutant genes - have increased resistance to geminivirus infection
e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
golden mosaic geminivirus
XX
XX
Claim 13: Page 115-116; 132pp; English.

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XX PN M0960573-A1.
XX ND 21-MAR-1996.
XX PE 15-SEP-1595; 95MO-FR01192.
XX PR 15-SEP-1994; 94FR-0011040.
XX PA (CNRS ) CENT NAT RECH SCL.
XX GI Gromenborn B;
XX HP1. 1996-179947/18.
XX P-PSDB: AAR88870.
XX PT Prodn. of virus-resistant transgenic plants - using mutated genomic
XX sequence from phytolectogenic DNA virus
XX
XX Disclosure: Fig 13; 93pp; French.
XX
XX Mutation of consensus amino acids in the NTP-binding site of
XX geminivirus Rep protein is used to produce replication deficient
XX viruses. The mutated viral nucleic acid is used for producing
XX transgenic plants that are resistant to, or tolerant of, the native
XX virus. The present sequence encodes a mutant form of the Rep (or CI)
XX protein from the serdianin isolate of tomato yellow leaf curl virus
XX (TYLCV). The mutated sequence was generated by site-directed mutagenesis
XX of a cDNA encoding the Rep protein of TYLCV. The resulting transgenic
XX plants transformed with the mutated virus were found to be resistant to
XX TYLCV, i.e. the mutation results in a dominant negative phenotype.
XX
XX Sequence 1080 BP; 355 A; 248 C; 210 G; 267 T; 0 other:
XX
XX alignment_scores:
XX Quality: 215.00 Length: 69
XX Ratio: 3.772 Gaps: 0
XX Percent Similarity: 82.609 Percent Identity: 55.072
XX
XX alignment_block:
XX US-09-289-346A-2 x AAT12904 ...
XX
XX Align seg 1/1 to: AAT12904 From: 1 to: 1080
XX
XX 2 LeavtltRFG;ygltubpghnigvlaspsjyAlAlaAlaAlaagj;gLyGlyC 18
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 331 CTTGAAAGGGGGCTCTTTCACGATCGACGAGCGATGCTCTAGCGGAGAGCA 380
XX
XX 18 sGlnThrSerAsnAspAlaAlaAlaAlaAlaAlaAlaAlaAlaSerSerItyG 35
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 381 ACACACACGACGACGACGCTTACGACACGACACATTAACGACGACGATAGG 430
XX
XX 35 IugLAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 51
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 431 CGCAGGCTCTGATGTATTAATTAACATTAACGCGCTACAGATTAACGCTCTA 480
XX
XX 52 GlnPheHisAsnLeuAsnSerSerAsnLeuAspArgIlePheAspLysThrPr 68
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 481 CATTTGATGATATATATATATATATATATATATATATATATATATATATAT 530
XX
XX seq_name: /cogn1_8/cgdata/geneseq/geneseqn/NA1996_DAT.AAT12905
XX seq_documentation_block:
XX ID AAT12905.standard; DNA; 1080 BP.
XX AC AAT12905;
XX
XX 07-NOV-1996 (first entry)
XX

```

XX Sardinian tomato yellow leaf curl virus mutated CI gene (K227H).
XX Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
XX modification of nucleic acid; replication;
XX viral resistance; geminivirus; tomato yellow leaf curl virus;
XX Sardinian isolate: SYICYV; transgenic plant; P-loop; CI gene;
XX All genes: ss.
XS Sardinian tomato yellow leaf curl virus.
OS
FH Key Location/Qualifiers
FH CDS 1..650
FT /product= Rep.(K227H)
FT /note= "encodes Rep protein in which wild-type Lys
FT binding site, is replaced by His"
FX
FX MO9608573-AL.
FX
FX 21-MAR-1996.
PD
PP 15-SEP-1995: 95NO-FR01192.
XX
XX 15-SEP-1994: 94FR-0011040.
XX
XX (CNRS) GENT NAT RECH SCI.
XX
XX Gronenborn B.
PI
DR WPI: 1996-179947/18.
DR P-PDB; AA88871.
XX
XX Prod'n. of virus-resistant transgenic plants - using mutated genomic
XX sequence from phytopathogenic DNA virus
XX
XX Disclosure: Fig 13: 93pp; French.

Mutation of consensus amino acids in the NTP-binding site of
geminivirus Rep protein is used to produce replication deficient
viruses. The mutated viral nucleic acid is used for producing
transgenic plants that are resistant to, or tolerant of, the native
protein. The present sequence encodes a mutant form of the Rep (or CI)
protein from the Tomato Yellow Geminivirus (TYSGV) that has been
engineered in which the wild-type Lys227 residue has been changed to a
His residue; transgenic Nicotiana benthamiana plants generated by a
transformation with the mutated virus were not resistant to SYICYV.
In contrast, plants transformed with a virus in which Lys227 had been
replaced by Ala were found to be resistant.

Sequence 1080 BP; 356 A; 248 C; 208 G; 268 T; 0 other:
SO

Alignment scores:

	Quality: 215.00	Length: 69
Ratio:	3.772	Gaps: 0
Percent Similarity:	82.609	Percent Identity: 55.072

alignment block:
US-09-289-346A-2 x AAT12905 ..

Align seg 1/1 from: AAT12905 From: 1 to: 1080

```

      2   Leauatfpgtgytlapbgcinalaspolyalaalaaialagctgcy 18
          |||                                     |||
331  CTGAAAGGGGTACTTCCTGCACATCGACCAAGCATCTCCTAGCGACACA 380
          |||||                                     |||||
18  sgltnhsrntsrnsaiaaiaglaiaaleuaasaiaser-serrlys 35
    |||||||         |||||         |||||         |||||
381  ACAGACGCCAACGACCTTACCGCAAGCCAAATPACACGACGAAGAATG 430
          |||||||         |||||||         |||||||         |||||||
35  ltuclualaleuglnlileahgcgtvlyslterogtguylstytleauphe 51
```

[illegible]

alignment-scores:
 Quality: 215.00 Length: 69
 Ratio: 3.772 Gaps: 0
 Percent Similarity: 82.609 Percent Identity: 55.072

alignment-block:
 US-09-289-346a-2 x AMT12906 ..

Align seq 1/1 to: AMT12906 from: 1 to: 1080

```

2  LeuValITPGLyGluPheGlnValAspGlyAlaAlaAlaGlyGly 18
331 CTTGAATGGCTACTTCCATCGACGACGACGATCTGTCAGGCGACCA 380
18  SGLTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST
381 ACACACACACACACACGCGCTTACGACGACGATTTACGACGACGAC 430
35  LAGCTAATGAGCTGATGATGATGATGATGATGATGATGATGATGAT 51
431 GCGAGCGCTTATGATGATGATGATGATGATGATGATGATGATGAT 480
52  GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThr 68
481 CATTTTCATATATTAATTAATTAATTAATTAATTAATTAATTAAT 530
68  GCLuPro 70
531 GCGACCT 537

```

seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AMT93314

seq_documentation_block:
 ID AMT93314 standard; DNA: 1183 BP.

AMT93314:
 27-APR-1998 (first entry)

DE Bean golden mosaic geminivirus CI open reading frame.
 XX
 XX Geminivirus; BGMV; CI gene; transdominant mutation;
 XX Transgenic plant; disease resistance; ss; cyclic; circular.
 XX
 OS Bean golden mosaic virus type II isolate Guatemala.
 XX
 XX
 FH Key Location/Qualifiers
 FT 1..1062
 FT /tag= a
 CDS
 MO9739110-A1.
 XX
 XX
 XX 23-OCR-1997.
 XX
 XX 15-APR-1997: 97MO-US06300.
 XX
 XX 16-APR-1996: 96US-0015517.
 XX
 XX (SEMI-) SPINITS VEGETABLE SEEDS INC.
 XX PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX
 XX Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT:
 XX
 XX WPI: 1997-526447/48.
 XX P-PSDB: AMW4338.
 XX
 XX Transgenic plants expressing geminivirus ACI and CI wild-type and
 XX mutant genes - have increased resistance to geminivirus infection
 XX e-9. tomato mottle virus, tomato yellow leaf curl virus or bean
 XX golden mosaic geminivirus
 XX
 XX Example 5: Page 100-102: 132pp: English.

CC This genomic DNA sequence includes the open reading frame (ORF) of
 CC the wild-type CI gene of bean golden mosaic virus (BGMV), a
 CC geminivirus that has a monopartite genome. The CI protein (see
 CC AMW4338) is required for replication. The wild-type CI ORF was
 CC inserted into a plasmid vector (see AMW4338) and the resulting
 CC involves production of transgenic plants containing DNA consisting
 CC of CI or ACI wild-type or mutant sequences that negatively interfere
 CC in trans with geminiviral replication during infection. Such
 CC transgenic plants are resistant to viral infection. The ACI/CI
 CC genes are especially from BGMV, tomato mottle virus or tomato
 CC yellow leaf curl virus (see AMW3242-93) and encode polypeptides
 CC (see AMW3242-35) that have mutations in the highly conserved
 CC DNA nicking domain and/or the ATP-binding domains.

Sequence 1183 BP: 372 A: 276 C: 248 G: 287 T: 0 other:

alignment-scores:
 Quality: 215.00 Length: 70
 Ratio: 3.644 Gaps: 0
 Percent Similarity: 84.286 Percent Identity: 57.143

alignment-block:
 US-09-289-346a-2 x AMT93314 ..

Align seq 1/1 to: AMT93314 from: 1 to: 1183

```

1  ThrLeuValITPGLyGluPheGlnValAspGlyAlaAlaAlaGlyGly 17
328 ACATCGAATGGCGACGACGATTCGACGACGACGATTCGACGACGAC 377
17  YCYGInThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
378 TCACGACGCTGCGCAAGCTCATATGCGCAAGCGATTTAAAGCGACATTC 427
34  YGCTAATGAGCTGATGATGATGATGATGATGATGATGATGATGAT 50
428 TTGATCTGCTTCACATATTAATTAATTAATTAATTAATTAATTAAT 477
51  PheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThr 67
478 CTTCAACATCCACACATCCGCTTCAATTCGACGACGATCTGCAAGGT 527
67  PProGluPro 70
528 GCGCGAACCA 537

```

seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AMT93290

seq_documentation_block:
 ID AMT93290 standard; DNA: 1183 BP.

AMT93290:
 27-APR-1998 (first entry)

DE Bean golden mosaic geminivirus CI mutant gene.
 XX
 XX Geminivirus; BGMV; CI gene; transdominant mutation;
 XX Transgenic plant; disease resistance; ss; cyclic; circular.
 XX
 OS Bean golden mosaic virus type II isolate Guatemala.
 XX
 XX
 FH Key Location/Qualifiers
 FT 1..1062
 FT /tag= a
 CDS
 MO9739110-A1.
 XX
 XX
 XX 23-OCR-1997.
 XX
 XX 15-APR-1997: 97MO-US06300.


```

PR 16-APR-1996: 96US-0015517.
XX
XX (SEMT-) SEMINIS VEGETABLE SEEDS INC.
PA (WISC-) WISCONSIN AIDMINT RES FOUND.
XX
XX Ahiquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT:
XX WPI: 1997-526447/48.
XX P-PSDB: AAM34332.
XX
XX Transgenic plants expressing geminivirus AC1 and C1 wild-type and
XX mutant genes - have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX
XX Claim 13: Page 103-105; 132pp: English.
XX
XX This DNA sequence comprises construct BGAC190 that codes for a
XX control mutant (see AAM34332) of the C1 protein (see AAM34338) of bean
XX golden mosaic virus (BGWV). It was obtained by kunkel mutagenesis
XX of the C1 gene of BGWV. The construct is required for
XX replication of the virus. The inventors have found that
XX plants containing DNA comprising geminivirus C1 or AC1 wild-type or
XX mutant sequences that negatively interfere in trans with
XX geminiviral replication during infection. Such transgenic plants
XX are resistant to viral infection. The AC1/C1 genes are especially
XX from BGWV, tomato mottle virus or tomato yellow leaf curl virus (see
XX AAM3432-35) and encode polypeptides (see AAM3432-35) that have
XX a high degree of homology to the C1 protein of the virus. The
XX domains in the highly conserved DNA-nicking and/or Cme NTP-binding
XX
XX Sequence 1183 BP: 371 A: 277 C: 249 G: 286 T: 0 other:
XX
XX alignment_scores:
XX Quality: 215.00 Length: 70
XX Ratio: 3.644 Gaps: 0
XX Percent Similarity: 84.286 Percent Identity: 57.143
XX
XX alignment_block:
XX US-09-289-346A-2 x AAT93290 ..
XX
XX Align seg 1/1 to: AAT93290 from: 1 to: 1183
XX
XX 1 ThrlenvalTrpGlyIuphGlnValAspGlyAlaAlaAlaAlaGlyG1 17
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 328 ACATTCAGTACGCGACAAATTCACAGTCGACCGACATCTCCAAAGAG 377
XX
XX 17 yCysGlnThrSerAsnAspAlaAlaGlyAlaAlaAlaAlaSerL 34
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 378 TCAGCAGTCTGCCACAGCATATTCAGCAAGACGATTAAACCGACATTC 427
XX
XX 34 ySgIuAlaLeuGlnIleLeaArgIuysIleProGluIuysTyrLeu 50
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 428 TTGAATCTGCTTCACATATTTCAGGAGGAAGAACACCGAAATATTCGTC 477
XX
XX 51 PheGlnPheHisAsnLeuAsnSerAsnIleuAspArgIlePheAspIy 67
XX ..... ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 478 CTTTCACATCTGCGCTTACATCTGACACGATCTTCGTCAAAAGT 527
XX
XX 67 PProGluPro 70
XX ||||| |||||
XX 528 CGCCCAACCA 537
XX
XX seq_name: /cgnl_8/seqdata/geneseq/geneseq/NA2000.DAT:AAA94700
XX seq_documentation_block:
XX ID AAA94700 standard: DNA: 1651 BP.
XX
XX AAA94700:
XX
XX 15-JAN-2001 (first entry)

```

```

DE PMRG 2288 35S-rep gene cassette.
XX
XX Geminivirus: DNA-A: geminivirus replication inhibition; ac3 gene;
XX Transgenic plant: antiviral; gene therapy; bean golden mosaic virus;
XX BGWV: alfalfa mosaic virus; AMV; cauliflower mosaic virus; CMV; ds.
XX
XX Bean golden mosaic virus.
XX Cauliflower mosaic virus.
XX Alfalfa mosaic virus.
XX Synthetic.
XX
XX US618048-A.
XX 12-SEP-2000.
XX
XX 24-APR-1998: 96US-0065999.
XX
XX 25-APR-1997: 97US-0044923.
XX
XX (WISC-) WISCONSIN AIDMINT RES FOUND.
XX
XX WPI: 2000-610861/58.
XX
XX Example: Column 15-16; 14pp: English.
XX
XX The present sequence is a 35S-rep gene cassette comprising the rep gene
XX of bean golden mosaic virus (BGWV)-5'cloned downstream of the CMV
XX 35S promoter and an alfalfa mosaic virus (AMV) leader sequence. The
XX sequence was integrated into pSIT-KS+ to produce a rep gene expression
XX vector. DNA-nicking domain mutations may be incorporated into rep gene
XX to produce a genetic construct that acts as a trans-dominant inhibitor
XX of geminiviral replication. When expressed in a plant cell, this
XX construct is able to dramatically reduce replication of geminivirus.
XX The present sequence is a transgenic plant that expresses the
XX ac3 gene in addition to the trans-dominant inhibitor exhibit increased
XX efficiency and broadened specificity of inhibition of geminiviral
XX production. Geminiviruses are one of the greatest constraints on
XX production of important crops, including cassava, beans, cowpeas,
XX peppers, tomatoes and cotton. The effects of the virus can be overcome
XX by using the genetic construct.
XX
XX Sequence 1651 BP: 517 A: 393 C: 342 G: 399 T: 0 other:
XX
XX alignment_scores:
XX Quality: 215.00 Length: 70
XX Ratio: 3.644 Gaps: 0
XX Percent Similarity: 84.286 Percent Identity: 57.143
XX
XX alignment_block:
XX US-09-289-346A-2 x AAA94700 ..
XX
XX Align seg 1/1 to: AAA94700 from: 1 to: 1651
XX
XX 1 ThrlenvalTrpGlyIuphGlnValAspGlyAlaAlaAlaAlaGlyG1 17
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 796 ACATTCAGTACGCGACAAATTCACAGTCGACCGACATCTCCAAAGAG 845
XX
XX 17 yCysGlnThrSerAsnAspAlaAlaGlyAlaAlaAlaAlaSerL 34
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 846 TCAGCAGTCTGCCACAGCATATTCAGCAAGACGATTAAACCGACATTC 895
XX
XX 34 ySgIuAlaLeuGlnIleLeaArgIuysIleProGluIuysTyrLeu 50
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 896 TTGAATCTGCTTCACATATTTCAGGAGGAAGAACACCGAAATATTCGTC 945
XX
XX 51 PheGlnPheHisAsnLeuAsnSerAsnIleuAspArgIlePheAspIy 67
XX ..... ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 946 CTTTCACATCTGCGCTTACATCTGACACGATCTTCGTCAAAAGT 995
XX

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/clone="CSB003809"
/clone_lib="TREC CSR Wheat Endosperm Library"
/tissue-type="endosperm"
/notes="Stage 1 wheat embryo post anthesis"
/insert-seq="seq1-100"
/notes="Vector: Lambda Zap/Bluescript; Site_1: XhoI;
Site_2: EcoRI; plants grown in phytocon with 16C/23C
(day/night) 16 hour light. M13 Reverse sequencing primer
used. 1.0 Kbp average insert size."
BASE COUNT      100 a      178 c      167 g      134 t
ORIGIN
alignment_scores:
Quality:       71.00      Length:       49
Ratio:         2.290      Gaps:        2
Percent Similarity: 63.265   Percent Identity: 42.857
alignment_block:
US-09-289-346A-2 x BEA01979 ...
Align seg 1/1 to: BEA01979 from: 1 to: 579
9 ValAspGlyAlaAlaAlaGlyGlyGlnThrSerAsnAspAlaAla 25
::: |||||:::|||||:::|||||:::|||||:::
283 ATCGTGCTGTGGTGTGGTGTGGTGTGGTCCACACATCGTGGAGTC 332
25 aa||G||AlaLeuAlaSerSerLysGluAlaAlaGlnIleLeuAa 42
|||||:::|||||:::|||||:::|||||:::
333 CCGTAGCCCCCAAGCGTGTGGAGAAGAA..... 366
42 rgGlutLysIleProCyluLyS.....TYrLeuPhe 51
|||||:::|||||:::|||||:::|||||:::
367 ..GAAGAGATTGAGAGAGACGACGACGACTGGCTCTCTACTCTTT 411
seq_name: gb_csti1:AV736082
seq_documentation_block:
LOCUS     AV736082             616 bp      mRNA           EST          17-OCT-2000
DEFINITION AV736082 CB Homo sapiens cDNA clone CHMAB09.5', mRNA sequence.
ACCESSION  AV736082
VERSION     AV736082.1 GI:10853663
KEYWORDS   EST.
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 616)
AUTHORS   Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,O., Zhou,J., Shen,Y., Han,Z.,
Chen,S., Mao,M. and Chen,Z.
COMMENTARY Other:SSS: Sheared DNA-51M3.TR
CONTACT: Jialin Wang, Shanghai Genomic Research Institute, Shanghai
Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-jin Hospital
197 Rui-jin II Road, Shanghai 200025, P. R. China
Tel.: 86-21-64740490
Fax: 86-21-64743206
Email: mshw@ems.sjtu.sh.cn
NOTES     This clone is available at Shanghai Hematology Institute in
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
Location/Qualifiers
1..616
/organism="Homo sapiens"
/adaptor="GenBank"
/clone_lib="CB"
/tissue-type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/notes="Vector: pBluescript; Site_1: EcoRI; The insert is

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BASE COUNT      173 a      149 c      171 g      118 t
ORIGIN
alignment_scores:
Quality:       71.00      Length:       51
Ratio:         1.919      Gaps:        2
Percent Similarity: 72.549   Percent Identity: 35.294
alignment_block:
US-09-289-346A-2 x AV736082 ...
Align seg 1/1 to: AV736082 from: 1 to: 616
12 AlaAlaAlaAlaGlyGlyGln...ThrSerAsnAspAlaAlaAct 27
|||||:::|||||:::|||||:::|||||:::
6 GGCGCCGCCTGCCGACGGCGAGAACGACACAGAGCGCTCCACAG 55
27 ValAlaSerAlaSerSerLysGluAlaAlaGlnIleLeuArgGlu 44
:::|||||:::|||||:::|||||:::|||||:::
56 AGCGCTACACCGCGCGCTGTGCTGCAAGCATGCTCATGATG 98
44 ysIleProCyluLySTrpLeuPheIlePheIleAsnLeuAlaSerSerLeu 60
|||||:::|||||:::|||||:::|||||:::
99 ..ATCCGTAAAAGTTCACAGATATTGTGGCATCTCAACACCAACATC 146
61 Asp 61
147 GAT 149
seq_name: AK050848
seq_documentation_block:
LOCUS     AK050848             572 bp      DNA           GSS          27-JAN-2000
DEFINITION Sheared DNA-51M3.TF Sheared DNA Trypanosoma brucei genomic clone
ACCESSION  AK050848
VERSION     AK050848.1 GI:6774113
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei.
ORGANISM   Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE  1 (bases 1 to 572)
AUTHORS   Li,Shobess,I., Zho,H., Gill,S., Sub,E., Malik,J., Fujii,C.,
Gerard,C., Jacob,V., de Jong,P., Olliv.E., Melville,S., Donelson,J.,
Fraser,C. and Adams,M.
COMMENTARY Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library
(unpublished (1999))
Other:SSS: Sheared DNA-51M3.TR
CONTACT: Jialin Wang, Shanghai Genomic Research Institute, Shanghai
Contact: Zhu Chen
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel.: 301 838 0200
Fax: 301 838 0208
Email: jnelsey@edlib.rig.org
NOTES     Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library through ATCC. This clone will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/db/mdb/dbdb/.
Seq primer: M13-forward
Class: Shotgun.
Location/Qualifiers
1..572
/organism="Trypanosoma brucei"
/strain="RM927/X GUTat 10.1"
/db_xref="taxon:5691"
/clone_lib="Sheared DNA-51M3"
/tissue-type="Sheared DNA"
/cell_type="Sheared DNA"
/lab_host="BM25.8"
/notes="Vector: pUC19; Site_1: SmaI; Constructed at Ybe

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/db.xref="taxon:3352"
/clone_lib="NXSI_148.D05"
/clone_lib="NXSI" (nsf xylem slide wood inclined)
/tissue_type="xylem"
/cell_type="slide"
/lab_host="XLI-Blue"
/note="Vector: Bluescript SK; Site 1: Eco RI; Site 2: XhoI
The library is from early (spring) wood taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form side
wood by bending to a 45 degree angle and tying them to the
trunk. The resulting xylem was harvested from the sides
of the inclined stems and cloned into the library. The
genotypes was used for the library. oligo-dT primed cDNA
vector arms. NOTE: The sequences contain a 'cDNA adapter'
between the EcoRI site and the start of the EST. The
adapter sequence is 'ATTCTGGACGAG'."

BASE COUNT
ORIGIN

112 a 115 c 108 g 151 t 17 others

alignment_scores:

Quality: 67.00 Length: 52
Ratio: 2.094 Gaps: 2
Percent Similarity: 61.538 Percent Identity: 34.615

alignment_block:

US-09-289-346A-2 x BGJ75828/rev ..

Align seq 1/1 to reverse of: BGJ75828 from: 1 to: 503

18 CysglnThrSerAsnAspAlaAlaGluAlaAsnAsnSerLeu 34
111
498 TGTGGCTGACACACAGATTCTTCAGACAGAAAGGCTCAATCT 449
34 sgluGluAlaLeuGlnIleIle-ArgGluLysIleProGluLysTyrLeu 50
448 GGACTGGTTTACACACATCTTTAAACACACATCCGACAGATAT... 402
51 PhocInPhenIleAsnLeuSerAsnLeuAspArgIleAspAspTyr 67
401CTGATATGGATTTATATACGACAGATTCGACAAATT 367

67 PPro 68
111
366 ACCC 363

seq_name: gb_ests: A1563120

seq_documentation_block:

LOCUS A1563120 314 bp mRNA EST 26-MAR-1999
DEFINITION WML5445 watermelon lambda zap library Citrullus lanatus cDNA clone

WML5445 similar to Photosystem I Accessory Protein E, mRNA

sequence.

ACCESSION A1563120
VERSION A1563120.1 GI:4521502

KEYWORDS
SOURCE watermelon

ORGANISM Citrullus lanatus

REFERENCE
AUTHORS Shih,J.S.
TITLE Watermelon leaf cDNAs
JOURNAL unpublished (1999)

COMMENT
Contact: Jeong Sheop Shin
Plant Molecular Genetics
Graduate School of Biotechnology, University of Korea
116-701 Anam-dong 5/1 Seoul, Korea
Tel: 00 82 2 3290 3430

Fax: 00 82 2 927 9028
Email: jsshie@kucn.korea.ac.kr
Seq primer: T3.
FEATURES
source
1..314
location/Qualifiers
/db_xref="taxon:3654"
/clone="WML5446"
/clone_lib="watermelon lambda zap library"
/dev_stage="seedling"
/note="Organ: leaf; Citrullus lanatus (Thunb.) Mansf."

BASE COUNT
ORIGIN

69 a 105 c 59 g 81 t

alignment_scores:

Quality: 66.50 Length: 62
Ratio: 1.750 Gaps: 2
Percent Similarity: 61.290 Percent Identity: 32.258

alignment_block:

US-09-289-346A-2 x A1563120/rev ..

Align seq 1/1 to reverse of: A1563120 from: 1 to: 314

11 G1YAlaAlaAlaIadGlyGlyGlnThrSerAsnAspAlaAlaIad 27
111
212 GAGACGCGACCGAGAGTGGAGAGCGAGCGAGCGAGCGAGCGAG 163
27 uAlaLeuAsnAsnSerAspGluGluAlaLeuGlnIleIleArgGlu 44
162 GATTAACCAATCTAGATGATCTTGAAACAGAGATGCGAATCTTGGGAGAG 113
44 yslleProGluLysTyrLeuPheGlnIlePheAsnLeuAsnSerAsnLeu 60
111
112 AGCCGACAGAA.....CATTAATCTTAAGAGAGAGAAAT 81
61 ASPArgIlePheAspLys.....ThProGlu 69
80 GAGATGGTGGTGAAGAGGATGACCATCCACAGAA 45

seq_name: gb_gss: TAZ231H070

seq_documentation_block:

LOCUS TAZ231H070 565 bp DNA GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 231H07, reverse sequence,
genomic survey sequence.

ACCESSION AL480948
VERSION AL480948.1 GI:11846717

KEYWORDS
SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei

REFERENCE
1 (bases 1 to 565)

AUTHORS Hall,N., Bowman,S., Lemard,N.J., Doggett,J., Alkio,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Mellville,S.E., Rajandream,K.A. and Barrett,L.B.C.

TITLE Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust genome Campus,
Cambridge CB0 1SA. E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk

COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TR927/24 Graft 10.11) was mechanically sheared
4 kb). The v. x.1 method used for the library construction is
described in detail in Smith, R. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).

/organism=
/strato="T

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 ility sequence stop: 618

0:508 row: 2 column: 2
 ility sequence stop: 618

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FEATURES                                POLYA-No.      Location/Qualifiers
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/organism="Drosophila melanogaster"
/sex="male and female"
/clone_lib="LD Drosophila melanogaster embryo pot2"
/clone="LD30829"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="X11 Blue"
/note="Organ: embryo; Vector: pot2; Site-1: EcoRI; Site-2:
pot2. Sized fractionated cDNAs were directly ligated into
pot2."
BASE COUNT      181 a      166 c      139 g      132 t
ORIGIN

alignment_scores:
      Quality: 66.50      Length: 54
      Ratio: 1.847      Gaps: 1
      Percent Similarity: 66.667      Percent Identity: 33.333

alignment_block:
US-09-289-346a-2 x AA950726 ..

Align seg 1/1 to: AA950726 from: 1 to: 618

18 CysGlnHrSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerLy 34
149 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
150 TCTCACTCTCGAAGCCGCTCTCGAATGCTGCTGCTCTCACTTC 199
34 sglugluAa..LeuGlnIleIleArgGluLyIleProGluLySTyrl 50
:::|||||::: :: :::::||||
200 GGAAGCAAGTCCCTCTGCTGCTGCAAGACCTCTCGACAAACCAAC 249
50 eupheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLy 66
249 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
250 TCGAGCGCAATATCATGAGTGGTCAATGAATAACTTCTCGAAGAGACGCT 299
67 ThrProGluPro 70
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300 ACTGCGAGCT 311

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? FILING DATE: 17-MAR-1997
? CLASSIFICATION: 800
? PRIOR APPLICATION DATA: FR 94.11040
? APPLICATION NUMBER: FR 94.11040
? PCT NUMBER: 94.11040
? PRIOR APPLICATION DATA: 1994
? APPLICATION NUMBER: WO PCT/FR95/01192
? FILING DATE: 15-SEP-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: PATCH, Andrew J. 32,925
? REGISTRATION NUMBER: US94AL CNR TOM
? REFERENCE/DOCKET NUMBER: US94AL CNR TOM
? TELEPHONE: (703) 521-2297
? TELEFAX: (703) 685-0573
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1145 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1077
? US-08-809-103B-7

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? Quality: 215.00 Length: 69
? Ratio: 3.772 Gaps: 0
? Percent Similarity: 82.609 Percent Identity: 55.072

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? US-09-289-346a-2 x US-08-809-103B-7
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331 CTGTAAATGGGGTACTTCCAGATCGACGACATCTGCTGAGGAGAC 380
18 sGlnTrpSerAsnGlnAlaAlaGlnGluAlaLeuAsnGlySerTyrG 35
||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACAGACGCCACACGACCTTACGCCAAGCATTTAGCGAGCACTAAGT 430
35 IuGluAlaLeuGlnIleIleTrpGluGlySerIleProGluTyrTLeuPhe 51
||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTTGATGTATTAAAGAAATTAGCCGCTGAGAAATTAGCTTCA 480
52 GlnProPheAsnIleAsnSerAsnIleuAsnArgIleIlePheAsnGlySerTr 68
||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTCATATATATATATATATATATATATATATATATATATATATAT 530
68 oGluPro 70
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531 GGCACCT 537

seq_name: /cgnl_7/prodata/1/lna/6a_COMB.seq:us-08-809-103B-1
seq_documentation_block:
? Sequence 1, Application US/08809103B
? Patent No. 6133505
? GENERAL INFORMATION:
? APPLICANT: GENE/BORN, Bruce
? INVENTOR: GENE/BORN, Bruce
? TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
? NUMBER OF SEQUENCES: 17
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: YOUNG & THOMPSON
? STREET: 745 South 33rd Street
? CITY: Arlington

```

```

? STATE: Virginia
? COUNTRY: U.S.A.
? ZIP: 22202
? COMPUTER READABLE FORM:
? MOLECULE TYPE: floppy disk
? OPERATING SYSTEM: IBM compatible
? SOFTWARE: Patent Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/809,103B
? FILING DATE: 17-MAR-1997
? CLASSIFICATION: 800
? PRIOR APPLICATION DATA:
? PRIOR APPLICATION NUMBER: FR 94.11040
? FILING DATE: 15-SEP-1994
? APPLICATION DATA:
? APPLICATION NUMBER: WO PCT/FR95/01192
? FILING DATE: 15-SEP-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: PATCH, Andrew J. 32,925
? REGISTRATION NUMBER: US94AL CNR TOM
? TELEPHONE: (703) 521-2297
? TELEFAX: (703) 685-0573
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1145 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1077
? US-08-809-103B-1

alignment_scores:
? Quality: 215.00 Length: 69
? Ratio: 3.772 Gaps: 0
? Percent Similarity: 82.609 Percent Identity: 55.072

alignment_block:
? US-09-289-346a-2 x US-08-809-103B-1
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||| ||||| ||||| ||||| ||||| ||||| |||||
331 CTGTAAATGGGGTACTTCCAGATCGACGACATCTGCTGAGGAGAC 380
18 sGlnTrpSerAsnGlnAlaAlaGlnGluAlaLeuAsnGlySerTyrG 35
||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACAGACGCCACACGACCTTACGCCAAGCATTTAGCGAGCACTAAGT 430
35 IuGluAlaLeuGlnIleIleTrpGluGlySerIleProGluTyrTLeuPhe 51
||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTTGATGTATTAAAGAAATTAGCCGCTGAGAAATTAGCTTCA 480
52 GlnProPheAsnIleAsnSerAsnIleuAsnArgIleIlePheAsnGlySerTr 68
||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTCATATATATATATATATATATATATATATATATATATATATAT 530
68 oGluPro 70
|||
531 GGCACCT 537

seq_name: /cgnl_7/prodata/1/lna/6a_COMB.seq:us-08-809-103B-3
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? Sequence 3, Application US/08809103B

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: Patent No. 6133505
: GENERAL INFORMATION:
: APPLICANT: GRENORBN, Bruno
: TITLE OF INVENTION: PHOTONTOGENIC DNA VIRUS RESISTANT
: INVENTOR: GRENORBN, Bruno
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: YOUNG & THOMPSON
: STREET: 745 South 23rd Street
: CITY: Arlington
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA: US-08-809-103B
: FILING DATE: 17-MAR-1997
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FR 94.11040
: FILING DATE: 15-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/FR95/01192
: FILING DATE: 15-SEP-1994
: NAME: PATCH, Andrew J.
: ATTORNEY/AGENT INFORMATION:
: REGISTRATION NUMBER: 32,925
: REFERENCE/DOCKET NUMBER: US94AL CNR TOM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 521-2297
: TELEFAX: 248425 EMON-0573
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1150 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: MOLECULE TYPE: DNA (genomic)
: NAME/KEY: CDS
: LOCATION: 1..1077
: US-08-809-103B-3

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alignment_scores:

Quality	Ratio	Length	Gaps
215.00	3.772	69	0
Percent Similarity:	82.609	Percent Identity:	55.072

alignment_block:

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US-09-289-346a-2 x US-08-809-103B-3 ..

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Align seg 1/1 to: US-08-809-103B-3 from: 1 to: 1150

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||| ||||| ||||| ||||| ||||| ||||| |||||
331 CTGAAATGGGACTTTCAGATCCAGCGACGATCTGCGAGGAGCA 380
18 sGlnThSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerLYSG 35
||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACAGACACCCACAGCGCTCTACAGCAAGCAATTACCGCGACGACT 430
35 lncglnlalnclnlllellakrgclulyslllepcgclulysrlytaupe 51
||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTGATGTAATTAAGATTACGCCCTGAGATTACGTTCTA 480
52 GlnPhelHlsAsnLeuAsnSerAsnLeuAspAlrGllephesPLytrHPr 68
||||| ||||| ||||| ||||| ||||| ||||| |||||

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481 CATTTTCATATATATAATAGTATTAGTAAAGGTTTCAGAGCGCC 530
69 oGluPro 70
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531 GGCCACT 537
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: Sequence 5, Application US/08809103B
: Patent No. 6133505
: GENERAL INFORMATION:
: APPLICANT: GRENORBN, Bruno
: TITLE OF INVENTION: PHOTONTOGENIC DNA VIRUS RESISTANT
: INVENTOR: GRENORBN, Bruno
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: YOUNG & THOMPSON
: STREET: 745 South 23rd Street
: CITY: Arlington
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA: US-08-809-103B
: FILING DATE: 17-MAR-1997
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FR 94.11040
: FILING DATE: 15-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/FR95/01192
: FILING DATE: 15-SEP-1994
: NAME: PATCH, Andrew J.
: ATTORNEY/AGENT INFORMATION:
: REGISTRATION NUMBER: 32,925
: REFERENCE/DOCKET NUMBER: US94AL CNR TOM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 521-2297
: TELEFAX: 248425 EMON-0573
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1150 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: MOLECULE TYPE: linear
: NAME/KEY: CDS
: LOCATION: 1..1077
: US-08-809-103B-5

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alignment_scores:

Quality	Ratio	Length	Gaps
215.00	3.772	69	0
Percent Similarity:	82.609	Percent Identity:	55.072

alignment_block:

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US-09-289-346a-2 x US-08-809-103B-5 ..

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Align seg 1/1 to: US-08-809-103B-5 from: 1 to: 1150

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2 LeuvalTrrpGjuphagclnvalagcglyalalalalaglycy 18
||| ||||| ||||| ||||| ||||| ||||| |||||
331 CTGAAATGGGACTTTCAGATCCAGCGACGATCTGCGAGGAGCA 380

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18 scdihhsrsmasapalialaiacilaaleunmsualaserfysc 35
19 |-----|-----|-----||-----|-----|
361 AGAGCAGGCACGACCCTTACCGAACATTMACCCGCAAGAATCT 430
373 acgaaiaagcaatlaiclatlgaagacluyallperocluystyleuphe 51
385 cccnacccttcattanttaataactaatmttatmacgtttccaagtgcctcc 530
431 ccgaccttcatcgattatttaaagatttagggcctcacaaanattncgtcta 480

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51 GCCACT 537

seq_documentation_block:
1 Sequence 43 application US/08B38151A
2 Date Rec'd: 08/08/2008
3 GENERAL INFORMATION:
4 APPLICANT: Stout, John T
5 APPLICANT: Lau, Hang T
6 APPLICANT: Maxwell, Douglas
7 APPLICANT: Ahlgvist, Paul
8 APPLICANT: Hanson, Steve
9 TITLE OF INVENTION: Transgenic Plants Expressing Geminaliviruses
10 NUMBER OF SEQUENCES: 63
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: Dressler, Rocky, Minnow & Katz
13 STREET: Two Prudential Plaza, suite 4700
14 CITY: Chicago
15 STATE: Illinois
16 COUNTRY: U.S.A.
17 ZIP: 60601
18 COMPUTER READABLE FORM:
19 MEDIUM TYPE: Floppy disk
20 OPERATING SYSTEM: IBM PC compatible
21 SOFTWARE: PatentIn Release #1.0, Version #1.30
22 CURRENT APPLICATION DATA:
23 FILING DATE: US/08/838,151A
24 CLASSIFICATION: B 800
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Mueller, Lisa V
27 REGISTRATION NUMBER: 38,978
28 REFERENCE/DOCKET NUMBER: SYS3801P0260
29 TELECOMMUNICATIONS INFORMATION:
30 FAX: 312-616-5460
31 TELEFAX: 312-616-5460
32 INFORMATION FOR SEQ ID NO: 43:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 1183 base pairs
35 type: nucleic acid
36 STRANDEDNESS: single
37 topology: circular
38 MOLECULE TYPE: DNA (genomic)
39 HYPERMETHYLATION MODIFIED: YES OR NO
40 AVTI-SENSE: NO
41 ORIGINAL SOURCE:
42 ORGANISM: Bean Golden Mosaic Geminalivirus
43 INVIVUAL ISOLATE: Guatemala
44 STRAIN: Type II Isolates
45 PREVIOUS PUBLICATION:
46 NAME KEY: GMS
47 LOCATION: 1, 1059
48 PUBLICATION INFORMATION:
49 AUTHORS: Farfa, JC
50 OTHER NAMES: Gilbertson, RL
51 AUTIORS: Hanson, SP
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? AUTHORS: Morales, FJ
? AUTHORS: Ahlquist, P
? AUTHORS: Lomeliio, AO
? AUTHORS: Maxwell, D
? TITLE: bean golden mosaic geminivirus type II
? JOURNAL: Journal of Virology
? TITLE: Genomic Organization and Sequence Analysis of Bean Golden Mosaic Virus
? JOURNAL: Journal of Virology
? TITLE: Pseudorecombinants, and Phylogenetic Relationships
? JOURNAL: Phytopathology
? VOLUME: 84
? ISSUE: 3
? PAGES: 321-329
? DATE: 1994
? US-08-636-151A-43

alignment_scores:
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    Ratio: 3.644         Gaps: 0
    Percent Similarity: 84.286   Percent Identity: 57.143

alignment_block:
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17 YGYSINPHTFSEFAAPSLAIAlAdIAlAlAlAlAlAlAlAlSerSert 34
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378 TCGAGCATCTCCACAGACGACATCTTCACAAAGCGATTTAACGCCGATTTAA 427
34 ysdLglnAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAl 50
428 PTGnATGTCCTCCATCTGACATTTTCACACACACACACACACACATTCATC 477
51 PhGnATGTCCTCCATCTGACATTTTCACACACACACACACACACATTCATC 67
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67 rProGUppro 70
528 GGCGGAGACCA 537

seq_documentation_block:
? Sequence 45, Application US/08838151A
? Patent No. 6281743
? GENALAB COMPOSITION: John T
? APPLICANT:
? APPLICANT: Luu, Hang T
? APPLICANT: Maxwell, Douglas
? APPLICANT: Ahlquist, Paul
? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing Geminiviruses
? NUMBER OF SEQUENCES: 3
? CORRESPONDENCE ADDRESS: 63
? ADDRESS: Dressler, Rocky, Milanow & Katz
? STREET: Two Prudential Plaza, Suite 4700
? CITY: Chicago
? STATE: Ill./IL
? COUNTRY: U.S.A.
? ZIP: 60601
? COMMERCIAL AVAILABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release v1.0. Version #1.30
? CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/838,151A
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: JAMES E. HARRIS
 REGISTRATION NUMBER: 38,978
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGIN: SOURCE:
 ORGANISM: Human
 STRAIN: Type II
 INDIVIDUAL ISOLATE: Guatemala
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1059
 US-08-838-151A-45

alignment_scores:
 Quality: 215.00 Length: 70
 Ratio: 3.644 Gaps: 0
 Percent Similarity: 84.286 Percent Identity: 57.143

alignment_block:
 US-09-289-346a-2 x US-08-838-151A-45

Align seg 1/1 to: US-08-838-151A-45 from: 1 to: 1183

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1 ThrLeuValTrpGlyIuphGlnValAspGlyAlaAlaAlaLactylG 17
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328 ACATGATGATGGGACATTCGACATCGACGACGACATTCGACAGG 377
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 YCysGlnThrSerAsnAspAlaAlaAlaAlaAlaAlaAlaSerG 34
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
378 TCACGATCTGCCACGACATTCGACATTCGACATTCGACATTCGA 427
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34 YGluGluAlaLeuGlnIleLeuGluIuysIleProGluuysTyrl 50
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428 TTAAATCTGCTTCACATATTGAAAGAGACACGACGAAAGATTAC 477
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51 PhagIphIleIleAsnLeuAsnSerTrsIleuAspAqIlePha 67
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478 CTCACATCATCAACATCTCGTTTAACTTCGACACGAACTTCGAA 527
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67 rProGluuPro 70
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528 GCCGAAACA 537

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seq_name: /cgnl_7/prodata/1/lna/6A.COMB.seq:US-09-065-999-5

seq_documentation_block:
 Sequence 5, Application US/09065999
 Patent No. 6118048
 GENERAL INFORMATION:
 APPLICANT: Hanson, Stephen F.
 ATTORNEY: Hanson, Stephen F.
 TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
 REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Quarles & Brady
 STREET: One South Pluckney Street

CITY: Madison
 STATE: WI
 COUNTRY: US
 DATE: 5/31/2113
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/065,999
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: SEAY, Nicholas J.
 REGISTRATION NUMBER: 27,386
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-251-5000
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1651 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-065-999-5

alignment_scores:
 Quality: 215.00 Length: 70
 Ratio: 3.644 Gaps: 0
 Percent Similarity: 84.286 Percent Identity: 57.143

alignment_block:
 US-09-289-346a-2 x US-09-065-999-5

Align seg 1/1 to: US-09-065-999-5 from: 1 to: 1651

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1 ThrLeuValTrpGlyIuphGlnValAspGlyAlaAlaAlaLactyl 17
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17 YCysGlnThrSerAsnAspAlaAlaAlaAlaAlaAlaAlaSerG 34
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
846 TCAGCATCTGCCACGACATTCGACATTCGACATTCGACATTCGA 895
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 YGluGluAlaLeuGlnIleLeuGluIuysIleProGluuysTyrl 50
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
896 TTAAATCTGCTTCACATATTGAAAGAGACACGACGAAAGATTAC 945
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 PhagIphIleIleAsnLeuAsnSerTrsIleuAspAqIlePha 67
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
946 CTCACATCATCAACATCTCGTTTAACTTCGACACGAACTTCGAA 995
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 rProGluuPro 70
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996 GCCGAAACA 1005

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seq_name: /cgnl_7/prodata/1/lna/6A.COMB.seq:US-09-065-999-6

seq_documentation_block:
 Sequence 6, Application US/09065999
 Patent No. 6118048
 GENERAL INFORMATION:
 APPLICANT: Hanson, Stephen F.
 ATTORNEY: Hanson, Stephen F.
 TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
 REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Quarles & Brady

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? STREET: One South Pinckney Street
? CITY: Madison
? STATE: WI
? COUNTRY: US
? ZIP: 53703-2113
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent in Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? FILING DATE: US/09/065, 999
? PILING DATE:
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: Seay, Nicholas J.
? REGISTRATION NUMBER: 27,386
? REFERENCE/DOCKET NUMBER: 960296, 94754
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 608-251-9166
? TELEFAX: 608-251-9166
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1651 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? MOLECULE TYPE: linear
? MOLECULE TYPE: DNA (genomic)
US-09-065-999-6

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alignment_scores:
? Quality: 215.00 Length: 70
? Ratio: 3.644 Gaps: 0
? Percent Similarity: 84.286 Percent Identity: 57.143

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alignment_block:

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Align seq 1/1 to: US-09-065-999-6 from: 1 to: 1651

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17 YCGGlnThserAmaspAlaAlaAlaGlnAlaLeuAsnAlaSerSertL 34
846 TCACAGCTGCGCAACGACTATATGCAAGGCAATTAAGCGCATTTCAA 895
34 YGClGlnAlaAlaGlnAlaLeuAsnAlaGlnAlaGlyIleProGlnuysTyleu 50
896 TTGAATCTGCTTGCATATTCAGCAAGCAACGAAAGATTTACGTC 945
51 PhedInpethAsnLeuAsnSerAsnLeuAspArgIlePhaAspIysTh 67
946 CTTCAACATCAACACATTCGTTCTATCTGACGAGCATCTTCGCAACT 995
67 TPCGluPro 70
996 GCGCGAACCA 1005
seq_name: /cogn_7/ptclata/1/lna/6A_COMB.seq:US-09-065-999-8
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? Sequence 8, Application US/09065999
? Patent No. 618048
? GENETIC INFORMATION:
? APPLICANT: Harrison, Stephen F.
? APPLICANT: Maxwell, Douglas P.
? TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:

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? ADDRESSEE: Quarles & Brady
? STREET: One South Pinckney Street
? CITY: Madison
? STATE: WI
? COUNTRY: US
? ZIP: 53703-2113
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent in Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? FILING DATE: US/09/065, 999
? PILING DATE:
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: Seay, Nicholas J.
? REGISTRATION NUMBER: 27,386
? REFERENCE/DOCKET NUMBER: 960296, 94754
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 608-251-9166
? TELEFAX: 608-251-9166
? INFORMATION FOR SEQ ID NO: 8:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1894 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? MOLECULE TYPE: linear
? MOLECULE TYPE: DNA (genomic)
US-09-065-999-8

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alignment_scores:
? Quality: 215.00 Length: 70
? Ratio: 3.644 Gaps: 0
? Percent Similarity: 84.286 Percent Identity: 57.143

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alignment_block:

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Align seq 1/1 to: US-09-065-999-8 from: 1 to: 1894

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17 YCGGlnThserAmaspAlaAlaAlaGlnAlaLeuAsnAlaSerSertL 34
846 TCACAGCTGCGCAACGACTATATGCAAGGCAATTAAGCGCATTTCAA 895
34 YGClGlnAlaAlaGlnAlaLeuAsnAlaGlnAlaGlyIleProGlnuysTyleu 50
896 TTGAATCTGCTTGCATATTCAGCAAGCAACGAAAGATTTACGTC 945
51 PhedInpethAsnLeuAsnSerAsnLeuAspArgIlePhaAspIysTh 67
946 CTTCAACATCAACACATTCGTTCTATCTGACGAGCATCTTCGCAACT 995
67 TPCGluPro 70
996 GCGCGAACCA 1005
seq_name: /cogn_7/ptclata/1/lna/6A_COMB.seq:US-09-065-999-7
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? Sequence 7, Application US/09065999
? Patent No. 618048
? GENETIC INFORMATION:
? APPLICANT: Harrison, Stephen F.
? APPLICANT: Maxwell, Douglas P.
? TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: One South Pinckney Street
CITY: Madison
STATE: WI US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/09/065, 999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seely, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296, 94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-9166
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-7

alignment_scores:
Quality: 215.00      Length: 70
Ratio: 3.644         Gaps: 0
Percent Similarity: 84.286   Percent Identity: 57.143

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846 TCACAGTCGTCCGACACGCTCATTCGACAAAGCGATTAAACGCGCATTC 895
34 YGlnGlnAlaAlaGlnGlnAlaAlaGlnGlnYllleProGlnYlYrleu 50
896 TTGATCTCCCTTCGACANTTTGAGAGAGACACACGCAAGATTTCGTC 945
51 PhsclPheHisAsnLeuAsnSerAsnLeuAspArglllePhcAspYlYr 67
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67 PProGlnPro 70
996 GCGGGAACCA 1005

seq_documentation_block:
Sequence ID: 297111 location US/08838151A
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Lau, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul

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APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Gemclinivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dresser, Rockey, Milamov & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: SYSTEM PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Steve
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Gemini Virus
INDIVIDUAL ISOLATE: Florida
FEATURE:
NAME/KEY: CDS
LOCATION: 44..1127
PUBLICATION INFORMATION:
AUTHORS: Gilbertson, RL
AUTHORS: Hayward, SF
AUTHORS: Johnson, EJ
AUTHORS: Rojas, MR
AUTHORS: Hou, YM
AUTHORS: Maxwell, DP
TITLE: Pseudorecombination between the infectious
TITLE: cloned DNA components of tomato mottle and bean
TITLE: mottle gemini viruses.
VOLUME: 7 J. Gen. Virol.
PAGES: 23-31
DATE: 1993
US-08-838-151A-1

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Percent Similarity: 84.286   Percent Identity: 54.286

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KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE

Tomato rugose mosaic virus.
Tomato rugose mosaic virus.
VIRUSES: ssRNA viruses: Geminiviridae: Begomovirus.
(bases 1 to 2622)
Forbes, J.J., Forbes, E. B., Brommonschenkel, S.H., Carvalho, M.G.,
Zambolim, E.M. and Zerbini, F.M.
Molecular Cloning and Characterization of Tomato rugose mosaic
virus (TRMV), a Begomovirus isolated from Tomatoes at Triangulo
Mineiro, Minas Gerais, Brazil
Unpublished
2. (bases 1 to 2622)
Zambolim, E.M., Zerbini, F.M.
Direct Submission
Submitted (31-JUL-2000) Dept. de Fitopatologia, Universidade
Federal de Vicosa, Av. P. H. Rolfs, s/n - Centro, Vicosa, MG
36571-000, Brazil
Location/Oualifiers
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Gerais"
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TRMV"
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GGSLHPIVLCIGPVHGVVSGLVGAPMNSCTWRI TNAPANI RCTSHVAPWGIALRHP
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/db_xref="GI:10281648"
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seq_documentation_block: 1193 bp DNA VR 01-APR-1997
DEFINITION genes, partial cds.
ACCESSION U92532
VERSION U92532.1 GI:1916444
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

Leonturus mosaic virus.
Leonturus mosaic virus.
VIRUSES: ssRNA viruses: Geminiviridae: Begomovirus.
1. (bases 1 to 1193)
Farja, J.C. and Maxwell, D.P.
Variability in geminivirus associated with Phaseolus vulgaris in
Brazil

alignment_scores:
Query: 291.00 Length: 70
Ratio: 4.654
Percent Similarity: 88.571 Percent Identity: 78.571

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17 YCYGlnThrSerGlnAspAlaAlaAlaAlaAlaAlaAlaSerG 34
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2248 YTGCGAGAGCTGACGAGCGTCCGAGAGACCTTGAACGACCTCA 2199

34 laalalaalaleughlglialaagldgliallsercglulstgryleu 50
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2198 AAGCACTCGCTTCACATTCATTCGCGGAGCAATCGCGGAAAGCTTCCTA 2149

51 PhagIphelilaanleuanSerAsnleuanPargIlelaaspyrth 67
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
2148 YTTCAAGTTTCAACATCTCAANAGTAAATTTGACAAATTTGCAAGGC 2099

67 PrcogIpro 70
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
2098 TCCGGAGCCA 2089

BASE COUNT 684 a 562 c 600 g 776 t
ORIGIN

[illegible]

ORGANISM	bean golden mosaic virus
REFERENCE	1 (sites)
AUTHORS	1. Gilbertson, R.L., Faria, J.C., Hanson, S.F., Morales, F.J.,
TITLE	Cloning of the Complete DNA Genomes of Four Bean-Infecting Geminiviruses and Determining Their Infectivity by Electric Discharge Particle Accelerator
JOURNAL	Phytopathology 81, 980-985 (1991)
AUTHORS	2 (sites)
REFERENCE	2. Gilbertson, R.L., Hidayat, S.H., Martinez, R.T., Leong, S.A., Faria, J.C.,
TITLE	Morales, F.J., and Maxwell, D.P. Infecting geminiviruses by nucleic acid hybridization probes and aspects of bean golden mosaic in Brazil
JOURNAL	Plant Dis. 75, 335-342 (1991)
REFERENCE	3 (bases 1 to 2617)
AUTHORS	Gilbertson, R.L., Faria, J.C., Almqvist, P.G., and Maxwell, D.P.
TITLE	Genetic diversity in geminiviruses causing bean golden mosaic disease: The nucleotide sequence of the infectious cloned DNA components of a Brazilian isolate of bean golden mosaic geminivirus
JOURNAL	Phytopathology 81, 980-985 (1991)
FEATURES	1 (sites)
source	1. 2617
	/organism="bean golden mosaic virus"
	/protein
	/isolate="Brazil"
	/strain="Type 1"
	/db_xref="taxon:10839"
	/db_xref="stage="replicative form"
	/gene="all"
	1..181
misc_feature	/standard_name="Common Region"
	/note="putative"
	/function="putative origin of replication"
gene	358..1113
	/gene="all"
	358..1113
	/gene="all"
	/note="putative"
	/codon_start=1
	/function="coat protein"
	/product="coat protein"
	/protein_10="AA66313.1"
	/db_xref="gi:331465"
	181..1508
	/gene="all"
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	/gene="all"
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	/codon_start=1
	/protein_10="AA66314.1"
	/db_xref="gi:331465"
	/translation="MDSRTGERITAHQENGVYIWEISNPLPKYVVEDQVYTRV
	YHILQIRNNLRKRLGLDKRLPLNFQDWTISLQASPTPLNFRVYLITLQVYISL
	NNVIAHARATDQSVYINVLDEHINLFT"
gene	1508..1556
	/gene="all"
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	/gene="all"
	/note="putative"
	/codon_start=1
	/protein_10="AA66315.1"
	/db_xref="gi:331465"
	/translation="MANSSTSPSTXYQHRAKRAKLRPRVDELCGTYIHNKS
	GHQFHGHCSPSSSEMYVLGDKISLFDQVQRKSTLHNSQIFPPNIVQPNQRE
	QTSQFHPGHCSPSSLSIDISPPNDIFK"
	complement(101in(1556..2617,1..24))
	/gene="all"
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1   TheNvalATrPdyJgUpheGluValAspGIYarSerAlaArgylVGI 17
2   ||||| 17790681 ||||| 17790681 ||||| 17790681 ||||| 17790681
3   374 ACCATCGAAGTGGGAGGTGGTGACATTGATGACGAAAGAAGTCCTGAGCAGCG 325
4   ||||| 17790681 ||||| 17790681 ||||| 17790681 ||||| 17790681
5   17 YCYSGIunThSerpSeAspAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 34
6   ||||| 17790681 ||||| 17790681 ||||| 17790681 ||||| 17790681
7   34 lalalaialaleuagilalelalefargluylyleptroglulytyrfelu 50
8   ||||| 17790681 ||||| 17790681 ||||| 17790681 ||||| 17790681
9   274 AGGAGGCGCCATCGAGAAACTCATGAGGAGGAATGCCGGAAGATTTCTTC 225
10  ||||| 17790681 ||||| 17790681 ||||| 17790681 ||||| 17790681
11  51 pHCdINpeHlSnslueLsnserLsnLeuSpgrlllePhasplysm 67
12  ||||| 17790681 ||||| 17790681 ||||| 17790681 ||||| 17790681
13  224 TTTCAATATCAACAACATTCACATTAACCTGATAGAGATTTTATGAGAGGA 175
14  ||||| 17790681 ||||| 17790681 ||||| 17790681 ||||| 17790681
15  67 rPGGluPro 70
16  ||||| 17790681 ||||| 17790681 ||||| 17790681 ||||| 17790681
17  174 TCAGGAGAACCA 165
18  seq documentation block:
19  LOCUS      Sdu6/7926     554 bp    DNA                VRL          28-JAN-1998
20  DEFINITION Sdu6 golden mosaic geminivirus Rep protein (NCI) gene, partial cds.
21  ACCESSION  U67926
22  VERSION    U67926.1 GI:1546801
23  KEYWORDS
24  SOURCE     sida golden mosaic virus.
25  ORGANISM   sida golden mosaic virus
26  AUTHORS    Williams, J.L., West, Geminiviridae; Begomovirus.
27  TITLE      1 (bases 1 to 554)
28             Royce M.E., McLaughlin, R.A., Nabha, N.K. and Maxwell, D.P.
29             Genetic Diversity among geminiviruses associated with the weed
30             species Sida spp. Macropodium lathyroides, and Missadua
31             amplissima from Jamaica
32             Plant Dis. 81, 1251-1258 (1997)
33             2 (bases 1 to 554)
34             Royce M.E., McLaughlin, R.A. and Maxwell, D.P.
35             Submitted 23-AUG-1996. Plant Pathology, University of Wisconsin,
36             1630 Linden Drive, Madison, WI 53706-1598, USA
37  FEATURES
38     source            1..554
39                        /organism="Sida golden mosaic virus"
40                        /strain="Jamaica"
41                        /isolate="Jamaica, May 1993"
42                        /db_xref="taxon:51034"
43                        /mol_map="complement(1..554)"
44                        /gene="AC1"
45                        /complement(<1..554)
46                        /gene="AC1"
47                        /note="(replication-associated protein"
48                                "/codon_start=1
49                                "/product="Rep protein"
50                                "/protein_id="AB07865.1"
51                                "/translation="STSPKALSSQTLQTKTPYKKFKIKCEHLNGEPLHLNLITDPE
52                                GKXNTNNRDFEDLVSCFPHKNIENGLAKASSDSKSYEKDQTIIMCKVRIDGSRSA
53                                RGGOQTADNAAEALNSPTSEDEKAITREKLPERLYGVHNLSNIDRFISPPKPMWS
54                                HRPPLDPFNVAWQMGEMAWGFGR"
55  BASE COUNT      121 a      127 c      139 g      167 t
56  ORIGIN
57
58 alignment_scores:
59     Quality: 259.00      Length: 70
60     Ratio: 4.246        gaps: 0
61     Percent Similarity: 87.143      Percent Identity: 68.571
62
63 alignment_block:

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US-09-289-346A-3 x SGU67926/rev ..
Align seq 1/1 to reverse of: SGU67926 from: 1 to: 554
1   ThrLeuValTctGcgcYphchicgVnAlapgcLrNkrgseRtlaacgtGcL 17
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290 ACCTCATCAATCGAGCGGGGTTCCTCCACGCACGGAAGAAGATCCTCCGSGAG 241
17 YCYGSLInThSeSaNaNsPAdLaLaLaLaLaLaLeuLaLaLaSeSera 34
    | |||||:::|||||
240 TCGACAAACACGCTACGAGCGACGCCGCGAGCGATTGAAATCTTGACACA 191
34 LaLaLaLaLaLeuLnInTeIleatagcLlLlllllllgeRcgCllySTytleu 50
    |||||:::|||||
190 ACGAGATGCGCTGAAATAATCTACAGAGAKAGTTCCACGAAGAAATATCTC 141
51 PhiedInPhetIsanIsleuNusSerSanIsleuSpArpCIlephaSaApLyStH 67
140 YTYCACATPCACACACACATCCGTAATATCATGATGAGATTTCATGATGAGC 91
67 ProGluPro 70
    |||||
90 TCCGACACCG 81
seq_name: gb_vf:AB001315
seq_documentation_block: 570 bp DNK VRT 13-FEB-1999
DESCRIPTION Tobacco leaf curl virus CI and C4 genes, clone YOKOHAMA3-1, partial
ACCESSION AB001315
VERSION AB001315.1 GI:3798714
KEYWORDS tobacco leaf curl virus CI and C4 genes, clone YOKOHAMA3-1, partial
and complete cds.
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
DIRECT SUBMISSION
Submitted (19-FEB-1997) to the DDBJ/EMBL/GenBank databases.
Kazuyuki Ooi, Kyushu University, Department of Biology; 6-10-1
Hakozaki Higashi-Ku, Fukuoka, Fukuoka 812, Japan
E-mail: koo@biochem.kuc.kyushu-u.ac.jp, Tel.: 81-92-642-2624,
Fax: 81-92-642-3333
2 (bases 1 to 570)
C.O.I.K., Onishi,S., Ishii,I. and Yahara,T.
Molecular phylogeny of geminiviruses infecting wild plants in Japan
J. Plant Res. 110, 247-257 (1997)
FEATURES
source
1..570
/organism="tobacco leaf curl virus"
/species="YOKOHAMA3-1"
/specific_host="Euphorbia makinoi"
/db_xref="taxon:57762"
/clone="YOKOHAMA3-1"
/complement(1..570)
/gene="C1"
complement(<1..>570)
/gene="C4"
start=1
/protein_id="BAA34034.1"
/db_xref="GI:4426541"
/translatation="EPALISQIDLNTPFNKLTKICREIHDCDSPLHLYLDPEKRY
CONNFEDYAFSPRSAPHHNPINIGAKSSSDYSVDYDKDSTDLEKSTODISGRAGG
OANNDADLANNSAKBALATIREKLPFOFTYHNLSMDIRFAPLEVPFCPTFF
ASSTFGVPEELIESAEENVSAAAREWKP"
complement(231..488)
/protein_id="BAA34034.1"
/codon_table="standard"

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/db_xref="GI:3798715"
 /translation="MEALISMCKFSSKANTNAKTDSSTWYPPDQHISIRTFRELNP
 APTSSPTSRTRTETRSNSENHSSTEVLEEAARMLTHVORR"
 BASE COUNT 141 a 121 c 126 g 182 t
 ORIGIN

alignment_scores:
 Quality: 251.00 Length: 85
 Ratio: 4.115 Gaps: 1
 Percent Similarity: 71.765 Percent Identity: 58.824

alignment_block:

us-09-289-346a-3 x AB001315/rev ..

Align seq 1/1 to reverse of: AB001315 from: 1 to: 570

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1  THTLeuValTTPbLyGluPhagInvalAspGlyArgSerAlaArgGlyG 17
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 AGCTCGAATGGGSMACATTCGAGATCGAGAGAGAGAGAGAGAGAGAG 269
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17  YCYGInThrSerAsnAspAlaAlaAlaAlaLeuAlaAlaSerSera 34
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
268 CTGCAGAAATCTCAAGACGCGATGCGAGAGCGCTTAATGCAAGTTCT 219
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34  lAlaAlaAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
218 AGCGAAGACCTTACCAATATTTAGGAGAAAGCTGCTAAGATTTATA 169
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51  PhcGluPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
168 TTTCATATCATATTAATTTAATAGTAATTAAGATTTTCCTCTCTCC 119
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
64  ..... PhaeApLysThr 68
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
118 CTTGAGAGCTTTTGTGTTCCTTCACAGCTCATCTTCATCATCAATTG 69
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
68  PGLu 69
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
68  CAGAA 64

```



```

2216 AGCTATGATGTCGCCGAGAGCCCTTAATGACAGGTTCAGTGAGCG 2167
37 lalenglnlletlãrglulyslleprogluystylleuphcinphe 53
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
2166 CTTTACGACATTAATGAGAGAGCCCTTAATGACATTTATTTCAAT 2117
54 HlsanleuanserAsanleuaspRlgilePheaplysthrp 68
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
2116 CATATTTAATTAATTTAGTACGATTTT.....ACCGCT 2078

seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT:AA084371
seq_documentation_block:
ID AA084371 standard: DNA, 434 BP.
XX
XX AA084371:
XX
AC 19-AUG-1995 (first entry)
XX
XX Gemini virus-specific polyribozyme-E target sequence.
XX
XX rbozyme target sequence: polyribozyme-E;
XX
XX tomato leaf curl virus: RN3 cleavage; tomato transgenic plant;
XX
XX virus disease-resistance: ss.
XX
XX Tomato leaf curl virus.
XX
XX Key Location/Qualifiers
XX
XX misc_feature 13..43
XX /tag a
XX /note "Ribozyme R1 target sequence"
XX
XX misc_feature 26..28
XX /tag b
XX /note "Ribozyme R1 cleavage site"
XX
XX misc_feature 312c342
XX /tag c
XX /note "Ribozyme R2 target sequence"
XX
XX misc_feature 325..337
XX /tag d
XX /note "Ribozyme R2 cleavage site"
XX
XX misc_feature 384..414
XX /tag e
XX /note "Ribozyme R3 target sequence"
XX
XX misc_feature 397c399
XX /tag f
XX /note "Ribozyme R3 cleavage site"
XX
XX W09503404-A.
XX
XX 02-FEB-1995.
XX
XX 22-JUL-1993: 93MO-EP01946.
XX
XX 22-JUL-1993: 93AU-0047014.
XX
XX 22-JUL-1993: 93MO-EP01946.
XX
XX (R10C-) R10CWM SA
XX
XX (GSTR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Baudino S, Comau D, Dry IB, Graber V, Lenee P;
XX
XX Mason J, Rezaian MA, Ridsen JE, Rezaian MA;
XX
XX WPI: 1995-075332/10.
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX
XX of gemini viruses by cleaving target virus sequence,
XX
XX useful for preparing resistant plants. esp tomatoes.
XX
XX Example 10: Fig 11b: 90pp: English.
XX
XX The sequence is a tomato leaf curl virus target sequence for
XX
XX polyribozyme-E, which hybridizes to and cleaves the sequence and
XX
XX thereby reduces replication, infection and/or assembly of the virus

```

```

CC substantially. The ribozyme may be expressed in a transgenic plant.
XX e.g. tomato, to confer virus disease-resistance.
XX
XX Sequence 434 BP; 125 A, 86 C, 91 G, 131 T, 0 other:
XX
XX Alignment scores:
XX
XX Alignment: 222.00 Length: 85
XX Ratio: 3.763 Gaps: 1
XX Percent Similarity: 69.412 Percent Identity: 52.941
XX
XX alignment_block:
XX
XX 05-03-209-346a-3 x AA084371
XX
XX Align seg 1/1 to: AA084371 from: 1 to: 434
XX
XX 1 TRLTLEVALTRPGILYUPEHGINVAZLAPGCIYARSGERLãATGCLYCI 17
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 95 ACCCTGAGATGAGAGAGCTTCAGATGATGAGAGCTTCAGAGAGGCG 144
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 17 YCYGILPHISORPãNSPRLãALãALãALãALãALãALãALãASCTRA 34
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 145 ACAACATACGACATACCCCTTACGCCAGCCGCTTACATCGAAGRA 134
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 34 lãAlãAlãAlãAlãAlãAlãAlãAlãAlãAlãAlãAlãAlãAlãAlã 50
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 195 ACCTGACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTT 244
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 51 PhecinPhecinAsanleuanserAsanleuaspRlgile..... 63
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 245 TTAACATTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 294
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 64 .....PheaspRlysthrp 68
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 295 GTTTCAGACTTATGTTCTCTTTTATCTTCTTCTTCTTCTTCTTCTT 344
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 68 PGGlu 69
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 345 CAGAA 349
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XX seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT:AA084372
XX
XX seq_documentation_block:
XX
XX ID AA084372 standard: DNA, 479 BP.
XX
XX AA084372:
XX
AC 19-AUG-1995 (first entry)
XX
XX Gemini virus-specific polyribozyme-F target sequence.
XX
XX rbozyme target sequence: polyribozyme-F;
XX
XX tomato leaf curl virus: RN3 cleavage; tomato transgenic plant;
XX
XX virus disease-resistance: ss.
XX
XX Tomato leaf curl virus.
XX
XX Key Location/Qualifiers
XX
XX misc_feature 46c49c
XX /tag a
XX /note "Ribozyme R4-R5 target sequence"
XX
XX misc_feature 58..60
XX /tag b
XX /note "Ribozyme R4 cleavage site"
XX
XX misc_feature 81..83
XX /tag c
XX /note "Ribozyme R5 cleavage site"
XX
XX misc_feature 356c365
XX /tag d
XX /note "Ribozyme R2 target sequence"
XX
XX misc_feature 370..372
XX /tag e
XX /note "Ribozyme R2 cleavage site"
XX
XX

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D7 27-APR-1998 (first entry)
 XX Tomato mottle virus AC1 mutant TOMOV-AC1dln23 gene.
 DE Gemlinivirus; TOMOV-AC1dln23, AC1 gene; transposon insertion;
 KM transgenic plant; disease resistance; ss; cycloid; circular.
 OS Tomato mottle virus isolate Florida.
 SS Synthetic.
 FH Key Location/Qualifiers
 FT CDS 44..1129
 FX /cds = a
 PN MO9739110-A1.
 PD 23-OCT-1997.
 PP 15-APR-1997; 97MO-U0506300.
 PR 16-APR-1996; 96MS-0015517.
 PX (SWM-) SEMINIS VEGETABLE SEEDS INC.
 PY (WISC) WISCONSIN ALOMONI RES FOUND.
 PA Ahlquist PG, Hanson SF, Liu HT, Maxwell DP, Stout JT;
 PI WO1, 1997-526447/48.
 PM P-PISR, AMM34326.
 DR Transgenic plants expressing geminivirus AC1 and CI wild-type and
 PT mutant genes - have increased resistance to gemlinivirus infection
 PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
 PT golden mosaic gemliniviruses
 XZ
 XZ Claim 11: Page 67-69; 12pp. English.
 CC This DNA sequence comprises a transdominant lethal mutant,
 CC designated TOMOV-AC1dln23, of the AC1 gene of tomato mottle virus
 CC virus (TOMOV). It encodes an AC1 protein (see AMM34326) that carries
 CC 2 mutations in an NTP-binding domain. The AC1 gene (see also
 CC AM93294) must be expressed for efficient replication of the two
 CC complementary DNAs. Infection of transgenic plants containing
 CC DNA comprising gemlinivirus AC1 or CI wild-type or mutant sequences
 CC that negatively interfere in trans with gemliniviral replication
 CC during infection. Such transgenic plants are resistant to viral
 CC infection. The AC1/CI genes are especially from TOMOV, tomato
 CC yellow leaf curl virus or bean golden mosaic gemlinivirus (see
 CC AM93282-93) and encode polypeptides (see AMM34324-35) that have
 CC homology in the highly conserved DNA-nicking and/or the NTP-binding
 CC domains.
 XZ
 XZ Sequence 1169 BP: 364 A; 278 C; 257 G; 270 T; 0 other:
 Alignment scores:
 Query: 218.00 Length: 70
 Subject: 3.695 Identical: 0
 Percent Similarity: 84.286 Percent Identity: 57.143
 Alignment_Block:
 US-09-289-346A-3 x AM93284 ..
 Align seg 1/1 to: AM93284 from: 1 to: 1169
 1 ThrlentatATGPGUjCUpheJupheJupheJasegVtAaseAlaaandlncI 17
 ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 371 ACAATCCAAATCGAGCGGAATTTCCTCCACATCGACGGCAACTGTCCGAGAAGAG 420
 17 yCysGLTIrTeSeASasApalaaialaaialaaialaaiauaaialaaiaSeSeSa 34
 ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 421 CGAGGACGTCTCATTAAGTTCTATATGATCGAAGAAAGGCTTAATGTCAAAGTGCG 470

```

seq_name: /cnrl_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AA193309
ID      ID
seq_documentation_block:
AC      AD      AA193309 standard; DNA: 2602 bp.
XX
AC      AAT93309:
XX
DE      27-APR-1998 (first entry)
XX
DE      Tomato mottle virus full-length A-component clone.
XX
KM      Geminivirus: TOMOV; ACI gene; transposant mutation:
KM      transgenic plant; disease resistance: ss; cyllcic: circular.
XX
OS      Tomato mottle virus isolate Florida.
XX
XX      W09739110-A1.
XX
PA      23-OCT-1997.
XX
PE      15-APR-1997: 97W0-US06300.
XX
PR      16-APR-1996: 96US-0015517.
XX
PR      (SEM1 - SEPTINIS VEGETARI FEEDS INC.
PR      (WISC ) WISCONSIN ALUMINI RES FOUND.
XX
AB         Ahlquist PC, Hanson SF, Linn HT, Maxwell DP, Stout JT;
DR         NPI: 1997-526447/48.
XX
PT      Transgenic plants expressing geminivirus ACI and CI wild-type and
PT      mutant genes - have increased resistance to geminivirus infection
PT      e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
PT      golden mosaic geminiviruses
XX
PS      Example 3.1: Page 76-77; 132pp; English.
XX
CC      This genomic DNA sequence comprises a full-length A-component clone
CC      of tomato mottle virus (TOMOV), a geminivirus that has a bipartite
CC      genome comprising DNA-A and DNA-B. It was isolated from TOMOV
CC      infected Nicotiana benthamiana and tomato plant DNA by restriction
CC      digestion. The DNA-B component (see AY93310) was also isolated.
CC      TOMOV DNA contains the ACI gene (see AY933294) that must be
CC      co-infectious with the A component for replication. Infection
CC      involving production of transgenic plants containing DNA
CC      comprising ACI or CI wild-type or mutant sequences that negatively
CC      interfere in trans with geminiviral replication during infection.
CC      Such transgenic plants are resistant to viral infection.
XX
XX      Sequence 2602 BP; 671 A; 561 C; 586 G; 784 T; 0 other;
XX
alignment_scores:
Quality: 218.00          length: 70
Ratio: 3.695             gaps: 0
Percent Similarity: 84.286 Percent Identity: 57.143

```


PS Claim 13: Page 111-112, 132pp: English.

XX This DNA sequence comprises construct BGAC228 that codes for a

CC transdominant lethal mutant (see AM34334) of the CI protein (see

CC AM34338) of bean golden mosaic virus (BGMV). It was obtained by

CC mutagenesis of the wild-type CI gene (see AM93314). CI is

CC required for replication. The invention involves production of

CC transgenic plants containing DNA comprising geminiviruses CI or ACI

CC wild-type or mutant sequences that negatively interfere in trans

CC with geminiviral replication during infection. Such transgenic

CC plants are resistant to viral infection. The ACI/CI genes are

CC especially from BGMV, tomato mottle virus or tomato yellow leaf

CC curl virus (see AM93282-93) and encode polypeptides (see AM34324-35)

CC that have mutations in the highly conserved DNA-nicking and/or the

CC NTP-binding domains.

XX Sequence 1062 BP: 338 A; 247 C; 218 G; 259 T; 0 other:

50

alignment_scores:

Quality: 217.00 Length: 70

Ratio: 3.741 Gaps: 0

Percent similarity: 82.857 Percent identity: 58.571

alignment_block:

US-09-289-346a-3 x AM933292 ..

Align seg 1/1 to: AM933292 from: 1 to: 1062

1 ThleuvaltrpGlyupheGlnvalAspGlyARGserAlaATGtGtGt 17

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

328 ACATGCAATGGGCGCAATTCGACATCGACGGCGACATCTCCAAAGAGAG 377

17 YCYGlnThSerAsnAspAlaAlaAlaAlaAlaAlaAlaSerSera 34

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

378 TCACAGCTGCTGCACACATTCGACAGGCGCATTTACACGCAATTCGAA 427

34 laAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 50

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

428 TTGAATCTGCTTCGACAAATTCGAGGAGAACACCAAGATTCGTC 477

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspArg 67

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

478 CTTCAACATCGACAAATTCGCTTAACTTCGACAGGACATTCGCAAG 527

67 rProGluPro 70

528 GCCGGAACCA 537

seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AM933293

seq_documentation_block:

ID AM933293 standard: DNA: 1062 BP.

XX AM933293:

AC 27-APR-1998 (first entry)

XX Bean golden mosaic geminivirus CI mutant ORF BGAC262.

XX Bean golden mosaic geminivirus CI mutant ORF BGAC262.

XX Geminivirus: BGMV; CI gene: transdominant mutation;

XX Transgenic plant: disease resistance: ss: cycloic: circular.

XX Bean golden mosaic virus type II isolate Guatemala.

XX MO9731110-A1.

XX 23-OCT-1997.

XX 15-APR-1997: 97MO-US06300.

XX 16-APR-1996: 560US-0015517.

PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.

PA (WISC) WISCONSIN ALUMNI RES FOUND.

XX Abiquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT.

XX PFT: 1997-526447/48.

XX P-PSDB: AM34335.

XX Transgenic plants expressing geminivirus ACI and CI wild-type and

XX mutant genes - have increased resistance to geminivirus infection

XX PT 9; tomato mottle virus, tomato yellow leaf curl virus or bean

XX golden mosaic geminivirus

XX Claim 13: Page 115-116, 132pp: English.

XX This DNA sequence comprises construct BGAC262 that codes for a

CC transdominant lethal mutant (see AM34335) of the CI protein (see

CC AM34338) of bean golden mosaic virus (BGMV). It was obtained by

CC Kuikel mutagenesis of the wild-type CI gene (see AM93314). CI is

CC required for replication. The invention involves production of

CC transgenic plants containing DNA comprising geminiviruses CI or ACI

CC wild-type or mutant sequences that negatively interfere in trans

CC with geminiviral replication during infection. Such transgenic

CC plants are resistant to viral infection. The ACI/CI genes are

CC especially from BGMV, tomato mottle virus or tomato yellow leaf

CC curl virus (see AM93282-93) and encode polypeptides (see AM34324-35)

CC that have mutations in the highly conserved DNA-nicking and/or the

CC NTP-binding domains.

XX Sequence 1062 BP: 340 A; 245 C; 219 G; 258 T; 0 other:

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alignment_scores:

Quality: 217.00 Length: 70

Ratio: 3.741 Gaps: 0

Percent similarity: 82.857 Percent identity: 58.571

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US-09-289-346a-3 x AM933293 ..

Align seg 1/1 to: AM933293 from: 1 to: 1062

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328 ACATGCAATGGGCGCAATTCGACATCGACGCGACATCTCCAAAGAGAG 377

17 YCYGlnThSerAsnAspAlaAlaAlaAlaAlaAlaAlaAlaAla 34

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378 TCACAGCTGCTGCACACATTCGACAGGCGCATTTACACGCAATTCGAA 427

34 laAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 50

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

428 TTGAATCTGCTTCGACAAATTCGAGGAGAACACCAAGATTCGTC 477

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspArg 67

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478 CTTCAACATCGACAAATTCGCTTAACTTCGACAGGACATTCGCAAG 527

67 rProGluPro 70

528 GCCGGAACCA 537

seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AM93314

seq_documentation_block:

ID AM93314 standard: DNA: 1183 BP.

XX AM93314:

AC 27-APR-1998 (first entry)

XX Bean golden mosaic geminivirus CI open reading frame.

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[illegible]


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/clone_lib="CB"
/tissue_type="cord blood"
/clone_type="CD34+ hematopoietic stem/progenitor cell"
/notes="Vector plasmid; Site 1: EcoRI. The insert is
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Percent Similarity: 64.062      Percent Identity: 31.250

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DEFINITION AV744285 CB Homo sapiens cDNA clone CBNAY06.5, mRNA sequence.
ACCESSION  AV744285
VERSION     BF493366
KEYWORDS    EST
SOURCE      human
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 559)
AUTHORS     Zhang, Q., Yao, X., Wu, X., Gu, D., Huang, Q., Zhou, J., Shen, Y., Han, Z.,
Hou, S., and Chen, Z.
JOURNAL     Human Genome Database (HGD)
COMMENT     Unpublished (2000)
CONTACT     Zhu Chen
Shanghai Institute of Hematology, Rui-jin Hospital
197 Rui-jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
E-mail: zhuch@shanghai.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shouling Road, Zhangjiang Hi-Tech Park, Pudong.
Location/Qualifiers
  1..559
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  /tissue_type="cord blood"
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/notes="Vector plasmid; Site 1: EcoRI. The insert is
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seq_documentation_block:
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DISTINCTION Drosophila melanogaster cDNA clone AT01702.3, mRNA sequence.
ACCESSION  BF493366
VERSION     BF493366.1 GI:1157667
KEYWORDS    EST
SOURCE      fruit fly
ORGANISM    Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;
Muscomorpha; Ephyridia; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 288)
AUTHORS     Stapleton, M., Brokstein, P., Hong, L., Aboyan, A., Baxter, E., Berman
B., Carlson, J., Champ, M., Chavez, C., Chew, M., Dorsett, V., Farfan
L., Fiske, E., George, R., Gonzalez, M., Guatin, H., Harris, N., Li, P.,
Liao, G., Miranda, A., Misra, S., Mungall, C. J., Nuno, J., Paclob, J.,
Cordoba, V., Park, S., Phoumthavong, S., Wan, K., Yu, C., Lewis, S. E.,
BCRP/HMT AT Drosophila EST project
JOURNAL     Unpublished (2000)
COMMENT     Other ESTs: AT01702.5, Sprime
CONTACT     Stapleton, M.
BDGP
Lawrence Berkeley National Lab
P.O. Box 808
Berkeley, CA 94720, USA
Fax: 510 486 6798
E-mail: http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu
hit genomic AB003566: arm:2L [1212407,1518758]
estimated-cyto:21P2-22A: 04/07/2001
Plate: AT 17 row: A column: 2
High quality sequence scop: 155.
Location/Qualifiers
  1..288
  /organism="Drosophila melanogaster"
  /db_xref="taxon:7227"
  /clone="AT01702"
  /clone_lib="AT Drosophila melanogaster adult testes POTB7"

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716 - Ludwig Institute for Cancer Research) profiles
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stringency conditions."
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Origin
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96 GGAGCTTTTCAGCTCCTGATTAAGAAAGTGGCAGAAAGCCCTGGATATCAACAC 145
20 rserGAAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 37
146 GCCAAGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 195
37 lalGAGATG 40
196 CTTCTCCAACTG 206
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seq_documentation_block:
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DEFINITION      PM2.HH0353-281299-003-H06 HH0353 Homo sapiens cDNA, mRNA sequence
ACCESSION      BH155633
VERSION      BH155633.1      GI:8618354
KEYWORDS      EST
SOURCE      human
ORGANISM      Homo sapiens
Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 353)
Dias Neto,A.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A.E., da Silva,M.Jr., Zago,M.A., Bordin,S., Costa,F.P., D.R.
Brustolin,A.F., deLencastre,E., Matsushima,A., Bhatia,G.S.C., Verjovski-
Almeida,S., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
COMMENT
  202005 Simpson A.J.G.
  Laboratory of Cancer Genetics
  Ludwig Institute for Cancer Research
  Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
  Brazil
  Tel: +55-11-2704522
  Fax: +55-11-2707001
  Email: asimpson@ludwig.org.br
  This entry represents the FAPESP/ICR Human Cancer Genome
  Project. This entry can be seen in the following URL
  (http://www.ludwig.org.br/scripts/gethtml2.pl?L1=512-PM2-HH0353-281299-003-346A.3)
  Seq primer: puc 18 forward
  High quality sequence stop: 353.
  Location/Qualifiers
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    clone_lib="HH0353"
    /dev_stage="Adult"
FEATURES
  source

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1169 base pairs
; TYPE: nucleic acid
; STRAND: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Tomato Mottle Gemini Virus
; STRAIN: Florida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 44..1127
; PUBLICATION INFORMATION:
; AUTHORS: Gilbertson, RL et al.
; TITLE: Pseudorecombination between the infectious
; TITLE: Cloned DNA components of tomato mottle and bean
; TITLE: Dwarf mosaic geminivirus.
; JOURNAL: Journal of General Virology
; VOLUME: 74
; PAGES: 23-31
; DATE: 1993
; US-08-838-151A-3

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; Alignment: 218.00 Length: 70
; Ratio: 3.695 Gaps: 0
; Percent Similarity: 84.286 Percent Identity: 57.143

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17 ycygslnhrserasnaspalalalalalalalaserSera 34
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
421 CCACGACGTCTGATGATCATATGCGAAGACGTTAAATGCAAGTTCGG 470
34 laalalalaleuglnlaleatgltlysileprogltulytyrleu 50
::: ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
471 TTCAATCTGCTTACGAGTCTTACGAGCAACCAACCAAGATTTTGTA 520
51 PhcInPheIlaenleuasnserasnleuasparytlepnaaplytyth 67
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; Sequence 5, Application US/08838151A
; GENERAL INFORMATION:
; PATIENT: Patient No. 6201743
; APPLICANT: Scout, John T
; APPLICANT: Liu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Alquist, Paul
; APPLICANT: Johnson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz

```

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; STREET: Two Prudential Plaza, suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; CITY: 06061
; COUNTRY: 06061
; COMPUTER: IBM PC compatible
; MEDIUM TYPE: PC-DOS/MS-DOS
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentm Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/ACPT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SYS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5100
; FAX: 312-616-5100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1169 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; STRAIN: Florida
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; Alignment: 218.00 Length: 70
; Ratio: 3.695 Gaps: 0
; Percent Similarity: 84.286 Percent Identity: 57.143

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421 CCACGACGTCTGATGATCATATGCGAAGACGTTAAATGCAAGTTCGG 470
34 laalalalaleuglnlaleatgltlysileprogltulytyrleu 50
::: ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
471 TTCAATCTGCTTACGAGTCTTACGAGCAACCAACCAAGATTTTGTA 520
51 PhcInPheIlaenleuasnserasnleuasparytlepnaaplytyth 67
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; Sequence 7, Application US/08838151A

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? Patent No. 6291743
? GENERAL INFORMATION:
? APPLICANT: Stout, John T
? APPLICANT: Loui, Hang Douglas
? APPLICANT: Maxwell, Douglas
? APPLICANT: Ahlquist, Paul
? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
? TITLE OF INVENTION: Genes
? NUMBER OF SEQUENCES: 63
? CORRESPONDENCE ADDRESS: Rocky, Milnamow & Katz
? ADDRESS: Two Prudential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460
? INQUIRY: 312-616-5460
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1169 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? RECOMBINATION: NO
? HYPOTHEICAL: NO
? ORIGINAL SOURCE:
? ORGANISM: Tomato Mottle Gemini Virus
? STRAIN: Florida
? FEATURE:
? NAME/REV: CDS
? LOCATION: 44..1127
? US-08-838-151A-7

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alignment_scores:
? Quality: 218.00 Length: 70
? Ratio: 3.695 Gaps: 0
? Percent Similarity: 84.286 Percent Identity: 57.143

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alignment_block:

US-09-289-346a-3 x US-08-838-151A-7

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421 CACGACGTCTGCTATCATTCATTCAGACGATTCATTCAGACGATTCG 470
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Sequence 17,209,113 location US/08838151A

GENERAL INFORMATION:

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? APPLICANT: Stout, John T
? APPLICANT: Loui, Hang T
? APPLICANT: Maxwell, Douglas
? APPLICANT: Ahlquist, Paul
? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
? TITLE OF INVENTION: Genes
? NUMBER OF SEQUENCES: 63
? CORRESPONDENCE ADDRESS:
? ADDRESS: Dressler, Rocky, Milnamow & Katz
? STREET: Two Prudential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601

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COMPUTER READABLE FORM:

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? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE:

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CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

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? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460

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? SEQUENCE CHARACTERISTICS:
? LENGTH: 2602 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? HYPOTHEICAL: NO
? ORIGINAL SOURCE:
? ORGANISM: Tomato Mottle GeminiVirus
? STRAIN: Florida
? US-08-838-151A-17

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? Quality: 218.00 Length: 70
? Ratio: 3.695 Gaps: 0
? Percent Similarity: 84.286 Percent Identity: 57.143

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          Ratio: 3.741      Gaps: 0
          Percent Similarity: 82.857      Percent Identity: 58.571

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17  GCGTGGTTCCTGCAAGTTCGCAATTCGCAATTCGCAATTCGCAATTCGCA 34
378  TCAGCATCTTCGCAAGTTCGCAATTCGCAATTCGCAATTCGCAATTCGCA 427
34  IAAIaAaIaAaIaAaIaAaIaAaIaAaIaAaIaAaIaAaIaAaIaAaIa 50
428  TGAATATTCCTCCCTGCAATTTTGAGCAAGCAACAAAGCAAGATATCGC 477
51  PHECTIPPHaHSAaGdIaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 67
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67  rFGGSLupro 70
528  GCGGGAACCA 537

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seq_name: /cgnl_7/pdatabase/1/lna/5E_COMB.seq:US-08-838-151A-51
Sequence 51, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luo, Hang T
APPLICANT: Applegate, Douglas
APPLICANT: Ahlquist, Paul
TITLE OF INVENTION: Transgenic Plants Expressing Gemtulinus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rodney, Millumay & Katz
ATTORNEY/AGENT INFORMATION:
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: DOS/MS-DOS/MS-POS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 38,978
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NOS:
SEQUENCE CHARACTERISTICS
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA (genomic)

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[illegible]


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? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460
? INFORMATION FOR SEQ ID NO: 43:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1183 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Bean Golden Mosaic Geminivirus
? STRAIN: Type II Isolates
? INDIVIDUAL ISOLATE: Guatemala
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1059
? PUBLICATION INFORMATION:
? AUTHORS: Etila, OC
? AUTHORS: Shattuck, RL
? AUTHORS: Hanson, SP
? AUTHORS: Morales, PJ
? AUTHORS: Ahlquist, P
? AUTHORS: Lonsdale, AO
? AUTHORS: Maxwell, D
? TITLE: Bean Golden Mosaic Geminivirus Type II
? REFERENCE/DOCKET NUMBER: 38,978
? TITLE: Guatemala Nucleotide Sequence
? JOURNAL: Phytopathology
? VOLUME: 84
? ISSUE: 3
? PAGES: 321-329
? DATE: 1994
? PATENT: 151A-43
? US-08-838-151A-43

alignment_scores:
? Quality: 217.00 Length: 70
? Ratio: 3.741 Gaps: 0
? Percent Similarity: 82.857 Percent Identity: 58.571

alignment_block:
? US-09-289-346a-3 x US-08-838-151A-43 ..
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? Align seg 1/1 to: US-08-838-151A-43 from: 1 to: 1183
?
? 1 ThTLeuValTPpGlyGluPheGlnValAlaSPGlyAYGSeRAlaATGAGTGC 17
? |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
? 328 ACAGTGCAGATGGAGGACATTCACAGTGCAGGCGACGCTCTCCAGAGGAGG 377
? 1 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
? 17 YCYGAGlnThSerAnbSPAlaAlaAlaAlaAlaAlaAlaAlaAlaSerA 34
? |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
? 378 TCAGCAGCTCGCCAGACGACATCATATGCAAGGCGATTAAACCGAGATTCAA 427

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? 34 lAlaAlaAlaGlnGlnIleTieATGCTuLySLleProGlnuTyTyrLeu 50
? :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
? 428 TTCAGTCTCGCTTCAGCATATTATGAGGAGACGACGACGACATTCACCTC 477
? 51 PhcGlnPheHisAnLeuAnbSerAnLeuAnbAPAGlllePheAnpLySth 67
? :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
? 478 CTCAGTGCAGTCCACATCGCTGTATATCTGCAGACGACATCTGCTCAAGT 527
? 67 PProGluPro 70
? :|||||:|||||
? 528 GCCGAGACCA 537

seq_name: /cgn1_7/prodata/1/ina/65_COMPB.seq:US-08-838-151A-45
?
? seq.documentable_block:
? Sequence 45, Application US/08838151A
? Patent No. 6291743
? GENERAL INFORMATION:
? APPLICANT: Slout, John T
? APPLICANT: Liu, Hang T
? APPLICANT: Maxwell, Douglas
? APPLICANT: Shattuck, RL
? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
? NUMBER OF SEQUENCES: 63
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: Dressler, Rocky, Milnamov & Katz
? STREET: Two Prudential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? OPERATING SYSTEM: IBM OS/MS-DOS
? CURRENT APPLICATION DATA: Release #1.0, Version #1.30
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460
? INFORMATION FOR SEQ ID NO: 45:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1183 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Bean Golden Mosaic Geminivirus
? STRAIN: Type II Isolates
? INDIVIDUAL ISOLATE: Guatemala
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1059
? US-08-838-151A-45

alignment_scores:
? Quality: 217.00 Length: 70
? Ratio: 3.741 Gaps: 0
? Percent Similarity: 82.857 Percent Identity: 58.571

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Percent Similarity: 82.857 Percent Identity: 58.571

Alignment block:

US-09-289-346a-3 x US-09-065-999-6 ..
Align seg 1/1 to: US-09-065-999-6 from: 1 to: 1651

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796 ACATTCGAAATGGGAGCAATTCGAACTCGACCGCAACGCAATTCGAAAGAGS 845
17  YCysGlnThSerAsnApAlaAlaAlaAlaAlaAlaAlaAlaSerSerA 34
   |||::| |||::| |||::| |||::| |||::| |||::| |||::| |||::|
846 TCAGCACTCTCGCAACGCACTCATCTGCAAGCAAGCATTTAAACGCAATTCA 895
34  lAlAlAlAlAlaLeuGlnlAlAlaAglylulys11leproGluysTyrlau 50
   |||::| |||::| |||::| |||::| |||::| |||::| |||::| |||::|
896 TTGAATCTGCTTCACATATTTGAAGAGAAACGCAACGCAAGATTACGTC 945
51  PhcGlnPhhAlaAlaLeuAsnSerAsnSerAsnSerAsnGlyllePhAspLySth 67
   |||::| |||::| |||::| |||::| |||::| |||::| |||::| |||::|
946 CTTCAACATCAACACATCCCTCTTATCTTCACACGATCTTCGCAACGT 995
67  PProGluPro 70
   |||::| |||::| |||::| |||::| |||::| |||::| |||::| |||::|
996 GCCGCAACCA 1005

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seq_name: /cgnl_7/prodata/1/lna/6a_COMB.seq:US-09-065-999-8

seq_documentation_block:

Sequence 8, Application US/09065999

Patent No. 6118048

GENERAL INFORMATION:

APPLICANT: Hanson, Stephen F.

INVENTOR: Hanson, Stephen F.

TITLE OF INVENTION: TRANSDOMINANT INHIBITION OF GEMINIVIRAL

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady

STREET: One South Plinckney Street

CITY: Madison

STATE: WI

COUNTRY: US

ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: US/09/065, 999

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27,386

REFERENCE/DOCKET NUMBER: 960296, 94754

TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-9166

TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1894 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

MOLWGT: 1894

MOLECULE TYPE: DNA (genomic)

US-09-065-999-8

alignment_scores: Quality: 217.00 Length: 70

Ratio: 3.741 Gaps: 0

Percent Similarity: 82.857 Percent Identity: 58.571

Alignment block:

US-09-289-346a-3 x US-09-065-999-8 ..
Align seg 1/1 to: US-09-065-999-8 from: 1 to: 1694

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796 ACATTCGAAATGGGAGCAATTCGAACTCGACCGCAACGCAATTCGAAAGAGS 845
17  YCysGlnThSerAsnApAlaAlaAlaAlaAlaAlaAlaAlaSerSerA 34
   |||::| |||::| |||::| |||::| |||::| |||::| |||::| |||::|
846 TCAGCACTCTCGCAACGCACTCATCTGCAAGCAAGCATTTAAACGCAATTCA 895
34  lAlAlAlAlAlaLeuGlnlAlAlaAglylulys11leproGluysTyrlau 50
   |||::| |||::| |||::| |||::| |||::| |||::| |||::| |||::|
896 TTGAATCTGCTTCACATATTTGAAGAGAAACGCAACGCAAGATTACGTC 945
51  PhcGlnPhhAlaAlaLeuAsnSerAsnSerAsnSerAsnGlyllePhAspLySth 67
   |||::| |||::| |||::| |||::| |||::| |||::| |||::| |||::|
946 CTTCAACATCAACACATCCCTCTTATCTTCACACGATCTTCGCAACGT 995
67  PProGluPro 70
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996 GCCGCAACCA 1005

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seq_name: /cgnl_7/prodata/1/lna/6a_COMB.seq:US-09-065-999-7

seq_documentation_block:

Sequence 7, Application US/09065999

Patent No. 6118048

GENERAL INFORMATION:

APPLICANT: Hanson, Stephen F.

INVENTOR: Hanson, Stephen F.

TITLE OF INVENTION: TRANSDOMINANT INHIBITION OF GEMINIVIRAL

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady

STREET: One South Plinckney Street

CITY: Madison

STATE: WI

COUNTRY: US

ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE: US/09/065, 999

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27,386

REFERENCE/DOCKET NUMBER: 960296, 94754

TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-9166

TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 2072 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

MOLWGT: 2072

MOLECULE TYPE: DNA (genomic)

US-09-065-999-7

alignment_scores:

Quality: 217.00 Length: 70
 Ratio: 3.741 Gaps: 0
 Percent Similarity: 82.857 Percent Identity: 58.571

Alignment block:

US-09-289-346a-3 x US-09-065-999-7 ..

Align seq 1/1 to: US-09-065-999-7 from: 1 to: 2072

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1  THIDeValTFpGlyGluPhenIvalAspGlyATGSerAlaArgGlyG1 17
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796 ACATGCAATGGGAGCATTCACAAATCGACAGCGCATCTCCAAACAGCG 845
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
17  YCYGlnPhrSerAspAlaAlaAlaAlaLeuAlaIaSerSofa 34
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
846 TCACGAGTCGCGAACGCTCATATGCAAGGCTATTAAACGCGATTCGA 895
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
34  LaAlaAlaLeuGlnIleIleArgGluIysIleProGluIysTyrLeu 50
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
896 TTGAAATCGCTTTCACATATTCAGAGACAGACACGACGAAATTCAGTC 945
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
51  PhedIlnPheHisAanLeuAnSerAnLeuAspArgIlePheAspIysTh 67
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
946 CTTGACATGCACACATCGCTCTAATCTCGAACGSAATCTTCGCAAAGT 995
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
67  rProGluPro 70
   |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
996 GCGGAAACCA 1005

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34 ysglglualalaleuglnlleielaialaialleproglulstyreleu 50
|||||
2171 AAGAAAGAGCCCGAGAAATTAATTAAGAGAAANATCCGAGAAATAATTTA 2122
51 PhleboiphebiaSenleuSenSerSerleuSenAspArgIlePheAspArgIle 67
|||||
2121 TTTCAGTTCCACCAATTAATACCAATTAATAGATAGATATTGATACAC 2072
67 rProgluPro 70
|||||
2071 TCTCGAGCCA 2062
seq_name: gb_v1:AY029750
seq_documentation_block: 2588 bp DNA circular VRL 08-MAY-2001
LOCUS AY029750
DEFINITION Tomato severe rugose virus DNA-A, complete sequence.
ACCESSION AY029750
KEYWORDS AY029750.1 GI:14009278
SOURCE Tomato severe rugose virus.
ORGANISM Tomato severe rugose virus.
VIRUSES: ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE 1 (bases 1 to 2588)
AUTHORS Rezende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
TITLE Length DNA-R nucleotide sequence of a novel
TOMATO INFLUENTING BEGOMOVIRUS, Tomato severe rugose virus, in Brazil
JOURNAL Unpublished
2 (bases 1 to 2588)
REFERENCE 2 (bases 1 to 2588)
AUTHORS Rezende,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2001) Instituto de Genetica e Biologia,
Universidade Federal de Uberlandia, Av. Amazonas s/n, Bloco 2E,
Campus Umuarama, Uberlandia, Minas Gerais 38.400-000,
Brazil
FEATURES
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1..2588 location/Qualifiers
/organism="Tomato severe rugose virus"
/strain="Minas Gerais"
/db_xref="taxon:159463"
/country="Brazil"
/feature_key="complement: DNA-A"
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305..1060
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YKRPATIRLGLGADVPGCCGEGPCVOSTESRHDSYHVKVCYCSNVTYRNGITIRERK
ATVKNDRFOVMHMFVAKYATGGQVASNDQALVKRPKMYVANNVYHDEAGKYENHT
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/translation="MDSRGSLITARQENGYTWEISLPYFKINVEDPMTTSRY
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/product="Trap"

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/protein_id="AAK50361.1"
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SASQFOLODQDITLIDILFK"
complement(1533..2588)
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/protein_id="AAK50357.1"
/db_xref="GI:14009279"
/translation="MPSKAPRMLRAGTSVRSASNPAGSYGPKYKNAAMVNPMP
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ATVKNDRFOVMHMFVAKYATGGQVASNDQALVKRPKMYVANNVYHDEAGKYENHT
EVALILYACHTASNPYATVATKIRITFYDSTIN"
complement(12171..2434)
/gene="AC4"
complement(12171..2434)
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/protein_id="AAK50359.1"
/db_xref="GI:14009281"
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NRPSPSPSTRFELISNGSKSTAEVLBAVAQQLTMIDQKP"
note="common region"
rep-origin
BASE COUNT 660 a 525 c 598 g 805 t
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alignment_scores:
Quality: 297.00 Length: 70
Ratio: 4.714 Gaps: 0
Percent similarity: 90.000 Percent identity: 78.571
alignment_block:
US-09-289-346a-4 x AY029750/rev ..
Align seg 1/1 to reverse of: AY029750 from: 1 to: 2588
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2258 ACTATGCAATGAGGCGCAATTCAGACGCGCAACGCGCGC 2209
17 ysgglThSerAsnAspAlaIleGlnAlaIleAsnAlaSerSerL 34
|||||
2208 TTTCGACGACGCTTACGATCTCCGCGCAACGCTTGAACGACCTTCA 2159
34 ysglglualalaleuglnlleielaialaialleproglulstyreleu 50
|||||
2158 AAGACGTCGCTTCGAGTAATCCGCGAGACGACGGAATAATTTT 2109
51 PhleboiphebiaSenleuSenSerSerleuSenAspArgIlePheAspArgIle 67
|||||
2108 TTTCAGTTCCACCAATTAATACCAATTAATAGATAGATATTGATACAC 2059
67 rProgluPro 70
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2058 TCTCGAGCCA 2049
seq_name: gb_v1:AF291705
seq_documentation_block: 2622 bp DNA circular VRL 25-SEP-2000
LOCUS AF291705
DEFINITION Tomato severe mosaic virus DNA-A, complete sequence.
ACCESSION AF291705
VERSION AF291705.1 GI:10281644

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[illegible]

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/contig="AC1"
/feature="Rep"
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/db_xref="db:10281645"
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SVKDKDQD1EMGEFQIDKSRKAGCCQDANDAAEVLAWSQDIALI1RKRPKE
FQHLNLSKRLIFARALAPRPLSSFTNVRKMDADQVFRSAAARKE
E11RDSRQSTKSTKALCANLTLSDLPNRYEENVEETVETIDQILKLE
KSTVYKSTVYKSTVYKSTVYKSTVYKSTVYKSTVYKSTVYKSTVYK
KSTVYKSTVYKSTVYKSTVYKSTVYKSTVYKSTVYKSTVYKSTVYK
APRINELPSTQSSSC"
BASE COUNT      684 a      563 c      600 g      776 t

Alignment_scores:
      Quality:      295.00      Length:      70
      Score:      4.693      Gaps:      0
Percent Similarity: 90.000      Percent Identity: 78.571

Alignment_block:
US-09-289-346A-4 x AF291705/rev ..

Align seq 1/1 to reverse of: AF291705 from: 1 to: 2622

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      |||:::
2298 ACTATCGAATGCGGGGAGATTCGCAATGACGCGACGACATGCTGCAATGACGGG 2249

17 ycygslnthseraninspalaialaialaialelnaslaaser 34
      |||:::
      |||:::
2248 TTGCCAGACACGACACGACGCGCTCCGACACGCTTGACGACCTCCA 2199

34 ysglueluakalegnlletlaialaialelprogtuygrytieu 50
      |||:::
      |||:::
2198 AAGACATCGCCTTGCGAGATATTCGCGGACAGACGCGCGAAAGCTCTTA 2149

51 pheclnphelnslnleuansserszmlneusparyllepaauplyrth 67
      |||:::
      |||:::
2148 TTTCATGTTTCACATCAATGATACATTTATTAACATGAGATTTTCGACG 2099

67 pfroglupro 70
      |||:::
      |||:::
2098 TCCGAGACCA 2089

seq_name: gb_vl:U092532
seq_documentation_block: 1193 bp      DNA      VR      01-APR-1997
DEFINITION      leonurus mosaic virus Rep protein (rep) and coat protein (cp)
genes: partial cds.
accession      092532
version      092532.1 GI:1916544
KEYWORDS
SOURCE
ORGANISM      leonurus mosaic virus.
LEONURUS MOSAIC VIRUS
Virus; dsDNA (+sense); geminiviridae; begomovirus.
REFERENCE
Farrar,J.C. and Maxwell,D.P.
Title      Variability in geminivirus associated with Phaseolus vulgaris
Brazil

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gene	358. .1113
CDS	358. .1113

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CGGCATCCGAAGCATGATGCTT

111111
3AAGA

[illegible]

JOURNAL, J. Plant Res. 110, 247-257 (1997)
FEATURES
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Location/Qualifiers
1..570
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/organism_taxid="10088" *NC_001313.1*
/specific_host="Nicotiorum maktinol"
/db_xref="taxon:67762"
/clone="YOKOHAMA3-1"
complement(1..570)
/gene="CI"
complement(<1..570)
/gene="CI-RT1"
/protein="16" *BA34033.1*
/db_xref="GI:442641"
/translation="PRLSIQNIININPTNKLYIKICRELHEDSPHHIALLQPECKYK
CQNFPEFVSPFRNSRIHPHINQKASSSDVYSIPKIDSDILEMOTQIDORSKRGCC
QNNNDACVAILNNSKRIAPALILEKLIKDFIYHNLNSLRIIFAPLFLVPCPFL
ASSFQVPEELSEKSNVSNARWRPM"
comp.comp(231..488)
/gene="C2"
complement(231..488)
/gene="C4"
/codon_start=1
/protein_id="BA34034.1"
/db_xref="GI:3798715"
/translation="MRALISKQFESSKRNKRTDSSVYSPQPDHISITPFEILNP
APTPSPTRIELNSGHSNSTEVELEANNRLTHVOR"
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ORIGIN 141 a 121 c 126 g 102 t

Alignment scores:
Quality: 254.00 Length: 85
Ratio: 4.164 Gaps: 1
Percent similarity: 71.765 Percent identity: 56.624

alignment block:
US-09-289-346A-4 x AB001315/rev ..

Align seg 1/1 to reverse of: AB001315 from: 1 to: 570

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268 CTGCCAGATCTCAACACAGCCAGTGGCAGAGCCCTTAAGCAGACTTCA
34  YSGTGTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
11  TTTTCTGATTTTGGTTCCTTCACAGCTCCATCTTTCATCAAGTTC
218 ACCTCTCAATAGGGAGACATCTCCAGATCGAGGAGAGAGAGAGAG
51  PHEGIDPHEHISASLNLASASERASNLAEUASPARITTE
168 TTTTCATATCATATTTAAATAGTAATTTAGTATGATTTGGCTCTCTC
64  .....
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FT      /*aaq" d
FT      /note" "ribozyme R3 cleavage site"
PN      M09503404.A.
XX      02-FEB-1995.
XX      22-JUL-1993; 93MO-BP01946.
XX      22-JUL-1993; 93AJU-0047014.
XX      22-JUL-1993; 93MO-BP01946.
XX      (BIOC-) BIOCSM SA.
XX      (CSIR) COMBOWELLHIN SCI & IND RES ORG.
PI      Baudino S, Comrau D, Dry IR, Gruber V, Lemee P;
PI      Meson J, Rezian MA, Riden JR, Rezanan MA;
PI      MPI: 1995-075232/10.
DR      Synthetic DNA virus ribozyme(s) - reduce replication, infection
DR      and/or assembly of viruses by cleaving target virus sequence,
PT      useful for preparing resistant plants, esp tomatoes.
XX      Example 10; Fig 11c: 90pp: English.
XX
XX      The sequence is a tomato leaf curl virus target sequence for
XX      polyribozyme-F, which hybridizes to and cleaves the sequence and
XX      thereby reduces replication, infection and/or assembly of the virus
XX      e.g. tomato, to confer virus disease resistance.
XX
SQ      Sequence 479 BP; 145 A; 95 C; 97 G; 142 T; 0 other:
SQ
Alignment_scores:
      Quidity: 233.00      Length: 85
      Ratio: 3.820
      Percent Similarity: 71.765      Percent Identity: 54.118
Alignment_block:
US-09-289-346A-4 x AA084372 ..
Align seg 1/1 to: AA084372 from: 1 to: 479
1   Thtlewaiaipglsiguhpneiginnvayalaspqiyvrsorlratgvcsl 17
    |||||
140  ACCCTCGATGCGGAGGTTTCAGATCGATGGAGCATCTCCAGAGGGGG 189
17  ycsydlthrsraasaspaialaialagualaleuasnalaibse-ort. 34
    | |||||
190  ACACACATACCCAGATACCGCTTACGCCAGGCCCTTACATCACTGACATA 239
34  ysgsluglunlaionchilialalalalalalalaletrcojuygrytieu 50
    |||||
240  AGTCAGAGGCTCTACAGCTTCAGATGAGGATTCAGCCCTTAAGATATTCCT 289
51  phtglnphtlshlsluhsaslsrfauluhsaparglile..... 63
    : : : : :
290  FTACCATTCATCATATATATATATATATATATATATATATATATACCTCC 339
34  ..... phaeaplythrp 68
    |||||
340  GTTGAGGCTTATGCTTCCCTTTTATCTCTCTCTTTCGATCGAGTTC 389
    |||||
390  CAGAA 394
seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA195.DAT:AA084375
seq_documentation_block:
ID: AA084375 standard: DNA; 550 BP.

```

```

XX AC AA084375;
XX DN 19-AUG-1995 (first entry)
XX DE Tomato leaf curl virus Australian strain DNA sequence.
XX KM Tomato leaf curl virus; Australia strain; plant disease: ds.
XX OS Tomato leaf curl virus (Australia).
XX PN W09503404-A.
XX PD 02-FEB-1995.
XX PF 22-JUL-1993: 93WO-EP01946.
XX PR 22-JUL-1993: 93AU-0047014.
XX PR 22-JUL-1993: 93WO-EP01946.
XX PA (BIOC-) BIOCEN SA.
XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX PI Baudino S., Comeau D., Dry IB., Gruber V., Lence P.
XX PI Mason J., Rezaian MA., Riden JE., Rezaian MA.
XX WP: 1995-07532/10.
XX PP Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX PP and/or assembly of viruses by cleaving target virus sequence,
XX PP useful for preparing resistant plants, esp tomatoes.
XX PS Disclosure: Fig 1: 90pp: English.
XX CC The sequence represents the complementary sense DNA strand of an
XX CC cDNA clone of the tomato leaf curl virus. It is a 2744 bp
XX CC sequence. The sequence may be used in generation of transgenic plants
XX CC with disease-resistance.
XX SN Sequence 550 BP; 148 A; 120 C; 134 G; 142 T; 6 other:

alignment_scores:
  Quality: 232.50 Length: 86
  Ratio: 3.811 Gaps: 1
  Percent Similarity: 70.930 Percent Identity: 53.488

alignment_block:
  US-09-289-346a-4 x AA084375 ..
  Align seg 1/1 to: AA084375 from: 1 to: 550
  1 ThleauValTRGtYgluphGcInValaSPoLyATSSerAlaVgYcI 17
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  201 ACCCTGATAGGGGAGATTTCAGTCAGTCGACGATCTCGAAGACGG 250
  17 yCYsGlnThrSerAspAlaAlaIaGlnAlaLeuAsnAlaSerSe 34
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  251 KACACATACGCCAATACGCTTACGCCACGCTTACACATCAAGTA 300
  34 ySgInGlnAlaLeuGlnInIleIleAlaAlaAlaIleProGluYgTylen 50
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  301 AGTCAGAGGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACG 350
  51 PhcGlnPheIleAsnLeuAsnSerAsnLcASpATgIle..... 63
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  351 TTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTTNNNTK 400
  64 ..... PheAspLysT 67
  401 TCCGTTGAGGTTTATGTTCTCTTTTATCTTCTCTTATGTCAG 450
  67 htrProGlu 69

```

```

seqname: /cgnl_8/egcdat/geneseq/geneseq/NA1997.DAT:AA93317
451 TTCACGAA 458
:|||||
ID seq_documentation_block:
XX AA93317 standard; DNA: 2744 BP.
AC AA93317;
XX 27-APR-1998 (first entry)
XX DE Tomato leaf curl virus from Southern India (stem-loop begin).
XX KM Geminiivirus: TICV-IND; AC1 gene: transdominant mutation;
XX KM Transgenic plant; disease resistance; ss: cyclic; circular.
XX OS Tomato leaf curl virus from Southern India.
XX PN W09739110-A1.
XX PD 23-OCT-1997.
XX PF 15-APR-1997: 97WO-0506300.
XX PR 16-APR-1995: 9505-0015517.
XX PA (SEMT-) SEMTUS VECTABLE SEEDS INC.
XX PA (MISC) WISCONSIN ALOHAI RES FOUND.
XX PI Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX WP: 1997-526447/48.
XX DR Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX CC mutant genes have enhanced resistance to geminivirus infection
XX CC and geminivirus resistance in tomato yellow leaf curl virus or bean
XX CC golden mosaic geminivirus
XX PS Disclosure: Page 119-121: 132pp: English.
XX CC This genomic DNA sequence comprises a full-length sequence
XX CC (stem-loop begin) from a tomato leaf curl virus from Southern
XX CC India. The sequence is a 2744 bp cDNA clone of the tomato leaf
XX CC containing geminivirus AC1 or CI wild-type or mutant
XX CC sequences (see AA93317-93) that negatively interfere in trans with
XX CC geminiviral replication during infection. Such transgenic plants
XX CC are resistant to viral infection. The AC1/CI genes are especially
XX CC from tomato mottle virus, tomato yellow leaf curl virus or bean
XX CC golden mosaic virus.
XX SN Sequence 2744 BP; 742 A; 539 C; 637 G; 826 T; 0 other:

alignment_scores:
  Quality: 229.00 Length: 65
  Ratio: 4.241 Gaps: 1
  Percent Similarity: 83.077 Percent Identity: 69.231

alignment_block:
  US-09-289-346a-4 x AA93317/rev ..
  Align seg 1/1 to reverse of: AA93317 from: 1 to: 2744
  4 TTRpLYGlnPhcGlnValaSPoLyATSSerAlaVgYcIyCYsGln 20
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  2266 TGGGCTGAGTTTCATGATCGACATCTCGACGACGACGACATCA 27
  20 tSerAsnSPoLyAlaIaGlnAlaLeuAsnAlaSerSeTySgInGln 37
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
  2216 AGCTAATGATGCTCCGCGAGGCTTAAAGCGCTTAAAGCGTCA 42
  37 lalauGlnIleIleAlaAlaIleProGluYgTylenPhcGlnPhe 53

```


PD	21-MAR-1996.
PF	15-SEP-1995:
XX	95NC-FR01192.
XX	15-SEP-1994:
XX	94FR-0011040.
XX	(CNRS) CENT NAT RECH SOL.
PA	Gronenborn B:
PI	
PL	
DR	WPI: 1996-179947/18.
XX	P-PsDB; AAB8872.
XX	Prodn. of virus-resistant transgenic plants - using mutated genomic
PT	sequence from phytopathogenic DNA virus
PS	Disclosure: Fig 13: 34pp. French.
XX	
CC	Mutation of consensus amino acids in the NTP-binding site of
CC	geminivirus Rep protein is used to produce replication deficient
CC	viruses. The mutated viral nucleic acid is used for producing
CC	transgenic plants resistant to infection by the virus (not cit)
CC	virus. The present sequence encodes a mutant form of the Rep (or Rc)
CC	protein from the sardinian isolate of tomato yellow leaf curl virus
CC	(STYLCO) in which the wild-type Lys227 residue has been changed by an
CC	Arg residue; transgenic Nicotiana benthamiana plants generated by an
CC	transformation with the mutated virus were not resistant to STYLCO.
CC	In contrast, plants transformed with a virus in which Lys227 had been
CC	replaced by Ala were found to be resistant.
SQ	Sequence 1080 BP: 356 A: 247 C: 210 G: 267 T: 0 other:
alignment_scores:	
Quality:	222.00 Length: 69
Ratio:	3.895 Gaps: 0
Percent Similarity:	82.609 Percent Identity: 57.971
alignment_block:	
US-09-289-346A-4 x AAT12906 ..	
Align seg 1/1 to: AAT12906 from: 1 to: 1080	
2 LeuValTrpGlyAluPheGluValAspIleValArgSerAlaArgLysIcyc 18	
111	
331 CTTCGAATGGAGCTTTCACATCGCAGCAAGCATGTCTGCAGGAGCAACA 380	
18 scqInPhserAmrApAlaAlaAdgIdaAlaLeuAsnAlaseSerLys 35	
381 ACAGACGCCCAACAGCGTTACGCAAGCAAGCAATTAACGGACGAGAAGTAGT 430	
35 IugIalalaLeuGlnIleIleIleAlaAlaAlaIlePrpGluLysTryLeuPhe 51	
431 CGGAGCGCTTGATGATTGATTAAAGATAATTNCGGCGCTAACAGANTTAAGTGA 480	
52 GluPheIsaMetLeuAsnSerLysSerLysAlaScylIlePheAspLysThrPr 68	
::::::::::::::::::::IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII 11	
481 CATTTTGAATAATTAATTAAGTAAATTAATTAACATTAACGCTTTCAGGCGCCYC 530	
68 oGUlUPRO 70	
131 CGCACACT 537	
seq_name: /cgnl_8/gcgdate/geneseq/geneseqp_NAI1995.DAT :AA084378	
seq_documentation_block:	
ID AA084378 standard: DNA: 1695 BP.	
AA	
AX	AA084378:
XX	
XT	19-AUG-1995 (first entry)
XE	Tomato yellow leaf curl virus DNA sequence.

```

XX Tomato yellow leaf curl virus; plant disease;
KW ribozyme target sequence; ds.
OS Tomato yellow leaf curl virus (S).
PH
PI Key Location/Qualifiers
PI misc_feature 405
FT /tag= a
FT /note= "Ribozyme cleavage site"
FT 1069- b
FT /note= "Ribozyme cleavage site"
FT 1286
FT /tag= c
FT /note= "Ribozyme cleavage site"
XX W09503404-A.
XX 02-FEB-1995.
XX 22-JUL-1993: 93MO-EP01946.
XX 22-JUL-1993: 93AU-0047014.
XX 22-JUL-1993: 93MO-EP01946.
XX (BIOC-) BIOGEN SA.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX Baudino S, Comeau D, Dry IB, Graber V, Ienne P;
XX Mason J, Rezaiian MA, Rydgen JB, Rezaiian MA;
XX MPI: 1995-075232/10.
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX of tobacco etch virus (TEV) using cleavage target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX Disclousre: Fig B: 90pp: English.
XX The sequence represents the complementary sense DNA strand of
XX tomato yellow leaf curl virus-S strain. Ribozyme cleavage sites
XX are indicated. Ribozymes against this sequence may be used in
XX generation of transgenic cometo plants with disease resistance.
XX Sequence 1695 BP: 568 A: 366 C: 308 G: 453 T: 0 other:
XX
XX alignment_scores:
XX Quality: 222.00 Length: 69
XX Ratio: 0.988 Gaps: 0
XX Percent Similarity: 82.009 Percent Identity: 57.971
XX
XX alignment_block:
XX US-09-289-346a-4 x AA084378
XX
XX Align seg 1/1 to: AA084378 from: 1 to: 1695
XX
XX 2 leuValATrGclgUlpHocInVaIsocIyATgSerAlaAGclGlyCy 18
XX ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 487 CTGAAATGCGGACTTCAGATCGACGACGACATCTGCGAGGGAGACA 536
XX
XX 18 sGlnrHrSerAsnAspAlaAlaIaGuaIaAluAsnAlaSerLeuLyg 35
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 537 ACAGACACCCACACGCTTACACAAAGCCATATTAACGACGAAATGACT 586
XX
XX 35 lUGlUAlaLeuGcllGcllAlaAlaAlaAlaIleRgcGlyUstRoumpe 51
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 587 CCGACGCTCTGATGCAATTAAGATTACCCCTACACATTACGCTCTA 636
XX
XX 52 GlnPheHIsAsnLeuAsnSerAsnLeuAspArg1LePheAspUstRhp 68
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 637 CATTTTCATATATATATATAGATTAGATTACGCTTCCAGCTGCTCC 686

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68 oClupro 70
1 |||
687 GCGACCT 693
seq_name: /cgnl_8/cydata/geneseq/geneseq/NA1997.DAT:AA793291
seq_documentation_block:
10 AA793291 standard: DNA: 1062 BP.
XX
XX AA793291:
XX
XX 27-APR-1998 (first entry)
XX
XX Bean golden mosaic geminivirus CI mutant ORF BGAC221.
XX
XX Geminivirus; BGWV; CI gene; transdominant mutation;
KW transgenic plant; disease resistance; ss; cyclic; circular.
XX
XX Bean golden mosaic virus type II isolate Guatemala.
XX W09739110-AI.
XX
XX 23-OCT-1997.
XX
XX 15-APR-1997: 97MO-0506300.
XX
XX 16-APR-1996: 9605-0015517.
XX (SEMT-) SEMINIS VEGETABLE SEEDS INC.
XX (MISC) MISCOSIN ALUMINI RES FOUND.
XX
XX Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Scout JT;
XX MPI: 1997-526447/48.
XX P-PSDB; AA04333.
XX
XX Transgenic plants expressing geminivirus ACI and CI wild-type and
XX mutant genes - have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX
XX Claim 13: Page 107-109; 132pp: English.
XX
XX This DNA sequence comprises construct BGAC221 that codes for a
XX transdominant lethal mutant (see AA04333) of the CI protein (see
XX AA04338) of bean golden mosaic virus (BGWV). It was obtained by
XX Kunek mutagenesis of the wild-type CI gene (see AA793314). CI is
XX required for replication. The invention involves production of
XX transgenic plants containing DNA comprising geminivirus CI or ACI
XX wild-type or mutant sequences that negatively interfere in trans
XX replication of the virus. The invention also involves transgenic
XX plants that are resistant to viral infection. The ACI/CI genes are
XX especially from BGWV, tomato mottle virus or tomato yellow leaf
XX curl virus (see AA793282-93) and encode polypeptides (see AA043324-35)
XX that have mutations in the highly conserved DNA-nicking and/or the
XX NTP-binding domains.
XX
XX Sequence 1062 BP: 339 A: 245 C: 219 G: 259 T: 0 other:
XX
XX alignment_scores:
XX Quality: 219.00 Length: 70
XX Ratio: 3.776 Gaps: 0
XX Percent Similarity: 82.857 Percent Identity: 60.000
XX
XX alignment_block:
XX US-09-289-346a-4 x AA793291
XX
XX Align seg 1/1 to: AA793291 from: 1 to: 1062
XX
XX 1 ThrleuValATrGclgUlpHocInVaIsocIyATgSerAlaATgclYgI 17
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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328 ACAATCGAATGGGACATTCACATTCAGACGGCAGATCTGCACAGCAGC 377
17 YCysGlnThrSerAsnAspAlaAlaIleAlaLeuAsnAlaSerL 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
378 TCGACAGTCGCGACAGCACTCATATGACGACATTAAAGCATTTTCA 427
34 YGluGlnAlaLeuGlnIleIleAlaAlaAlaIleProGluLysTyrLeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
428 TTGAGATCTCCCTTCACATATTTAGAGAGACAGACCGCAATATTCCTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThr 67
   ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
478 CTTCAACATCAGCAACATCCGTCCTCATCTCAGACGATCTGTCTCAAGT 527
67 PProGluLupro 70
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
528 GCCGAGACCA 537
seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AA193292
seq_documentation_block:
ID AA193292 standard; DNA: 1062 BP.
AA193292:
AA193292:
27-APR-1998 (first entry)
Bean golden mosaic geminivirus CI mutant ORF BGAC228.
Geminivirus; BGWV; CI gene; transdominant mutation;
transgenic plant; disease resistance; ss; cyclic; circular.
XX Bean golden mosaic virus type II isolate Guatemala.
OS
XX MO9739110-A1.
23-OCT-1997.
15-APR-1997; 97MO-US06300.
PR 16-APR-1996; 96DS-0015517.
XX (SEMT-) SEMINUS VEGETABLE SEEDS INC.
XX (WISC) WISCONSIN ALDUMNI RES FOUND.
XX Abitajust PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX WPI; 1997-526447/48.
XX P-PSDB; AAM34334.
XX Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX mutant genes - have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX
XX Claim 13: Page 111-112; 132pp; English.
XX This DNA sequence comprises construct BGAC228 that codes for a
XX transdominant lethal mutant (see AAM34334) of the CI protein (see
XX AAM34338) of bean golden mosaic virus (BGWV). It was obtained by
XX Kniel/48) and is deposited with the WIPO International Patent
XX required for replication. The invention involves production of
XX transgenic plants containing DNA comprising geminivirus CI or AC1
XX wild-type or mutant sequences that negatively interfere in trans
XX plant geminiviral replication during infection. Such transgenic
XX plants are resistant to viral infection. The AC1/CI genes are
XX especially from BGWV, tomato mottle virus or tomato yellow leaf
XX curl virus (AYDV) and encode polypeptides (see AAM3434-35)
XX that have mutations in the highly conserved DNA-licking and/or the
XX NTP-binding domains.
XX
XX Sequence 1062 BP: 338 A; 247 C; 218 G; 259 T; 0 other;

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alignment_scores:
Quality: 219.00 Length: 70
Ratio: 3.776 Gaps: 0
Percent Similarity: 82.857 Percent Identity: 60.000
alignment_block:
US-09-289-346a-4 x AA193292
Align seq 1/1 to: AA193292 From: 1 to: 1062
1 ThrLeuValIrrGlyGlnPheGlnValAspGlyAArgSerAlaArgLysI 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
328 ACATCGAATGGGACAGCACTCATATGACGACGACGACATCTGCACAGCAG 377
17 YCysGlnThrSerAsnAspAlaAlaIleAlaLeuAsnAlaSerL 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
378 TCGACAGTCGCGACAGCACTCATATGACGACATTAAAGCATTTTCA 427
34 YGluGlnAlaLeuGlnIleIleAlaAlaAlaIleProGluLysTyrLeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
428 TTGAGATCTCCCTTCACATATTTAGAGAGACAGACCGCAATATTCCTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThr 67
   ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
478 CTTCAACATCAGCAACATCCGTCCTCATCTCAGACGATCTGTCTCAAGT 527
67 PProGluLupro 70
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
528 GCCGAGACCA 537
seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT:AA193293
seq_documentation_block:
ID AA193293 standard; DNA: 1062 BP.
AA193293:
AA193293:
27-APR-1998 (first entry)
Bean golden mosaic geminivirus CI mutant ORF BGAC262.
Geminivirus; BGWV; CI gene; transdominant mutation;
transgenic plant; disease resistance; ss; cyclic; circular.
XX Bean golden mosaic virus type II isolate Guatemala.
XX
XX MO9739110-A1.
23-OCT-1997.
15-APR-1997; 97MO-US06300.
XX (SEMT-) SEMINUS VEGETABLE SEEDS INC.
XX (WISC) WISCONSIN ALDUMNI RES FOUND.
XX Abitajust PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX WPI; 1997-526447/48.
XX P-PSDB; AAM34335.
XX Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX mutant genes - have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX
XX Claim 13: Page 115-116; 132pp; English.
XX This DNA sequence comprises construct BGAC262 that codes for a
XX transdominant lethal mutant (see AAM34335) of the CI protein (see
XX AAM34338) of bean golden mosaic virus (BGWV). It was obtained by

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CC Kunkel mutagenesis of the wild-type CI gene (see AAT93314). CI is
 CC required for replication. The invention involves production of
 CC transgenic plants containing DNA comprising geminivirus CI or ACI
 CC wild-type or mutant sequences that negatively interfere in trans
 CC with the replication of the virus. Such plants are resistant to viral
 CC infection. The ACI/CI genes are
 CC especially from BGMV, tomato mottle virus or tomato yellow leaf
 CC curl virus (see AAT93282-93) and encode polypeptides (see AAM34324-35)
 CC that have mutations in the highly conserved DNA-nicking and/or the
 CC NTP-binding domains.

XX Sequence 1062 BP: 340 A: 245 C: 219 G: 258 T: 0 other:

alignment_scores:
 Quality: 219.00 Length: 70
 Ratio: 3.776 Gaps: 0
 Percent Similarity: 82.857 Percent Identity: 60.000

alignment_block:
 US-09-289-346a-4 x AAT93293 ..
 Align seg 1/1 to: AAT93293 from: 1 to: 1062

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1  ThrLeuValITrPGlyGlnPhcGlnValaAspGlyAArgSerAlaATGtGlyC 17
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
328 KcATTCGATGAGGGGACcANTTCcAGTCcAGCGcAGcATCTcCAAGAGAGG 377
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
17  YcSGGlnThSerAsnAPAlaAlaGluAlaLeuAsnAlaSerSert 34
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
378 TCAGCGTCGTCCGcACGcCTCATTCGACcAGCATTTAAcCGcAGATTTCcAA 427
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
34  YcGluGlnAlaLeuGlnITleAlaAlaAlaAlaITleProGluuTyTleu 50
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
428 TTGcATCTcGCTTCcAGcATcATTCcAGcAGcAGcAGcATTCcAGTC 477
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
51  PhcGlnPhcHisAsnLeuAsnSerAsnLeuAsnAPArgITlePhcAspLySth 67
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
478 CTTCAcCATTCcAGcACATCCGTCCTTCATCTCGACcAGcATCTCTCGcAAAGT 527
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
67  PPGcGluPro 70
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
528 GCGGAGMcCA 537

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seq_name: /cgnl_8/gcdata/geneseq/geneseq/NA1997.DAT: AAT93314
 seq_documentation_block:
 ID AAT93314 standard: DNM: 1183 BP.

XX AAT93314:
 DT 27-APR-1998 (first entry)
 XX
 DE Bean golden mosaic geminivirus CI open reading frame.
 XX
 XX Gemintivirus: BGMV, CI gene: transdominant mutation;
 XX Transgenic plant: disease resistance, ss: cyclical; circular.
 XX Bean golden mosaic virus type II isolate Guatemala.

XX
 XX Key Location/Qualifiers
 XX CDS 1..1062
 XX /tag- a
 XX M09739110-A1.

XX
 XX 23-OCT-1997.
 XX
 XX 15-APR-1997: 97MO-US06300.
 XX
 XX 16-APR-1996: 960US-0015517.
 XX
 XX (SMT-) SPMINIS VEGETABLE SEEDS INC.

PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX
 XX Abijah PG, Hanson SF, Luu HT, Maxwell DP, Stout JT:
 XX WPI: 1997-526447/48.
 XX P-PSDB: AAM34338.

XX Transgenic plants expressing geminivirus ACI and CI wild-type and
 XX mutant genes - have increased resistance to geminivirus infection
 XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
 XX golden mosaic geminivirus

XX Example 5: Page 100-102; 132pp; English.

XX This genomic DNA sequence includes the open reading frame (ORF) of
 XX the wild-type CI gene of bean golden mosaic virus (BGMV). A
 XX geminivirus that has a monopartite genome. The CI protein (see
 XX AAM34338) is required for replication. The wild-type CI ORF was
 XX subjected to Kunkel mutagenesis (see AAT93290-93). The invention
 XX involves production of transgenic plants containing DNA comprising
 XX wild-type or mutant sequences that negatively interfere in trans
 XX with the replication of the virus. Such plants are resistant to viral
 XX infection. The ACI/CI
 XX genes are especially from BGMV, tomato mottle virus or tomato
 XX yellow leaf curl virus (see AAT93282-93) and encode polypeptides
 XX (see AAM34324-35) that have mutations in the highly conserved
 XX DNA-nicking domain and/or the NTP-binding domains.

XX Sequence 1183 BP: 372 A: 276 C: 248 G: 287 T: 0 other:

alignment_scores:
 Quality: 219.00 Length: 70
 Ratio: 3.775 Gaps: 0
 Percent Similarity: 82.857 Percent Identity: 60.000

alignment_block:
 US-09-289-346a-4 x AAT93314 ..
 Align seg 1/1 to: AAT93314 from: 1 to: 1183

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1  ThrLeuValITrPGlyGlnPhcGlnValaAspGlyAArgSerAlaATGtGlyC 17
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
328 KcATTCGATGAGGGGACcANTTCcAGTCcAGCGcAGcATCTcCAAGAGAGG 377
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
17  YcSGGlnThSerAsnAPAlaAlaGluAlaLeuAsnAlaSerSert 34
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
378 TCAGCGTCGTCCGcACGcCTCATTCGACcAGCATTTAAcCGcAGATTTCcAA 427
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
34  YcGluGlnAlaLeuGlnITleAlaAlaAlaAlaITleProGluuTyTleu 50
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
428 TTGcATCTcGCTTCcAGcATcATTCcAGcAGcAGcAGcATTCcAGTC 477
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
51  PhcGlnPhcHisAsnLeuAsnSerAsnLeuAsnAPArgITlePhcAspLySth 67
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
478 CTTCAcCATTCcAGcACATCCGTCCTTCATCTCGACcAGcATCTCTCGcAAAGT 527
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
67  PPGcGluPro 70
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
528 GCGGAGMcCA 537

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seq_name: /cgnl_8/gcdata/geneseq/geneseq/NA1997.DAT: AAT93290
 seq_documentation_block:
 ID AAT93290 standard: DNM: 1183 BP.

XX AAT93290:
 DT 27-APR-1998 (first entry)
 XX
 DE Bean golden mosaic geminivirus CI mutant gene.
 XX
 XX Gemintivirus: BGMV, CI gene: transdominant mutation;
 XX


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seq_name : /cgnl_8/scgdelta/geneseq/geneseqn/MK2000.DMT::AAA94700
seq_documentation_block: ID AAAA94700 standard; DNM: 1651 BP. AC AAAB94700; DE 15-JAN-2001 (first entry) pmwG 2288 JIS-rep gene cassette. XX geminivirus; DMN-A: geminivirus replication inhibitor; ac3 gene; transgenic plant; actival; gene therapy; bean golden mosaic virus; BMV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CaMV; DS. KW Bean golden mosaic virus. OS Cauliflower mosaic virus. CA Alfalfa mosaic virus. SS Synthetic. XX US6118048-A. PN 12-SEP-2000. PP 24-APR-1998: 98US-0065999. PR 25-APR-1997: 97US-0044925. PA (MISC ) WISONSNIN ALDMMI RES FOUND. DN WPt.: 2000-610861/58. DR Genetic construct comprising a mutant geminiviral rep gene, useful for producing a plant resistant to geminiviral infection." PT Example; Column 15-16; 14pp; English. CC The present sequence is a 35S-rep gene cassette comprising the rep gene of bean golden mosaic virus (BGMV)-GA cloned downstream of the GmY vector. This recombinant DNA was used as template to produce the expression sequence which was integrated into pBSIT-KST to produce the rep gene expression vector. DNA-nicking domain mutations may be incorporated into rep gene to produce a genetic construct that acts as a trans-dominant inhibitor of geminiviral replication. When expressed in a plant cell, this inhibitor is able to dramatically reduce replication of geminivirus. CC Genetic constructs that include sequences containing a portion of the ac3 gene in addition to the trans-dominant-inhibitor exhibit increased resistance to BGMV. These results suggest that the inclusion of ac3 gene replication enhancers are one of the greatest constraints on production of important crops, including cassava, beans, cowpeas, peppers, tomatoes and cotton. The effects of the virus can be overcome by using the genetic construct.. CC Sequence 1651 BP: 517 A: 393 C: 342 G: 399 T: 0 other: SO alignment_scores: Quality: 219.00 Length: 70 Ratio: 3.776 Gaps: 0 Percent Similarity: 82.857 Percent Identity: 60.000 alignment_block: US-09-289-346A-x XAA94700 .. Allign seg I/I to: AAA94700 from: 1 to: 1651
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I ThrtleuvdATrTgcCGAGTCagheGnvaJaapCjYAcsgSeAlatAgctGLL 17
|||||
528 GGCGGGACCA 537

[illegible]

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alignment_scores:
  Quality: 219.00
  Ratio: 3.776
  Percent Similarity: 82.857
  Length: 70
  Gaps: 0
  Percent Identity: 60.000
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alignment_block:
US-09-289-346A-4 x AAA94703
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Align seg 1/1 to: AAA94701 from: 1 to: 1651

[illegible]

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        /db_xref="taxon:9606"
        clone_library="NCI-CCAB-K1d3"
        /lab_host="DHIOB"
        note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with
        a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
        strand cDNA was primed with a Not I - oligo(dT) primer,
        double-stranded cDNA was ligated to Eco RI adaptors
        (Pharmacia), digested with Not I and cloned into the Not
        I site of the pGEM-3 vector. The recombinant vector was
        source 2 pooled kidney library through electroporation
        or normalization. Library constructed by Bento Soares and
        M. Felima Bonaldo."
BASE COUNT      98 a   90 c   102 g       53 t
ORIGIN
alignment_scores:
    Quality:      69.50      Length:      64
    Ratio:         1.782     Gaps:         3
Percent Similarity: 60.938      Percent Identity: 37.500
alignment_block:
US-09-289-346A-4 x AA863354 ..
Align seg 1/I: CO: AA863354 from: 1 to: 343
3 ValTrp...GIYLDIPNheIVAl.....ASgCYLArgSerAlAr 15
||||| .....|.....|.....|.....|.....|.....|
43 GTGTGCACGGTGCAAAAGCAGATGCTCCCGGACCAACCGAGTCGTAC 92
|||..|..|..|..|..|..|..|..|..|..|..|..|..|..|..|
15 gGjyGlyCySLnThrSerAsnspALalalaglualeluasAlas 32
AGAGAGTGAAGAAGACCTGGAAATGACCAAGCATGCCCGACTG..... 135
93 AAGAGTGAAGAAGACCTGGAAATGACCAAGCATGCCCGACTG..... 135
32 eSerLySGlGuILeUglInleIAleAlAlAlleIpobLuys 48
||||| ::: |||||::|::|::|::|::|::|::|::|::|::|::|::|
136 .....GAGCGMAAGATGCTATTATCCACACCAAGACGCTGCCAG 177
49 TyLeuPheGlnPheHISanLeuasnSerAsnleuSparg 62
178 TACCAGATCGAGACCTGCTCTCCACCCACCAAGCTGCAGAA 219
seq_name: pj_est1.A1731422
seq_documentation_block:
LOCUS      A1731422          546 bp      mRNA           EST              11-DUN-1999
DEFINITION BRLHD19565 Six-day Cotton fiber Gossypium hirsutum CDA-5' similar
to mitochondrial processing peptidase (EC 3.4.99.41) alpha-II chain
peptidase [Solanium tuberosum], mRNA sequence.
ACCESSION  A1731422
KEYWORDS
SOURCE
ORGANISM   Gossypium hirsutum
            Solanum tuberosum plantae; Streptophyta; Embryophyta; Tracheophyta;
            Eudicotyledons; Malvales; Malvaceae; Gossypium.
REFERENCE  1 (bases 1 to 546)
            Bielavicz,M., Metz,E.C., Davy,D.F. and Burr,B.
            ESTs from developing cotton fiber
            unpublished (1999)
COMMENT
            Contact: Ben Burr
            Department of Plant Biology
            Brookhaven National Laboratory
            Upton, NY 11973 USA
            Tel.: 516-344-3396
            Fax: 516-344-3407
            Email: burrd@bnl.bnl.gov
            Seq primer: T3 Primer.
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[illegible]

TITLE Chen, S., Mao, M. and Chen, Z.
JOURNAL Homo sapiens CB library cDNA clones
COMMENT Unpublished (2000)
Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: mshliems.stn.sh.cn

This clone is available at Shanghai Hematology Institute in Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.

FEATURES
source
1. 586
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CBMAC03"
/cell_line="CB"
/tissue_type="cord blood"
/note="Vector: pBluescript; Site 1: EcoRI; The insert is cloned randomly with the EcoRI digestion"

BASE COUNT 162 a 140 c 166 g 115 t
ORIGIN

alignment_scores:
Quality: 67.00 Length: 53
Ratio: 1.811 Gaps: 2
Percent Similarity: 69.811 Percent Identity: 32.075

alignment_block:
US-09-289-346a-4 x AV373185 ..

Align seg 1/1 to: AV373185 from: 1 to: 585

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1  AATTCGCGCGCCGCTGCACGCGCTGCAGAACGACGACGAGCGCTTC 50
   ::::::::::: ||| ::::::::::: ||| ::::::::::: |||
25 AAlaGAlaIleuAsnAlaSerSerIySglUglUleuGlnIleuA 42
   ::::::::::: ||| ::::::::::: ||| ::::::::::: |||
51 CACGAGAGCGCTACACGCGCGCTGCTGCTGCACGCTGCTCTGAG 99
   ::::::::::: ||| ::::::::::: ||| ::::::::::: |||
42 IAlaIleAlIleProGluIyGlyTleuPheGlnPheIleAsnIleuSer 58
   ::::::::::: ||| ::::::::::: ||| ::::::::::: |||
100 .....ATCCCTGAAGATGTCACGATATTTCGAGTCACTCAACGC 141

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59 AsnIleuAsp 61
||||:||||
142 AACATCGAT 150

seq_name: gb_cst1:AV736552

seq_documentation_block: 596 bp mRNA EST 17-OCT-2000
LOCUS AV736552 CB Homo sapiens cDNA clone CBBNHE0 5', mRNA sequence.
DEFINITION AV736552
ACCESSION AV736552.1 GI:10854133
VERSION AV736552.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 596)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS Zhang, Q., Ye, M., Wu, X., Gu, J., Huang, Q., Zhou, J., Shen, Y., Han, Z.,
Chen, S., Mao, M. and Chen, Z.
Homo sapiens CB library cDNA clones
Unpublished (2000)
CONTACT: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital

197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: mshliems.stn.sh.cn
This clone is available at Shanghai Hematology Institute in Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.

FEATURES
source
1. 586
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CBMAC03"
/cell_line="CB"
/tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/note="Vector: pBluescript; Site 1: EcoRI; The insert is cloned randomly with the EcoRI digestion"

BASE COUNT 158 a 142 c 168 g 116 t
ORIGIN

alignment_scores:
Quality: 67.00 Length: 53
Ratio: 1.811 Gaps: 2
Percent Similarity: 69.811 Percent Identity: 32.075

alignment_block:
US-09-289-346a-4 x AV736552 ..

Align seg 1/1 to: AV736552 from: 1 to: 586

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10 AsdGlyArGerAlaArgIgyIcYsGin...ThrSerAsnAspAlaI 25
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1  AATTCGCGCGCCGCTGCACGCGCTGCAGAACGACGACGAGCGCTTC 50
   ::::::::::: ||| ::::::::::: ||| ::::::::::: |||
25 AAlaGAlaIleuAsnAlaSerSerIySglUglUleuGlnIleuA 42
   ::::::::::: ||| ::::::::::: ||| ::::::::::: |||
51 CACGAGAGCGCTACACGCGCGCTGCTGCTGCACGCTGCTCTGAG 99
   ::::::::::: ||| ::::::::::: ||| ::::::::::: |||
42 IAlaIleAlIleProGluIyGlyTleuPheGlnPheIleAsnIleuSer 58
   ::::::::::: ||| ::::::::::: ||| ::::::::::: |||
100 .....ATCCCTGAAGATGTCACGATATTTCGAGTCACTCAACGC 141

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59 AsnIleuAsp 61
||||:||||
142 AACATCGAT 150

seq_name: gb_cst1:AV741448
seq_documentation_block: 596 bp mRNA EST 17-OCT-2000
LOCUS AV741448 CB Homo sapiens cDNA clone CBBRC02 5', mRNA sequence.
DEFINITION AV741448
ACCESSION AV741448
VERSION AV741448.1 GI:10859029
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 596)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS Zhang, Q., Ye, M., Wu, X., Gu, J., Huang, Q., Zhou, J., Shen, Y., Han, Z.,
Chen, S., Mao, M. and Chen, Z.
Homo sapiens CB library cDNA clones
Unpublished (2000)
CONTACT: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: mshliems.stn.sh.cn
This clone is available at Shanghai Hematology Institute in

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Alignment_scores:

Quality: 222.00 Length: 69
 Ratio: 3.895 Gaps: 0
 Percent Similarity: 82.609 Percent Identity: 57.971

Alignment_block:

US-09-289-346a-4 x US-08-809-103b-1 ..

Align seq 1/1 to: US-08-809-103b-1 from: 1 to: 1148

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331 CTTGAATGGAGTACTTCCAGATCCAGCGAGATCTGCTAGGAGAGCA 380
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18 sGlnThSerAsnSPAlaAlaGlnAlaLeuAsnAlaSerSerLysG 35
|||||
381 ACAGACGCCACACGCGCTTCCAGCGAGATTAACCGAGAGTAAGT 430
|||||
35 LucAlaIleGlnGlnIleTlAlaAlaAlaIlePpGluGlySTyLeuPb 51
|||||
431 CGCAGCGCTTGATGATTAATTAAGATTAAGCGCCCTACGAGTTCCTCA 480
|||||
52 GlnPheHIsAsnLeuAsnSerAsnLeuAspArgTlIephAspLysThr 68
|||||
481 CATTTTCATATATTAATTAAGTATTAATTAAGTATTAAGTTCCTCCAGTCC 530
|||||
68 GclUpPro 70
531 GCGACCT 537

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seq_name: /cgnl_7/p2data/1/lna/6a_COMB.seq:US-08-809-103b-3

seq_documentation_block:

Sequence 3, Application US/08809103B

Patent No. 6335010

General Information:

Applicant: GROENBORN, Bruno

Title of Invention: PHYTOPATHOGENIC DNA VIRUS RESISTANT

Number of Sequences: 17

Correspondence Address:

Address: YOUNG & THOMPSON

City: 445 South 23rd Street

State: Virginia

Country: U.S.A.

ZIP: 22202

Computer Readable Form:

Medium Type: Floppy disk

Operating System: PC-DOS/MS-DOS

Software: PatentIn Release #1.0, Version #1.30

Current Application Data:

Filing Date: 17-MAR-1997

Application Number: US/08/809,103B

Classification: 800

Prior Application Data:

Prior Application Number: FR 94,11040

Prior Application Date: 15-SEP-1994

Filing Date: 15-SEP-1995

Application Number: NO PCT/FR95/01192

Attorney/Agent Information:

Name: PATCH, Andrew J.

Registration Number: 32,925

Reference/DocId Number: US94AL CNR TOM

Telephone: (703) 521-2297

Telefax: (703) 685-0573

Telex: 248425 EMBON

Information for SEQ ID NO: 3:

Sequence Characteristics:

Length: 1150 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE: CDS

LOCATION: 1..1077

US-08-809-103b-3

alignment_scores:

Quality: 222.00 Length: 69
 Ratio: 3.895 Gaps: 0
 Percent Similarity: 82.609 Percent Identity: 57.971

alignment_block:

US-09-289-346a-4 x US-08-809-103b-3 ..

Align seq 1/1 to: US-08-809-103b-3 from: 1 to: 1150

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|||||
18 sGlnThSerAsnSPAlaAlaGlnAlaLeuAsnAlaSerSerLysG 35
|||||
381 ACAGACGCCACACGCGCTTCCAGCGAGATTAACCGAGAGTAAGT 430
|||||
35 LucAlaIleGlnGlnIleTlAlaAlaAlaIlePpGluGlySTyLeuPb 51
|||||
431 CGCAGCGCTTGATGATTAATTAAGATTAAGCGCCCTACGAGTTCCTCA 480
|||||
52 GlnPheHIsAsnLeuAsnSerAsnLeuAspArgTlIephAspLysThr 68
|||||
481 CATTTTCATATATTAATTAAGTATTAATTAAGTATTAAGTTCCTCCAGTCC 530
|||||
68 GclUpPro 70
531 GCGACCT 537

```

seq_name: /cgnl_7/p2data/1/lna/6a_COMB.seq:US-08-809-103b-5

seq_documentation_block:

Sequence 5, Application US/08809103B

Patent No. 6335010

General Information:

Applicant: GROENBORN, Bruno

Title of Invention: PHYTOPATHOGENIC DNA VIRUS RESISTANT

Number of Sequences: 17

Correspondence Address:

Address: YOUNG & THOMPSON

City: 445 South 23rd Street

State: Virginia

Country: U.S.A.

ZIP: 22202

Computer Readable Form:

Medium Type: Floppy disk

Operating System: PC-DOS/MS-DOS

Software: PatentIn Release #1.0, Version #1.30

Current Application Data:

Filing Date: 17-MAR-1997

Application Number: US/08/809,103B

Classification: 800

Prior Application Data:

Prior Application Number: FR 94,11040

Filing Date: 15-SEP-1994

Application Number: NO PCT/FR95/01192

Filing Date: 15-SEP-1995

Attorney/Agent Information:

```

? NAME: PATCH, Andrew J.
? REGISTRATION NUMBER: 32, 925
? REFERENCE/DOCKET NUMBER: US954AL CNR TOM
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 685-0523
? TELEFAX: (703) 685-0573
? INFORMATION FOR SEQ ID NO: 5:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1150 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1077
? US-08-809-103B-5

alignment_scores:
? Quality: 222.00 Length: 69
? Ratio: 3.895 Gaps: 0
? Percent Similarity: 82.609 Percent Identity: 57.971

alignment_block:
US-09-289-346a-4 x US-08-809-103B-5
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2 LeuValITPGLIuphEdInValAspGLyTAspSerAlaArgIyGlyCY 18
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331 CTTGAATGGGGTACTCTTCACATCGACGACGACATCTCCTACGCGAGACACA 380
18 SGLINThSerAsnSPAlaAlaGluAlaLeuAsnAlaSerIleuSG 35
381 ACAGACCCACACGCGCTTACGCAAGCAATTTAACCGAGACTNAGT 430
35 LuGluAlaLeuGlnIleIleAlaAlaAlaIleProGluIuSTyLeuPhe 51
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTGATGTAATTAAGATTACGCGCTTACGATTACGTTCTA 480
52 GTPhehIAsnLeuAsnSerAlaLeuAsnAlaIleProGluIuSTyLeu 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTCATTAATAATAATTAATTGATTAAGGTTTCCAGGCGCTCC 530
68 GGLuPro 70
531 GCGACCT 537

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? Patent No. 6291743
? GENERAL INFORMATION:
? APPLICANT: Stout, John T
? APPLICANT: Stout, Douglas
? APPLICANT: Maxwell, Paul
? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
? NUMBER OF SEQUENCES: 63
? CORRESPONDING ADDRESS: Rocky, Milwaukee & Katz
? STREET: Two Prudential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk

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? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? REGISTRATION NUMBER: US/08/838,151A
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: 38, 978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (312) 616-4600
? TELEFAX: 312-616-4646
? INFORMATION FOR SEQ ID NO: 48:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1062 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Bean Golden Mosaic GeminiVirus
? STRAIN: Type II
? INDIVIDUAL ISOLATE: Guatemala
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1059
? US-08-838-151A-48

alignment_scores:
? Quality: 219.00 Length: 70
? Ratio: 3.778 Gaps: 0
? Percent Similarity: 82.857 Percent Identity: 60.000

alignment_block:
US-09-289-346a-4 x US-08-838-151A-48
Align seq 1/1 to: US-08-838-151A-48 from: 1 to: 1062

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328 ACATCGAAGGCGACATTCGATCGACGCGCATTCGATCGACAGAGG 377
17 YCYGlnThSerAsnSPAlaAlaGluAlaLeuAsnAlaSerIleu 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
378 TCACAGCTCGCCACGATCATATCGCAAGGCGCTTAACGCGACATTCNA 427
34 YSGluGluAlaLeuGlnIleIleAlaAlaAlaIleProGluIuSTyLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
428 TTGATCTCGGCTTCACATTTAAGAGAGAACACCGAATTAATTACGTC 477
51 PhEdInPhehIAsnLeuAsnSerAlaLeuAsnAlaIleProGluIuSTyLeu 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
478 GTTCACATCGACACATTCGTTATCTCGACGAGATCTTGCTCAAGT 527
67 PROGLuPro 70
528 GCGCGACCA 537

seq_name: /cgnl_7/ptcdatc1/1na/6b_COMB.seq:us-08-838-151A-51
seq_documentation_block:
? Sequence 51, Application US/08838151A
? Patent No. 6291743
? GENERAL INFORMATION:
? APPLICANT: Stout, John T
? APPLICANT: Stout, Douglas
? APPLICANT: Maxwell, Paul
? APPLICANT: Hanson, Steve

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1 APPLICANT: Hanson, Steve
2 TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
3 NUMBER OF INVENTION: Genes
4 NUMBER OF SEQUENCES: 63
5 CORRESPONDENCE ADDRESS:
6 ADDRESS: Dressler, Rocky, Milnow & Katz
7 CITY: Chicago
8 STATE: Illinois
9 COUNTRY: U.S.A.
10 ZIP: 60601
11
12 COMPUTER READABLE FORM:
13 COMPUTER: IBM PC compatible
14 OPERATING SYSTEM: PC-DOS/MS-DOS
15 SOFTWARE: Patentin Release #1.0, Version #1.30
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/08/838-151A
18 FILING DATE: 800
19 CLASSIFICATION: 800
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Mueller, Lisa V
22 REGISTRATION NUMBER: 38,978
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: 312-616-5400
25 TELEFAX: 312-616-5460
26 INFORMATION FOR SEQ ID NO: 51:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 1062 base pairs
29 TYPE: nucleic acid
30 STRANDEDNESS: single
31 TOPOLOGY: circular
32 MOLECULE TYPE: DNA (genomic)
33 BIOPHETICAL: NO
34 ORIGINAL SOURCE:
35 ORGANISM: Bean Golden Mosaic GeminiVirus
36 STRAIN: Type II
37 INDIVIDUAL ISOLATE: Guatemala
38 FEATURE:
39 NAME/KEY: CDS
40 LOCATION: 1..1059
41 US-08-838-151A-51
42
43 alignment_scores:
44 Quality: 219.00 Length: 70
45 Ratio: 3.776 Gaps: 0
46 Percent Similarity: 82.857 Percent Identity: 60.000
47
48 alignment_block:
49 US-09-289-346a-4 x US-08-838-151A-51 ..
50
51 Align seg 1/1 to: US-08-838-151A-51 from: 1 to: 1062
52
53 1 Thleuvaltrpgcygyluphegnvalaspqlyatgserrlatargqlygl 17
54 |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
55 328 ACATGCAATGGGAGCAATTCACATCGACGCGACGACATTCACAGAGG 377
56 |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
57 17 ycygclntrhserrasapnalalalagialalulenasalaserse 34
58 |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
59 378 TCAGCGAGTCGCCACACATTCATCCACAAAGCATTAAAGCGAATTCA 427
60 |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
61 34 ysglualalaleuclnllleialalalalleptroglytyrtleu 50
62 |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
63 428 TTGATATCCTCCATCAATATTAAGAGAACACACCGAAGATTACGTC 477
64 |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
65 51 phgclnpheliasenleuaserrnleuasrlylllephaslyyeth 67
66 |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
67 478 CTTCAACATCACACATCCGCTTCATATCTCGACAGGATCTTGTCAAAGT 537
68 |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
69 67 pTroglyupro 70

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1 seq_name: /cgnl_7/plcdela/1/lna/6E_COMB.seq:US-08-838-151A-54
2 528 GCGCGAACCA 537
3 ::::::::::
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5 seq_documentation_block:
6 : Sequence 54: Application US/08838151A
7 : Patent No. 6291743
8
9 GENERAL INFORMATION:
10 : APPLICANT: Stout, John T
11 : APPLICANT: Luu, Hang T
12 : APPLICANT: Maxwell, Douglas
13 : APPLICANT: Ahlquist, Paul
14 : APPLICANT: Sall
15 : TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
16 : NUMBER OF SEQUENCES: 63
17 : CORRESPONDENCE ADDRESS:
18 : ADDRESS: Dressler, Rocky, Milnow & Katz
19 : CITY: Chicago
20 : STATE: Illinois
21 : COUNTRY: U.S.A.
22 : ZIP: 60601
23
24 COMPUTER READABLE FORM:
25 : MEDIUM TYPE: Floppy disk
26 : COMPUTER: IBM PC compatible
27 : OPERATING SYSTEM: PC-DOS/MS-DOS
28 : SOFTWARE: Patentin Release #1.0, Version #1.30
29 : CURRENT APPLICATION DATA:
30 : APPLICATION NUMBER: US/08/838-151A
31 : FILING DATE:
32 : CLASSIFICATION: 800
33 : ATTORNEY/AGENT INFORMATION:
34 : NAME: Mueller, Lisa V
35 : REGISTRATION NUMBER: 38,978
36 : TELECOMMUNICATION INFORMATION:
37 : TELEPHONE: 312-616-5400
38 : TELEFAX: 312-616-5460
39 : INFORMATION FOR SEQ ID NO: 54:
40 : SEQUENCE CHARACTERISTICS:
41 : LENGTH: 1062 base pairs
42 : TYPE: nucleic acid
43 : STRANDEDNESS: single
44 : TOPOLOGY: circular
45 : MOLECULE TYPE: DNA (genomic)
46 : BIOPHETICAL: NO
47 : ANTI-SENSE: NO
48 : ORIGINAL SOURCE:
49 : ORGANISM: Bean Golden Mosaic GeminiVirus
50 : STRAIN: Type II
51 : INDIVIDUAL ISOLATE: Guatemala
52 : FEATURE:
53 : NAME/KEY: CDS
54 : LOCATION: 1..1059
55 : US-08-838-151A-54
56
57 alignment_scores:
58 Quality: 219.00 Length: 70
59 Ratio: 3.776 Gaps: 0
60 Percent Similarity: 82.857 Percent Identity: 60.000
61
62 alignment_block:
63 US-09-289-346a-4 x US-08-838-151A-54 ..
64
65 Align seg 1/1 to: US-08-838-151A-54 from: 1 to: 1062
66
67 1 Thleuvaltrpgcygyluphegnvalaspqlyatgserrlatargqlygl 17
68 |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
69 328 ACATGCAATGGGAGCAATTCACATCGACGCGACGATTCACAGAGG 377

```

[illegible]

APPLICATION NUMBER: US/08/838,151A
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY INFORMATION:
 NAME: Mueller, Lisa Y
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 45:
 STRANDEDNESS: single
 LENGTH: 1183 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOHETICAL TYPE: NO
 ANTI-SENSE: NO
 ORIGIN: GenBank
 ORGANISM: BORN Golden Mosaic Geminivirus
 STRAIN: Type II
 INDIVIDUAL ISOLATE: Guatemala
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1059
 US-08-838-151A-45

alignment_scores:
 Quality: 219.00 Length: 70
 Ratio: 3.776 Gaps: 0
 Percent Similarity: 82.857 Percent Identity: 60.000

alignment_block:
 US-09-289-346a-4 x US-08-838-151A-45

Align seg 1/1 to: US-08-838-151A-45 from: 1 to: 1183

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1 1ThrluValtFrgLygluphEgInvalAspGlyVrgserAlaTgCyl 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
328 ACATCGAATGGAGACAAATTCACAGTCACGACGACGACGACGACG 377
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
17 1CysglFmhsrserAspAlaAlaAlaAlaAlaAlaAlaAlaAla 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
378 TCAGCAGTCCTCCCAAGACCTCATATGCAAGGCAATTAAACGCAAT 427
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
34 1YsglGluAlaLeuGlnIleIleAlaAlaAlaAlaAlaAlaAla 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
428 TTGACATCTGCTTCACAAATATTAAGAGAACACGACGACGACG 477
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
51 1PhcIlnPheIleAsnLeuAsnSerAsnLeuAspArgIlePheAsp 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
478 CTTCAACATCAACACATCCGTTTATCTTCACAGGATCTTCGTAAG 527
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
67 1FProGluPro 70
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
528 GCGCGACCA 537

```

seq_name: /cgnl_7/plodata/1/lna/6a_COMB.seq:US-09-065-999-5

seq_documentation_block:
 : Sequence 5, Application US/09065999
 : Patent No. 6118048
 : GENERAL INFORMATION:
 : APPLICANT: Hanson, Stephen P.
 : TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
 : NUMBER OF SEQUENCES: 8
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Quarles & Brady
 : STREET: One South Pluckney Street

CITY: Madison
 STATE: WI
 COUNTRY: US
 LENGTH: 5760/2113
 COMPUTER REPEATABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: Iw PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/065,999
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27,186
 REFERENCE/DOCKET NUMBER: 960296, 94754
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-251-5000
 TELEFAX: 608-251-9186
 INFORMATION FOR SEQ ID NO: 5:
 LENGTH: 1651 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-065-999-5

alignment_scores:
 Quality: 219.00 Length: 70
 Ratio: 3.776 Gaps: 0
 Percent Similarity: 82.857 Percent Identity: 60.000

alignment_block:
 US-09-289-346a-4 x US-09-065-999-5

Align seg 1/1 to: US-09-065-999-5 from: 1 to: 1651

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1 1ThrluValtFrgLygluphEgInvalAspGlyVrgserAlaTgCyl 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
796 ACATCGAATGGAGACAAATTCACAGTCACGACGACGACGACG 845
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
17 1CysglFmhsrserAspAlaAlaAlaAlaAlaAlaAlaAlaAla 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
846 TCAGCAGTCCTCCCAAGACCTCATATGCAAGGCAATTAAACGCAAT 895
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
34 1YsglGluAlaLeuGlnIleIleAlaAlaAlaAlaAlaAlaAla 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
896 TTGACATCTGCTTCACAAATATTAAGAGAACACGACGACGACG 945
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
51 1PhcIlnPheIleAsnLeuAsnSerAsnLeuAspArgIlePheAsp 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
946 CTTCAACATCAACACATCCGTTTATCTTCACAGGATCTTCGTAAG 995
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
67 1FProGluPro 70
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
996 GCGCGACCA 1005

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seq_name: /cgnl_7/plodata/1/lna/6a_COMB.seq:US-09-065-999-6

seq_documentation_block:
 : Sequence 6, Application US/09065999
 : Patent No. 6118048
 : GENERAL INFORMATION:
 : APPLICANT: Hanson, Stephen P.
 : TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
 : NUMBER OF SEQUENCES: 8
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Quarles & Brady

STREET: One South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA
 APPLICATION NUMBER: US/09/065,999
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27,386
 REFERENCE/DOCKET NUMBER: 960296,94754
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-251-9160
 TELEFAX: 608-251-9166
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1651 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: linear
 MOLFEEL TYPE: DNA (genomic)
 US-09-065-999-6

alignment_scores:
 Quality: 219.00 Length: 70
 Ratio: 3.776 Gaps: 0
 Percent Similarity: 82.857 Percent Identity: 60.000

alignment_block:
 US-09-289-346a-4 x US-09-065-999-6 ..

Align seq 1/1 to: US-09-065-999-6 from: 1 to: 1651

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1  ThrlenvaITrGlyGlpbheGlnValapGlyAgsrAlaAtgGlyG 17
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796 ACATGCAATGGGCAACATTCGAATGACGACGCAATTCGACAAAGC 845
17  YCYGlnThSerAsnspAlaAlaIaGlnValaLeuAsnAlaSeSerL 34
   | ||||| ||||| ||||| ||||| ||||| ||||| |||||
846 TCACGACGTCCCAACGACTCATATGCAACGCAATTAACCGCAATTCA 895
34  YGAGlGlnAlaGlnGlnIleIleAlaAlaAlaIleProGluuTyTleu 50
896 TTGAATCTGCTTCACATATTCAGAGAAACACCAAGATTCAGTC 945
51  PhedIlnPhelAsnLeuAsnSerAsnLeuAspArgIlePhaAspLysTh 67
   ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
946 CTTCAACATCAACACATTCGCTTAATCTGACGACGATCTTCGAAGT 995
67  FPRGluPro 70
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996 GCGCAACCA 1005
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seq_name: /cgnl_7/plodeta/1/lna/fa_COMB.seq:us-09-065-999-8

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seq_documentation_block:
? Sequence 8, Application US/09065999
? GENERAL INFORMATION:
? APPLICANT: Hanson, Stephen F.
? APPLICANT: Maxwell, Douglas P.
? TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
? TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Quarles & Brady
 STREET: One South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA
 APPLICATION NUMBER: US/09/065,999
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27,386
 REFERENCE/DOCKET NUMBER: 960296,94754
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-251-9160
 TELEFAX: 608-251-9166
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1894 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: linear
 MOLFEEL TYPE: DNA (genomic)
 US-09-065-999-8

alignment_scores:
 Quality: 219.00 Length: 70
 Ratio: 3.776 Gaps: 0
 Percent Similarity: 82.857 Percent Identity: 60.000

alignment_block:
 US-09-289-346a-4 x US-09-065-999-8 ..

Align seq 1/1 to: US-09-065-999-8 from: 1 to: 1894

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1  ThrlenvaITrGlyGlpbheGlnValapGlyAgsrAlaAtgGlyG 17
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796 ACATGCAATGGGCAACATTCGAATGACGACGCAATTCGACAAAGC 845
17  YCYGlnThSerAsnspAlaAlaIaGlnValaLeuAsnAlaSeSerL 34
   | ||||| ||||| ||||| ||||| ||||| ||||| |||||
846 TCACGACGTCCCAACGACTCATATGCAACGCAATTAACCGCAATTCA 895
34  YGAGlGlnAlaGlnGlnIleIleAlaAlaAlaIleProGluuTyTleu 50
896 TTGAATCTGCTTCACATATTCAGAGAAACACCAAGATTCAGTC 945
51  PhedIlnPhelAsnLeuAsnSerAsnLeuAspArgIlePhaAspLysTh 67
   ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
946 CTTCAACATCAACACATTCGCTTAATCTGACGACGATCTTCGAAGT 995
67  FPRGluPro 70
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996 GCGCAACCA 1005
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seq_name: /cgnl_7/plodeta/1/lna/fa_COMB.seq:us-09-065-999-7

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seq_documentation_block:
? Sequence 7, Application US/09065999
? GENERAL INFORMATION:
? APPLICANT: Hanson, Stephen F.
? APPLICANT: Maxwell, Douglas P.
? TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
? TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
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seq_id documentation block:
LOCUS AF291705 2622 bp DNA circular VRL
DEFINITION Tomato rugose mosaic virus DNA-A, complete sequence.
ACCESSION AF291705
VERSION AF291705.1 GI:10281644

seq_name: qb_v1:AF291705

seq documentation block:
LOCUS AF291705 2622 bp DNA circular VRL
DEFINITION Tomato rugose mosaic virus DNA-A, complete sequence.
ACCESSION AF291705
VERSION AF291705.1 GI:10281644
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[illegible]

alignment_scores:
 Quality: 271.00 Length: 70
 Ratio: 4.517 Gaps: 0
 Percent Similarity: 88.235 Percent Identity: 79.412

alignment_block:
 US-09-289-346a-5 x SCU67926/rev

Align seg 1/1 to reverse of: SCU67926 from: 1 to: 554

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1 1ThleuValITrGlyLuphGlnValaJpGlyAgsSrAlaAglyGyl 17
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290 ACATGCAATGAGGGGGTCTTCCATGCGAGAAAGATCTCTCTGAGG 241
  17 YCysGlnThrSerAspAlaIalAglAlaLeuAsnAlaSerL 34
  |||
240 TCAGCAAAACGCTAGACGCGACCGCGATTTGATGAGCA 191
  34 YSGlUGlAlaLeuGlnIleIleIleAGlyLysIleProAlaIleu 50
  190 ACAGGATCGACTGAATCATCTGACAGAAATTCACGAAAGATTC 141
  51 PhcIInPhleIaSnLeuAsnSerIleuAspArgIlePhaAspLysTh 67
  |||
140 TTTCAGTACACAACTGATCCACTAATTCAGATGATTTTCTACTACCC 91
  67 pProGluPro 70
  90 TCCAGAACCC 81
  seq_name: gb_v1:AF288227

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seq_documentation_block: 1383 bp DNA VRL 20-AUG-2000
 LOCUS AF288227 Sweet potato leaf curl virus replication association protein (AC1)
 DEFINITION Sweet potato leaf curl virus replication association protein (AC1)
 ACCESSION AF288227
 VERSION AF288227.1 GI:9858125

KEYWORDS
 SWEET POTATO LEAF CURL VIRUS.
 ORGANISM
 VIRUSES; ssDNA viruses; Geminiviridae; Begomovirus.
 REFERENCE
 1 (bases 1 to 1383)
 Lotrakul, P., Valverde, R.A., Clark, C.A., Sim, J. and De la Torre, R.
 Detection of a geminivirus infecting sweet potato in the United States.
 TITLE
 Plant Dis. 82, 1253-1257 (1998)
 2 (bases 1 to 1383)
 Lotrakul, P. and Valverde, R.A.
 Direct Submission
 Submitted (18-JUL-2000) Plant Pathology and Crop Physiology,
 Louisiana State University, 302 Life Sciences Bldg., Baton Rouge,
 LA 70803, USA

FEATURES
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 1..1383
 /organism="sweet potato leaf curl virus"
 /db_xref="taxon:100755"
 /note="subgenomic DNA"
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 /note="AC1"
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 /protein_id="AF288227.1"
 /translation="MAPPKREIOAKNYETTPKCSISKEDCIQAOLITQPSKKRYT
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 YVNDKGGITTEGFOVGSARAGQOINTAAALANSGEALQITREKLPEKYS
 OFHNLVSNIDRISPPSYSSPSSSSFNAPDILISMAAEVWDSARDDPSIV
 ICSPRIRGIVTWARSLGPHNVLCOHLDLSPKYSNSAWNYIDVNPVYLKRFEPKNG

gene
 complement(815..1072)
 /gene="AC4"
 complement(815..1072)
 /note="AC4"
 /codon_start=1
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 /protein_id="AF288227.1"
 /db_xref="GI:9858127"
 /translation="MSGMNSKCSKANSNAQADSSINSHRTDITFTPSRELP
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BASE COUNT 359 a 296 c 327 g 401 t
 ORIGIN

alignment_scores:
 Quality: 271.00 Length: 68
 Ratio: 4.517 Gaps: 0
 Percent Similarity: 88.235 Percent Identity: 79.412

alignment_block:
 US-09-289-346a-5 x AF288227/rev

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902 KCOTACCTGCGGTGATGATCTCAGGTGCGACGACATCTCTCTAGAGG 853
  17 YCysGlnThrSerAspAlaIalAglAlaLeuAsnAlaSerL 34
  |||
852 CCACGACGCTGCTAGACGCGACCGCGATTTGATGAGCA 803
  34 YSGlUGlAlaLeuGlnIleIleIleAGlyLysIleProAlaIleu 50
  |||
802 AAGGACGCTGCTGATGATCTCAGGTGCGACGACATCTCTAGAGG 753
  51 PhcIInPhleIaSnLeuAsnSerIleuAspArgIlePhaAspLysTh 67
  |||
752 TTTCAGTACACAACTGATCCACTAATTCAGATGATTTTCTACTACCC 703
  67 pPro 68
  111
  702 KCOT 699
  seq_name: gb_v1:AF104036

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seq_documentation_block:
 LOCUS AF104036 2828 bp DNA circular VRL 05-AUG-1999
 DEFINITION Sweet potato leaf curl virus DNA A, complete sequence.
 ACCESSION AF104036
 VERSION AF104036.1 GI:5702158

KEYWORDS
 SWEET POTATO LEAF CURL VIRUS.
 ORGANISM
 VIRUSES; ssDNA viruses; Geminiviridae; Begomovirus.
 REFERENCE
 1 (bases 1 to 2828)
 Lotrakul, P., Valverde, R.A., Clark, C.A., Sim, J. and De la Torre, R.
 Detection of a geminivirus infecting sweet potato in the United States.
 TITLE
 Plant Dis. 82, 1253-1257 (1998)
 2 (bases 1 to 2828)
 Lotrakul, P. and Valverde, R.A.
 Cloning of a DNA-A-like genomic component of sweet potato leaf curl virus: nucleotide sequence and phylogenetic relationships
 Molecular Plant Pathology On-line (1999)
 http://www.bispp.org.uk/mpdol/1999/0422lotrakul/
 REFERENCE
 Lotrakul, P. and Valverde, R.A.
 Direct Submission
 Submitted (02-NOV-1998) Plant Pathology and Crop Physiology,
 Louisiana State University, 302 Life Sciences Bldg., 150, Baton

[illegible][illegible]

```

34 yscglunghabndnldlletleekrgtuglysierrcalalatalaleu 50
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194 AGGAGGGCCATCGAAGAATTGCACGAAGAAATTCGCCGAATAATTTCTC 145
   ||||| |-----|-----|-----|-----|-----|
51 plichiPhenilSensitizansSermentumPurplilheaselysyn 67
   ||||| |-----|-----|-----|-----|-----|
144 TTTTCAATTCACACTATTCCTGTAACCTGATGGATTTTCGAAAGA 95
   ||||| |-----|-----|-----|-----|-----|
67 PProclupro 70
   ||||| |-----|-----|-----|-----|-----|
94 TCAGCAACA 85
seq_name: gb_vl:AB001315

seq document location, block:
LOCUS       AB001315             570 bp     DNA                VRL           13-FEB-1999
DEFINITION  Tobacco leaf curl virus CI and C4 genes, clone YOKOHAMA3-1, partial
            and complete cds.
ACCESSION   AB001315
VERSION     AB001315.1 GI:3798714
KEYWORDS    SOURCE
SOURCE      ORGANISM
            Nicotiana glauca virus [Isolate:YOKOHAMA3,
            specific host plant: tobacco makino] DNA, clone: YOKOHAMA3-1,
            tobacco leaf curl viruses
            Viruses; ssRNA viruses; Geminiviridae; Begomovirus.
REFERENCE   1 (bases 1 to 570)
AUTHORS     Ooi,K.
JOURNAL     Direct Submission
            Submitted (19-Feb-1997) to the DDBJ/EMBL/Genbank databases.
            Kazuyuki Ooi, Kyushu University, Department of Biology: 6-10-1
            Kasuga-koji, Kasuga University, Fukuoka 812, Japan
            (E-mail:koois@post.kyushu-u.ac.jp, Tel:+81-92-642-2624,
            Fax:-81-92-642-2645)
REFERENCE   2 (bases 1 to 570)
AUTHORS     Ooi,K., Ohshita,S., Ishii,T. and Yahara,T.
JOURNAL     Molecular phylogeny of geminiviruses infecting wild plants in Japan
            J. Plant Res. 110, 247-257 (1997)
FEATURES
     source          1..570
                     /organism="Nicotiana glauca"
                     /isolate="YOKOHAMA3"
                     /specific_host="Empetrium makinoi"
                     /db_xref=taxon:67762
                     /clone="YOKOHAMA3-1"
                     complement(1..570)
                     /gene=C1
                     complement(<1..>570)
                     /codon_start=1
                     /protein_id="BA3403.1"
                     /db_xref=gi:4426541
                     /translation="EPKLSQQLNTPFNKIYIKTKTEILHIGDSPHLAVIQLQPKRYKA
                     CONNFEDLVSTRTSGSHRNITOGAKSSSDVSYDDTDLTSMQTQIDGSAROCGQ
                     ONMNDGADLMASNSAKALATIREKIPDPTFOYNISMDIRFAPLEVPFCPTFF
                     ASSFDQPEELDEMASNAWMSAAHWRRKM"
                     complement(231..486)
                     /gene=C4
                     /codon_start=1
                     /protein_id="BA3403.1"
                     /db_xref=gi:3798715"
                     /translation="MTAILSKOTCSKANNTKIDTSSTTVYPOPDIIISTRELFANL
                     APSPSSPTSTETLSENGSRHSRFTSEVAENRAHLRHIVOR"
                     I21 c 126 g 182 t

Alignment_scores:
Quality: 264.00      Length: 85
Ratio: 4.258        Gaps: 1
Percent Similarity: 72.941 Percent Identity: 62.353

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Alignment_block:
US-09-2893-346A-5 x AB001315/rev ..
Align seg 1/1 to reverse of: AB001315 from: 1 to: 570

    1 TTTTAAATATTGTCCTGTCAGGCCTCCTACAGCCCTCATCTTAAGAATGGC 17
      ||||| .....|||||.....|||||.....
   318 ACCTCGCAATGGCAACAATTCGCAATCATGCCGAACAAGACTGTACGAGG 269

    17 ycyaslnThrSerAsnaspAlaIalaIagUlaLleaaSalalaseSerL 34
      |.....|.....|.....|.....|.....|.....|.....|.....|
   268 CTGGCACAAATCAACCAACGCTGCAGAGGCCCTTAATCAACAGTTTCA 219

    34 yscUGUAUUldeagUlIllellAggUcUggUgcGUgCUttaaUlaIaleu 50
      |||||.....|.....|.....|.....|.....|.....|.....|.....|
   218 AGCGAACCACTTAGCAAATAATTAGGGAACAACTCCCTTAAGATTNTNA 169

    51 PhaeInPhenIsarIsaIsanSerAsnLeuaaprrJlle..... 63
      |||||.....|.....|.....|.....|.....|.....|.....|.....|
   168 TTTCATATCATCAATTAATTAATGTAATTAGTATGATTTTGTCCTCTCC 119

     64 .....|.....|.....|.....|.....|.....|.....|.....|
   118 GTTGSAGCTTTTGTGTTGTCCTTCACAGCCCTCATCTTAAGAATGGC 69

     68 tccglu 69
        ||||
     68 CAGA 64

seg_name: qb.v1:AB001318
seq_documentation_block:
LOCUS       AB001318                    570 bp            DNA                   VRL               13-FEB-1999
DEFINITION  Tobacco leaf curl virus CJ and CA genes, clone YOKOHAMA5-2, partial
ACCESSION   AB001318
VERSION     AB001318.1 GI:3738720
KEYWORDS
SOURCE      tobacco leaf curl virus (isolate,YOKOHAMA5, specific clones:Riputorium makinoi) DNA, clone:YOKOHAMA5-2, tobacco leaf curl virus; genome viruses; geminiviridae; Begomovirus.
ORGANISM    1 (bases 1 to 570)
REFERENCE   1 (bases 1 to 570)
AUTHORS     Ooi,K.R.
TITLE       Direct Submission
JOURNAL     Submitted (19-FEB-1997) to the DDBJ/EMBL/Genbank databases.
           Kazuyuki Ooi, Kyushu University, Department of Biology; 6-10-1 Hakozaki, Higashi-Ku, Fukuoka, Fukuoka 812, Japan
           Nakazaki,Hidashi-Ku, Fukuoka, Fukuoka 812, Japan
           Fax:+81-92-642-2645 ; Kyushu-u.ac.jp, Tel:+81-92-642-2624,
           2 (bases 1 to 570)
           Ooi,K., Onshita,S., Ishii,I. and Yahara,T.
           Molecular phylogeny of geminivirus infecting wild plants in Japan
           J. Plant Res. 110, 247-257 (1997)
FEATURES
             Location/Qualifiers
               1..570      "tobacco leaf curl virus"
                 /isolate="YOKOHAMA5"
                 /specific_host="Riputorium makinoi"
                 /db_xref="taxon:67762"
                 /clone="YOKOHAMA5-2"
                 complement(1..570)
                 /gene=C1"
                 complement<1..>570)
                 /gene=C1"
                 /name=C1"
                 /comment="start=1"
                 /contig="qb.v1:BA33039.1"
                 /date="Feb-14-2000"
                 /db_xref="GI:342644"
                 /translation="EPKASLSQNLNTPINKLYIKICRELDHDSPEHYAVLLDPECKRYWV
CONNFDFLVSTRHSFHNHTNGAKSSIVSYIDKGDDLEMTGDIDRSARSGC
OANNPQACVAEKAASKAEALAIIEKLKDKEIFDYHNLSNDLRITFAPIPLVEVCPT
ASSFPQVPEELBESMAENVSPARKRMPM"
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gene complement(231..488)
/gene="C4"
CDS complement(231..488)
/gene="C4"
/protein_start=1
/protein_end=4336584.1*
/protein_id="A001318.1"
/translation="MGLISNCRSSSKANAKITTSSTWYPPQPHISIRFRELAN
APTSSPFRIRSENEFSRSTEEYLEAAMLTTHVQR"

BASE COUNT 140 a 121 c 129 g 180 t

ORIGIN

alignment_scores:
Quality: 264.00 Length: 85
Ratio: 4.258 Gaps: 1
Percent similarity: 72.941 Percent identity: 62.353

alignment_block:
US-09-289-346a-5 x AB001318/rev ..

Align seg 1/1 to reverse of: AB001318 from: 1 to: 570

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1 1ThrluValtRfPolYgluphGlnValaSpGlyVnYgSerLAtaGtG1 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
318 ACCTCGAATGGGAGCATTCACATCGACGACGAGAGATCTCAGACGAG 269
17 YCYGlnThrSerAspAlaIaG1aLaLeuAsnAlaSerSeT 34
||||| ||||||| ||||||| ||||||| ||||||| |||||||
268 CTCCAGAACTGTCAGACAGCGATGTCAGACGAGATTCAGACGAG 219
34 YGlnuLaIaLeuGlnIleIleArgLyuLyIleProAlaIaLaLeu 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
218 AGGCAAGACATTAGCATTAATAGCGAAAGCTCCCAAGAGATTMTA 169
51 PhcInPhelIaSnLeuAsnSerLauAspYgIle..... 63
168 TTTCATATCATANTTAATTAAGTATTTAAAGCATTTTGGTCTCC 119
64 ..... PhasApLyS7thp 68
118 GTTCAGAGTTTTTTGTTGCTTCCTTCACGCCCTCATCTTCAGATTC 69
68 TCGLu 69
|||||
68 CAGA 64

```

seq_name: gb-v1:AF098940

seq_documentation_block: 1405 bp DNA 04-MAR-1999

LOCUS AF098940 Macropitillium golden mosaic geminivirus strain Jamaica

DEFINITION Macropitillium golden mosaic geminivirus strain Jamaica

partial cds.

ACCESSION AF098940.1 GI:4336584

VERSION AF098940

KEYWORDS Macropitillium golden mosaic geminivirus.

SOURCE Macropitillium golden mosaic geminivirus.

ORGANISM Macropitillium golden mosaic geminivirus.

REFERENCE 1 (bases 1 to 1405)

AUTHORS Roye, M.E.

TITLE Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica

JOURNAL Unpublished

ATTNIONS Roye, M.E., McLaughlin, M.A. and Maxwell, D.P.

TITLE M. latyrolides from Jamaica

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1405)

AUTHORS Roye, M.E., McLaughlin, M.A. and Maxwell, D.P.

TITLE Direct Submission

JOURNAL Submitted (14-OCT-1998) Biotechnology Centre, University of the West Indies, Mona, Kingston 7, Jamaica

FEATURES

source

1. 1405

/organism="Macropitillium golden mosaic geminivirus"

/strain="Jamaica strain 1"

/db_xref="genbank:AF098940.1"

/country="Jamaica"

/clone="pMCJaz2; pMCJaz3"

gene complement(<1..701)

/gene="rep"

/gene="rep"

/product="replication associated protein"

/protein_id="A001318.1"

/db_xref="GI:4336586"

/translation="MPKSGFSIKRANFLYTPQCSLYIKREBALSLTNLNPVKKFT
KCEHPRBDGHLHVLIOFGKPNCTNNKLFDLVSPRSKSHENIDGASSDVKS
YVKGDTLENGYFDIGSAGSGQTSNMAAASLSTFEAKARIVKELKPEFL
DHNKSLTMDLMDWAPPLSTFNPVDKMDKADITFQKSNAPRPMAS1
119859757KMAC

misc_feature

/note="Intergenic region"

1031..>1405

gene

/gene="cp"

1031..>1405

/gene="cp"

/protein_id="A001318.1"

/protein_start=1

/protein_end="coat protein"

/db_xref="GI:4336585"

/translation="MPKRCQSMRTPTGVANRLVYSPRGYGFPSNKAQENVNPP
YRRPVRITLSPDVGCEGSPCKVQSYEQRHDSHVKGWICISDTRGVYTHRVK
RCYKRVYILKRIWDSNINSC

BASE COUNT 328 a 333 c 357 g 386 t 1 others

ORIGIN

alignment_scores:
Quality: 264.00 Length: 70
Ratio: 4.328 Gaps: 0
Percent similarity: 87.143 Percent identity: 70.000

alignment_block:
US-09-289-346a-5 x AF098940/rev ..

Align seg 1/1 to reverse of: AF098940 from: 1 to: 1405

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1 1ThrluValtRfPolYgluphGlnValaSpGlyVnYgSerLAtaGtG1 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
374 ACATCGATGAGGAGGTGTCACATCGACGACGAGATTCGAGGACG 325
17 YCYGlnThrSerAspAlaIaG1aLaLeuAsnAlaSerSeT 34
||||| ||||||| ||||||| ||||||| ||||||| |||||||
324 TCACCAACATCTAAGATGACGCCGACGAGCTTAATTTTGTGACCA 275
34 YGlnuLaIaLeuGlnIleIleArgLyuLyIleProAlaIaLaLeu 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
274 AGGACGCGCGCATGAKMTAGTCAGACGAGATTCGAGGAGGATTC 225
51 PhcInPhelIaSnLeuAsnSerLauAspYgIlePhasApLyS7th 67
||||| ||||||| ||||||| ||||||| ||||||| |||||||
224 TTTCATATCATACATTCAGTACCTGATGAGATTTTCATGAGGA 175
67 TCGLu 70
|||||
174 TCGAGACA 165

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[illegible]

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FT misc_feature 429..459
FT /tag= e
FT /note= "Ribozyme R3 target sequence"
FT /size= 444
FT /type= 4
FT /note= "ribozyme R3 cleavage site"
XX
XX WO503404-A.
XX
XX 02-FEB-1995.
XX
XX 22-JUL-1993. 93MO-EP01946.
XX
XX 22-JUL-1993. 93AU-0047014.
XX
XX 22-JUL-1993. 93MO-EP01946.
XX
XX (BIOC-) BIOCEM SA.
XX (CSTR-) COMMONWEALTH SCI & IND RES ORG.
XX
XX Baudino S., Comeau D., Dry IB., Gruber V., Lemes P.,
XX Mason J., Rezalan MA., Riggden JE., Rezalan MA.
XX WPI: 1995-075232/10.
XX
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX and/or assembly of viruses by cleaving target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX
XX Example 10: Fig 11c: 90pp: English.
XX
XX The sequence is a tomato leaf curl virus target sequence for
XX poly-ribozyme-F, which hybridizes to and cleaves the sequence and
XX thereby reduces replication, infection and/or assembly of the virus
XX substantially. The ribozyme may be expressed in a transgenic plant,
XX e.g. tomato, to confer virus disease-resistance.
XX
XX Sequence 479 BP: 145 A; 95 C; 97 G; 142 T; 0 other:
XX

```

```

alignment_scores:
  Quality: 232.00      Length: 85
  Ratio: 3.803        Gaps: 1
  Percent Similarity: 71.765   Percent Identity: 55.294
alignment_block:
  US-09-289-346a-5 x AA084372

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Align seq 1/1 to: AA084372 from: 1 to: 479

```

1  ThrLeuValITrPGIyGlnPheGlnValaIspGIyATgSerAlaTargIyG1 17
140  ACCCTCGAATGGGAGAGATTTCAGTCGATCGATCGATCGATCGATCGAGG 189
17  YCYsGlnPheSerGlnAspAlaIaAlaGlnAlaLeuAsnAlaSerSort 34
190  ACAACATCAACCAAGACGACCTTACGCCACGACGCTTACATCGACATCA 239
34  ysgIuGlalaleuGlnIleIleIleATargIuysIleIleAlaIaAlaleu 50
240  ACCTCGAATGGGAGAGATTTCAGTCGATCGATCGATCGATCGATCGATG 289
51  PheGlnPheIleAsnLeuAsnSerGlnLeuAspArgIle..... 63
290  TTACATTTTCATTAATTTAAATAGTAATTAAGATTAAGATTAAGATTAAC 339
64  .....PheAspIysThrP 68
340  GTTCGAGCTTATGCTTCCTCTTTTATCTCTCTCTCTCTTTGATGAGATTC 389
68  TGGIu 69
390  CAGNA 394

```

```

seq_name: /cgn1.8/cydate/geneseq/genesequ/NAI995.DAT:AA084375
seq_documentation_block:
  ID AA084375 standard: DNM: 550 BP.
  AC
  AA084375:
  DE
  DT 19-AUG-1995 (first entry)
  XX
  XX Tomato leaf curl virus Australian strain DNA sequence.
  XX
  XX Tomato leaf curl virus: Australia strain: plant disease: ds.
  XX
  XX Tomato leaf curl virus (Australia).
  XX
  XX WO503404-A.
  XX
  XX 02-FEB-1995.
  XX
  XX 22-JUL-1993. 93MO-EP01946.
  XX
  XX 22-JUL-1993. 93AU-0047014.
  XX
  XX 22-JUL-1993. 93MO-EP01946.
  XX
  XX (BIOC-) BIOCEM SA.
  XX (CSTR-) COMMONWEALTH SCI & IND RES ORG.
  XX
  XX Baudino S., Comeau D., Dry IB., Gruber V., Lemes P.,
  XX Mason J., Rezalan MA., Riggden JE., Rezalan MA.
  XX WPI: 1995-075232/10.
  XX
  XX
  XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
  XX and/or assembly of viruses by cleaving target virus sequence,
  XX useful for preparing resistant plants, esp tomatoes.
  XX
  XX Disclosure: Fig 11. 90pp: English.
  XX
  XX The sequence represents the complementary sense DNA strand of an
  XX Australian strain of tomato leaf curl virus. Ribozymes specific
  XX for this sequence may be used in generation of transgenic plants
  XX with disease-resistance.
  XX
  XX Sequence 550 BP: 148 A; 120 C; 134 G; 142 T; 6 other:
  XX

```

```

alignment_scores:
  Quality: 231.50      Length: 86
  Ratio: 3.795        Gaps: 1
  Percent Similarity: 70.930   Percent Identity: 54.651
alignment_block:
  US-09-289-346a-5 x AA084375

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Align seq 1/1 to: AA084375 from: 1 to: 550

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1  ThrLeuValITrPGIyGlnPheGlnValaIspGIyATgSerAlaTargIyG1 17
201  ACCCTCGAATGGGAGAGATTTCAGTCGATCGATCGATCGATCGATCGAGG 250
17  YCYsGlnPheSerGlnAspAlaIaAlaGlnAlaLeuAsnAlaSerSort 34
251  ACAACATCAACCAAGACGACCTTACGCCACGACGCTTACATCGACATCA 300
34  ysgIuGlalaleuGlnIleIleIleATargIuysIleIleAlaIaAlaleu 50
301  ACCTCGAATGGGAGAGATTTCAGTCGATCGATCGATCGATCGATCGATG 350
51  PheGlnPheIleAsnLeuAsnSerGlnLeuAspArgIle..... 63
351  TTACATTTTCATTAATTTAAATAGTAATTAAGATTAAGATTAAGATTAAC 400
64  .....PheAspIysT 67

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[illegible]

Percent Similarity: 84.286 Percent Identity: 58.571

alignment_block:

US-09-289-346a-5 x AAT93294 ..

Align seg 1/1 to: AAT93294 from: 1 to: 1160

```

1 ThrlwvAlrPgLygluPhgInVaIhApLyAqSeraIlaAgLyG1 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
371 ACAATGAAATGAGGAGATTTCAGATCGACGACGACGACGAG 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 YCysGlnThrSerAsnAspAlaIaIaGluAlaLeuAsnIaSer 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
421 CCACGAGCTGCTAAAGATTCTATGAGGACGACGACGACGAG 470
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 YSGluGluAlaLeuGlnIleIleIaTgLuYsIleProAlaIaIaLeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
471 TTCAATCTGCTTACGAGTCTTACGACGACGACGACGACGAG 520
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 PhdGlnPheHisAsnLeuAsnSerAsnLeuAspAqIlePheAspLySrh 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
521 TTCAAAATATCATACATCCGCTCTACGCTAAGACGACGATTCGCAAGAGC 570
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 PProGluPro 70
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
571 YCGSAGACCG 580

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seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAT93282

seq_documentation_block:

ID AAT93282 standard: DNA: 1169 BP.

XX AAT93282:

27-APR-1998 (first entry)

Tomato mottle virus AC1 mutant TOMOV-AC1dIm gene.

Geminivirus: TOMOV-AC1dIm: AC1 gene; transdominant mutation;

transgenic plant; disease resistance; ss; cyclic; circular.

XX Tomato mottle virus isolate Florida.

XX Synthetic.

XX Key Location/Qualifiers

XX CDS 44..1129

XX /*tag= a

XX W09739110-A1.

XX 23-OCT-1997.

XX 15-APR-1997: 97NO-US06300.

XX 16-APR-1996: 96US-0015517.

XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.

XX (WISC) WISCONSIN AGRICULTURAL RES FOUND.

XX Ahlgquist PG, Hanson ST, Luu HT, Maxwell DP, Stout JT;

XX P-PSDB: AAM34324.

XX WPI: 1997-526447/48.

XX Transgenic plants expressing geminivirus AC1 and CI wild-type and

XX mutant genes - have increased resistance to geminivirus infection

XX e.g. Tomato mottle virus, tomato yellow leaf curl virus or bean

XX golden mosaic geminivirus

XX Claim 11: Page 60-62; 132pp: English.

XX This DNA sequence comprises a transdominant lethal mutant,

XX designated TOMOV-AC1dIm, of the AC1 gene of tomato mottle virus

CC virus (TOMOV). It encodes an AC1 protein (see AAM34324) that carries
 CC mutations in its NTP-binding domains. The AC1 gene (see also
 CC AAT93294) must be expressed for efficient replication of the two
 CC genomic components, DNA-A and DNA-B, of the bipartite TOMOV genome.
 CC The invention involves production of transgenic plants containing
 CC the negatively interfering in trans with geminivirus replication
 CC during infection. Such transgenic plants are resistant to viral
 CC infection. The AC1/CI genes are especially from TOMOV, tomato
 CC yellow leaf curl virus or bean golden mosaic geminivirus (see
 CC AAT93282-93) and encode polypeptides (see AAM34324-35) that have
 CC mutations in the highly conserved DNA-nicking and/or the NTP-binding
 CC domains.

Sequence 1169 BP; 363 A; 281 C; 255 G; 270 T; 0 other;

alignment_scores: Quality: 220.00 Length: 70
 Ratio: 3.729 Gaps: 0
 Percent Similarity: 84.286 Percent Identity: 58.571

alignment_block:

US-09-289-346a-5 x AAT93282 ..

Align seg 1/1 to: AAT93282 from: 1 to: 1169

```

1 ThrlwvAlrPgLygluPhgInVaIhApLyAqSeraIlaAgLyG1 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
371 ACAATGAAATGAGGAGATTTCAGATCGACGACGACGACGAG 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 YCysGlnThrSerAsnAspAlaIaIaGluAlaLeuAsnIaSer 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
421 CCACGAGCTGCTAAAGATTCTATGAGGACGACGACGACGAG 470
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 YSGluGluAlaLeuGlnIleIleIaTgLuYsIleProAlaIaIaLeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
471 TTCAATCTGCTTACGAGTCTTACGACGACGACGACGACGAG 520
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 PhdGlnPheHisAsnLeuAsnSerAsnLeuAspAqIlePheAspLySrh 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
521 TTCAAAATATCATACATCCGCTCTACGCTAAGACGACGATTCGCAAGAGC 570
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 PProGluPro 70
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
571 YCGSAGACCG 580

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seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AAT93283

seq_documentation_block:

ID AAT93283 standard: DNA: 1169 BP.

XX AAT93283:

27-APR-1998 (first entry)

Tomato mottle virus AC1 mutant TOMOV-AC1dIm gene.

Geminivirus: TOMOV-AC1dIm: AC1 gene; transdominant mutation;

transgenic plant; disease resistance; ss; cyclic; circular.

XX Tomato mottle virus isolate Florida.

XX Synthetic.

XX Key Location/Qualifiers

XX CDS 44..1129

XX /*tag= a

XX W09739110-A1.

XX 23-OCT-1997.

XX 15-APR-1997: 97NO-US06300.

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XX 16-APR-1996: 9605-0015517.
XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX (MISC.) MISCONSIM ALUMINI RES FOUND.
XX Ahlquist PG, Hanson SF, Luv HT, Maxwell DP, Stout JT;
XX WPI: 1997-526447/48.
XX P-PSDB: AMW4325.
XX Transgenic plants expressing geminivirus ACI and CI wild-type and
XX mutant genes have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX Claim 11: Page 64-65; 132pp: English.
XX This DNA sequence comprises a transdominant lethal mutant,
XX designated TOMOV-ACIdlm23, of the ACI gene of tomato mottle virus
XX (ToMoV). It encodes an ACI protein (see AMW4326) that carries
XX a mutation in its NTP-binding domain. The ACI gene (see also
XX AMW3294) must be expressed for efficient replication of the two
XX genomic components, DNA-A and DNA-B, of the bipartite ToMoV genome.
XX The invention involves production of transgenic plants containing
XX DNA comprising geminivirus ACI or CI wild-type or mutant sequences
XX that negatively interfere in trans with geminiviral replication
XX and/or geminivirus-induced plant disease resistance to viral
XX infection. The ACI/CI genes are especially from ToMoV, tomato
XX yellow leaf curl virus or bean golden mosaic geminivirus (see
XX AMW3282-93) and encode polypeptides (see AMW4324-35) that have
XX mutations in the highly conserved DNA-nicking and/or the NTP-binding
XX domains.
XX Sequence 1169 BP: 361 A; 280 C; 258 G; 270 T; 0 other:
XX
XX alignment_scores:
XX Quality: 220.00 Length: 70
XX Ratio: 3.729 Gaps: 0
XX Percent Similarity: 84.286 Percent Identity: 58.571
XX
XX alignment_block:
XX US-09-289-346A-5 x AMW93284
XX
XX Align seq 1/1 to: AMW93284 from: 1 to: 1169
XX
XX 1 ThrTevAlTrpGlyGlnPheGlnValAspGlyAArgSerAlaArgGlyG1 17
XX |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
XX 371 ACAATCGAAGCGGAGATTTCACATCGACGCGCATTCGCCACAGAGG 420
XX 17 YCYGlnThrSerAsnAspAlaAlaGlnAlaLeuAsnAlaSerSerL 34
XX |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
XX 421 CCACGAGCTCGTAAATGATTCATATCGCAAAAGCGTTAATCACTTCG 470
XX
XX 34 YSGlnGlnAlaLeuGlnAlaLeuArgGlyAluysIlleProAlaAlaLeu 50
XX |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
XX 471 TTCACATCTGCTTACGACGCTCTACGGCAAGAACACAAAGATTTTGTA 520
XX PheGlnPheIleAsnLeuAsnSerAsnLeuAsnAspArgIlePheAspArg 67
XX |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
XX 521 TTACAAATATCATACATCGCTCTACACTACGATATTCGCCAAGAGC 570
XX
XX 67 rProGluPro 70
XX |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
XX 571 TCCGGAACCG 580
XX
XX seq_name: /cgnl_8/gcgdelta/geneseq/geneseq/MW1997.DAT:AMW93284
XX
XX seq_documentation_block:
XX ID AMW93284 standard: DNA; 1169 BP.
XX
XX AMW93284:

```

```

XX 27-APR-1998 (first entry)
XX XX Tomato mottle virus ACI mutant TOMOV-ACIdlm23 gene.
XX DE Geminivirus; TOMOV-ACIdlm23; ACI gene; transdominant mutation;
XX KW transgenic plant; disease resistance; ss; cyclic; circular.
XX XX
XX OS Tomato mottle virus isolate Florida.
XX
XX XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDL /fig- a
XX
XX W09739110-A1.
XX
XX 23-OCT-1997.
XX
XX 15-APR-1997: 57MO-US06300.
XX
XX 16-APR-1996: 9605-0015517.
XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX (MISC.) MISCONSIM ALUMINI RES FOUND.
XX Ahlquist PG, Hanson SF, Luv HT, Maxwell DP, Stout JT;
XX WPI: 1997-526447/48.
XX P-PSDB: AMW4326.
XX Transgenic plants expressing geminivirus ACI and CI wild-type and
XX mutant genes - have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX Claim 11: Page 67-69; 132pp: English.
XX This DNA sequence comprises a transdominant lethal mutant,
XX designated TOMOV-ACIdlm23, of the ACI gene of tomato mottle virus
XX (ToMoV). It encodes an ACI protein (see AMW4326) that carries
XX 2 mutations in an NTP-binding domain. The ACI gene (see also
XX AMW3294) must be expressed for efficient replication of the two
XX genomic components, DNA-A and DNA-B, of the bipartite ToMoV genome.
XX The invention involves production of transgenic plants containing
XX DNA comprising geminivirus ACI or CI wild-type or mutant sequences
XX that negatively interfere in trans with geminiviral replication
XX during infection. Such transgenic plants are resistant to viral
XX infection. The ACI/CI genes are especially from ToMoV, tomato
XX yellow leaf curl virus or bean golden mosaic geminivirus (see
XX AMW3282-93) and encode polypeptides (see AMW4324-35) that have
XX mutations in the highly conserved DNA-nicking and/or the NTP-binding
XX domains.
XX Sequence 1169 BP: 364 A; 278 C; 257 G; 270 T; 0 other:
XX
XX alignment_scores:
XX Quality: 220.00 Length: 70
XX Ratio: 3.729 Gaps: 0
XX Percent Similarity: 84.286 Percent Identity: 58.571
XX
XX alignment_block:
XX US-09-289-346A-5 x AMW93284
XX
XX Align seq 1/1 to: AMW93284 from: 1 to: 1169
XX
XX 1 ThrTevAlTrpGlyGlnPheGlnValAspGlyAArgSerAlaArgGlyG1 17
XX |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
XX 371 ACAATCGAAGCGGAGATTTCACATCGACGCGCATTCGCCACAGAGG 420
XX 17 YCYGlnThrSerAsnAspAlaAlaGlnAlaLeuAsnAlaSerSerL 34
XX |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

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```

421 CCACGAGCTGTGTCATTATGTTTAAATCGCAAGCCTTAATGCAGCATTCGG 470
34 ysgcudlualaleucloiaileatgcluhyllepfroaliaalaleu 520
471 TTCAATCTTGCTTACCCATGCTTAAACGGAAGAACAACAAAGATTTCGA 570
51 PhecltPPhetHccsttcaaaenasefrramlaagayaclyllephaspyent 627
:::||||| ::::::::::::::::::::||| ::::
521 TTCAAAAATTCATTCACATCCGCTCTACTACATAAGCAATATTGCCAAGCG 570
67 pfProgluPro 70
:::|||||
571 TCCGGAACCG 580

seq_name:/cgnl_b/gcgdata/geneseq/geneseq/MN1997.DAT:AA793309
seq_id:MN1997
seq_documentation_block:
ID: AA793309 standard; DNA; 2602 BP.
AA793309:
AA793309:
27-APR-1998 (first entry)
Tomato mottle virus full-length A-component clone.
XX
XX
XX Geminivirus: TOMOV; ACI gene; transduant mutation;
KM transgenic plant; disease resistance; ss: cyclic; circular.
XX
XX Tomato mottle virus isolate Florida.
XX
XX MO9739110-A1.
PN
PD 23-OCT-1997.
PF 15-APR-1997: 97MC-US06500.
PA 16-APR-1996: 96US-0015517.
XX
XX (SEM-) SEMINUS VEGETABLE SEEDS INC.
XX (WISC.) WISCONSIN ALUMNI RES FOUND.
XX
XX Ahlgust PG, Hanson SF, Liu HT, Maxwell DP, Stout JT,
XX NPT. 1997-526447/48.
XX
XX Transgenic plants expressing geminivirus ACI and CI wild-type and
PT mutant genes - have increased resistance to geminivirus infection
PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX
XX Example 3.1: Page 76-77; 132pp: English.
XX
XX This genomic DNA sequence comprises a full-length A-component clone
CC of tomato mottle virus (TOMOV), a geminivirus that has a bipartite
CC genome comprising DNA-A and DNA-B. It was isolated from TOMOV
CC infected Nicotiana benthamiana and tomato plant DNA by restriction
CC digestion. The DNA-B component (see AA793310) was also isolated.
CC TOMOV DNA-A contains the ACI gene (see AA793294) that must be
CC expressed for efficient replication of DNA-A and DNA-B. The
CC expression of the transgenic plants containing DNA
CC comprising ACI or CI wild-type or mutant genes have effectively
CC interfering in trans with geminiviral replication during infection.
XX Such transgenic plants are resistant to viral infection.
XX
XX Sequence 2602 BP; 671 A; 561 C; 586 G; 784 T; 0 other;
XX
alignment_scores:
Quality: 220.00 length: 70
Ratio: 3.729 gaps: 0
Percent Similarity: 84.286 Percent Identity: 58.571
alignment_block:

```

```

US-09-289;346a-5 x AA793309/few
Align seq 1/1 to reverse of: AA793309 from: 1 to: 2602
1 ThrileValTrIreGjAluehigElnvalAapGLVtAgSerAlatgLyGI 17
2282 ACATCTAGTATGGGAAGATTTCAGATCGACGGCAATCTCCDANAGAGG 2233
17 yCgInThrISerAmSpALalAbAladlAlAlaLtuASnAlaserSert 34
+ +++++++ ++++++ ++++++ ++++++ ++++++ ++++++
2232 CCACAGGTCTCATTAATTCATTAAGAAGAAAGCTTTAAATGAAGTTCG 2183
2182 TTCATCTGCCCTTACCGTGCTAAGSGAAGAACCAACAAGATT707A 2133
34 ysgUgluaLaLeugLinlelleatgcllystIIeProalAlalaLeu 50
+ ++++++ ++++++ ++++++ ++++++ ++++++ ++++++
51 PhelIPheHisAsnLeuAsnSerAnLeuAsPaGyllePhaeApLy97H 67
+ ++++++ ++++++ ++++++ ++++++ ++++++ ++++++
2132 TTTCACAACTCATMAATCCGCTCTACCTGAACGATATTCGCAGAGGC 2083
67 PPGcIGuUer 70
+ ++++++ ++++++ ++++++ ++++++ ++++++ ++++++
2082 TCCGCAACCG 2073

seq_name : /cnrl_8/gagataz/geneseq/geneseqp/NA1936.DAT:AA12904
seq_documentation_block:
ID AA12904 standard: DNA: 1080 BP.
XX
XX
XX AA12904:
XX
XX
XX 07-NOV-1996 (first entry)
XX
XX Sardinian tomato leaf curl virus mutated CI gene (K237A).
DE
XX
XX Sardinian tomato yellow leaf curl virus.
XX
XX Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
XX viral resistance; geminivirus; tomato yellow leaf curl virus;
XX viral resistance; geminivirus; tomato yellow leaf curl virus;
XX Sardinian isolate; SYRVCY; transgenic plant; P-loop; CI gene;
XX A11 gene; dominant negative phenotype; ss.
XX
XX Sardinian tomato yellow leaf curl virus.
OS
XX
XX Key Location/Qualifiers
XX FH /feature = a
XX CDS /product= Rep(K237A)
FT FT /note= "encodes Rep protein in which wild-type lys
FT FT at position 227, i.e. within the NP-
FT FT binding site, is replaced by Ala"
XX
XX W06060573-A1.
XX
XX PD 21-MAR-1996.
XX
XX PE 15-SEP-1995; 95NC-FR01192.
XX
XX PR 15-SEP-1994; 94FR-0011040.
XX
XX RA (CNNS ) CENT NAT RECH SCT.
XX
XX PI Greenhorn B.
XX
XX WP1: 1996-179947.1B.
XX DR P-PStDB: AAA88870.
XX
XX Prodn. of virus-resistant transgenic plants - using mutated genomic
XX sequence from phytoproctogenic DNA virus
XX
XX PS Disclosure: Fig 13: 93pp; French.
XX
XX Mutation of consensus amino acids in the NP-binding site of
XX geminivirus Rep protein is used to produce replication deficient

```


modification; mutation; viral replication; deficient; inhibition;
 KM viral resistance; geminivirus; tomato yellow leaf curl virus;
 KM Sardinian isolate; STVLCV; transgenic plant; P-loop; CI gene;
 KM AUI gene; ss.

Sardinian tomato yellow leaf curl virus.

Key Location/Qualifiers
 FT 1..1080

FT /tag= a
 FT /product= Rep-(K227R)
 FT /note= encodes Rep protein in which wild-type Lys
 FT at position 227, i.e. within the NTP-
 FT binding site, is replaced by Arg.

MO9608573-AI.

PD 21-MAR-1996.

XX 15-SEP-1995: 95MO-FR01192.

XX 15-SEP-1994: 94FR-00101040.

XX (CNRS) CENT NAT RECH SCI.

XX Gromenborn B;

XX WPI: 1996-170947/18.

XX P-750D; AM08872.

XX Prodn. of virus-resistant transgenic plants - using mutated genomic
 XX sequence from phytopathogenic DNA virus

XX Disclosure: Fig 13: 93pp; French.

XX Mutation of consensus amino acids in the NTP-binding site of
 XX the replicase of the Sardinian isolate of tomato yellow leaf
 XX curl virus. The mutated viral nucleic acid is used for producing
 XX transgenic plants that are resistant to, or tolerant of, the native
 XX virus. The present sequence encodes a mutant form of the Rep (or CI)
 XX protein from the Sardinian isolate of tomato yellow leaf curl virus
 XX (STVLCV) in which the wild-type Lys227 residue has been changed to an
 XX Arg residue; transgenic Nicotiana benthamiana plants generated by
 XX transformation with the mutated virus were not resistant to STVLCV.
 XX The plants were found to be resistant.
 XX replaced by Ala were found to be resistant.

XX Sequence 1080 BP: 356 A; 247 C; 210 G; 267 T; 0 other;

XX alignment_scores:

XX Quality: 219.00 Length: 69
 XX Ratio: 3.942 Gaps: 0
 XX Percent Similarity: 82.609 Percent Identity: 57.971

XX alignment_block:

XX 09-09-289-346a-5 x AA012906

XX Align seq 1/1 to: AA012906 from: 1 to: 1080

XX 2 leavYATPcYclucPheclInVAlAsGcYKtRSerAlArGcYcYlcy 18

XX 331 CTTGAATGGCGTACTTCCAGATCCAGCGACGACATCTGCTAGGGAGACCA 380

XX 18 sGlnPheASnAspAlaAlaAlaGluAlaLeuAlaSerSerLysG 35

XX 381 AAGAGACACCAACGACCTTACGCAAGGACCTTAAGACGACGATGACT 430

XX 35 InGluAlaGlnGlnIleAlaArgcYlucYsIlePheAlaAlaLeuPhe 51

XX 431 CGCAGCCTCTTGATTAATTAAGATTAGCCCTTCACGATTAACCTTCA 480

XX 52 GlnPheASnLeuAsnSerAsnLeuAspAlrIlePheAspLysThr 68

481 CATTTCATATATATAATAGTATATGATTAAGTTCACAGTCCTCC 530

68 oGUPro 70

531 GGCACCT 537

seq_name: /cynl_8/ycgdata/geneseq/geneseq/AN1995.DAT:AA084378

seq_documentation_block:
 ID: AA084378 standard: DNA: 1695 BP.

XX AA084378:

XX 19-AUG-1995 (first entry)

XX Tomato yellow leaf curl virus DNA sequence.

XX Tomato yellow leaf curl virus; plant disease;

XX Ribozyme target sequence; ds.

XX Tomato yellow leaf curl virus (S).

XX key location/Qualifiers

XX misc_feature

XX /tag= a

XX /note= "Ribozyme cleavage site"

XX /tag= b

XX /note= "Ribozyme cleavage site"

XX /tag= c

XX /note= "Ribozyme cleavage site"

XX misc_feature

XX /tag= a

XX /note= "Ribozyme cleavage site"

XX /tag= b

XX /note= "Ribozyme cleavage site"

XX /tag= c

XX /note= "Ribozyme cleavage site"

XX misc_feature

XX /tag= a

XX /note= "Ribozyme cleavage site"

XX /tag= b

XX /note= "Ribozyme cleavage site"

XX /tag= c

XX /note= "Ribozyme cleavage site"

XX misc_feature

XX /tag= a

XX /note= "Ribozyme cleavage site"

XX /tag= b

XX /note= "Ribozyme cleavage site"

XX alignment_scores:

XX Quality: 219.00 Length: 69
 XX Ratio: 3.942 Gaps: 0
 XX Percent Similarity: 82.609 Percent Identity: 57.971

XX alignment_block:

XX 09-09-289-346a-5 x AA084378

XX WPI: 1995-075232/10.

XX Synthetic DNA virus ribozyme(s) - reduce replication, infection

XX and/or assembly of viruses by cleaving target virus sequence,

XX useful for preparing resistant plants, esp. tomatoes.

XX Disclosure: Fig 8: 90pp; English.

XX The sequence represents the complementary sense DNA strand of

XX tomato yellow leaf curl virus-S strain. Ribozyme cleavage sites

XX are indicated. Ribozymes against this sequence may be used in

XX generation of transgenic tomato plants with disease-resistance.

XX Sequence 1695 BP: 568 A; 366 C; 308 G; 453 T; 0 other;

Align seq 1/1 to: AA084378 from: 1 to: 1695

```

2 LeuValTrpGlyLuphGlnValAspGlyArGserAlaArgGlyGlyCY 18
111 |||||.....
487 CTTCAATGGGGTACTCTCCAGATCCAGACGACATCTGCTAGGGAGACCA 536
18 sGlnTrSerAsnAspAlaAlaAGluAlaLeuAsnAlaSerSerLysG 35
|||||.....
537 ACAGACACCAACGACGCTCCACCAAGCCAAATTACCCGACGAGTAAGT 586
35 LUGluAlaLeuGlnIleIleArgGluLysIleProAlaAlaAlaLeuPhe 51
.....
587 CGCAGGCTCTTAATGATATTAACAAATTACGCCCTCAATCTACTTCA 636
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThr 68
|||||.....
637 CATTTTCATTAATATAATATGTAATATGATTAAGGTTTCCAGGCTCTC 686
68 oGluPro 70
111 |||||
687 GGCCACT 693

```

seq_name: /cgnl_b/gcgdata/geneseq/geneseq/NA197.DAT:AA193291

seq_documentation_block:

ID AA193291 standard; DNA; 1062 BP.

AA193291:

27-APR-1998 (first entry)

Bean golden mosaic geminivirus CI mutant ORF BGAC221.

Geminivirus, BGWV, CI gene, transdominant mutation;

transgenic plant; disease resistance; ss; cyclic; circular.

Bean golden mosaic virus type II isolate Guatemala.

W09739110-A1.

23-OCT-1997.

15-APR-1997; 57MO-US06300.

16-APR-1996; 9605-0015517.

(SEMI-) SEMINIS VEGETABLE SEEDS INC.

(WISC) WISCONSIN ALUMNI RES FOUND.

Ahiquist PG, Hanson SF, Lau HT, Maxwell DP, Stout JT;

WPI; 1997-526447/48.

F-PSDB: AAW34333.

Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean golden mosaic geminivirus

Claim 13: Page 107-109; 132pp: English.

This DNA sequence comprises construct BGAC221 that codes for a transdominant lethal mutant (see AAW34333) of the CI protein (see AAW34338) of bean golden mosaic virus (BGWV). It was obtained by recombinant gene synthesis of the wild-type CI gene (see AA193318) CI 15 transgenic plants containing DNA comprising geminivirus CI or AC1 wild-type or mutant sequences that negatively interfere in trans with geminiviral replication during infection. Such transgenic plants are resistant to viral infection. The AC1/CI genes are especially from BGWV, tomato mottle virus or tomato yellow leaf curl virus (see AA193282-93) and encode polypeptides (see AAW34324-35) that have mutations in the highly conserved DNA-nicking and/or the

CC NTP-binding domains.

XX Sequence 1062 BP; 339 A; 245 C; 219 G; 259 T; 0 other;

50 alignment_scores:

Quality: 218.00 length: 70
Ratio: 3.695 gaps: 0
Percent similarity: 84.286 Percent identity: 60.000

alignment_block:

US-09-289-346a-5 x AA193291

Align seq 1/1 to: AA193291 from: 1 to: 1062

```

1 ThrLeuValTrpGlyLuphGlnValAspGlyArGserAlaArgGlyGly 17
|||||.....
328 ACAATCGAATGGGAGACAAATTCGAAATCGACCGCAGCAATCTCGAAGAGAG 377
17 YGyGlnTrhSerAsnAspAlaAlaAGluAlaLeuAsnAlaSerL 34
|||||.....
378 TCAGCGATCTCCAGACACATCATCTCAAGACCATTAAGGACATTCGA 427
34 YSGluAlaAlaLeuGlnIleIleArgGluLysIleProAlaAlaLeu 50
|||||.....
428 TTGAATCTGCTTACCAATATCAATGAAGACAGACCAACGAAATTAAGTCG 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLys 67
|||||.....
478 CTTCAATCATCACATCCCTCTTATCTCCAGACGATCTCTCAAGT 527
67 rProGluPro 70
528 GGCGGACCA 537

```


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```

ACCESSION      AJ272897
VERSION        AJ272897.1 GI:6432270
KEYWORDS       EST
SOURCE         Metarhizium anisopliae
ORGANISM       Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
               Hypocryales; Clavicipitaceae; mitospore-forming;
REFERENCE      1 (bases 1 to 623)
AUTHORS        Screen,S.E., Mahbur,P. and St. Leger,J.T.
TITLE          Seren analysis of the insect pathogenic fungus Metarhizium anisopliae
PUBLISHED     unpublished (1999)
COMMENT        Complete genome sequence
              Entomology Department
              University of Maryland
              4112 Plant Sciences Building, College Park, MD 20742, USA.

FEATURES
             location/Qualifiers
Source=Metarhizium anisopliae"
            /organism="Metarhizium anisopliae"
            /db_xref="taxon:5280"
            /strain="AFSP-1"
            /date="Feb 1999"
            /clone="Maz29"
            /note="Metarhizium anisopliae ARSEF 2575"/
            /note="Vector: UniZap; Metarhizium anisopliae was grown on insect cuticle for 24 hours. A cDNA library was constructed in the unidirectional Lambda vector, UniZap"
```

```
BASE COUNT    161 a   159 g   159 t   164 T

ORIGIN

alignment_scores:
Quality:      73.00           Length:      63
Ratio:        1.872          Gaps:      2
Percent Similarity: 61.905 Percent Identity: 33.333

Alignment Block:
US-09-289-346A-5 x AJ272897 ..

Align seg 1/1 to: AJ272897 from: 1 to: 623

15 ATGATGCATCAGTCTTTTCGGTAAGAATAAAAGTAGCAAAAACAAGCG.. 30
...|||||.....
175 CAGAGTGCCATTACTAACGTCTGCCAGCATGGAATGACGCCCCGACCACCA 224
31 .....AlbsereerLyssgicugialatlaaleagcintlelailagtlv 44
225 AAATPTGCATGCGCACCTCCCAAGATGCTGAAAAATCAAACCAATTCAGAAG 274
44 yslieProalalaiaaaabheacInPheliasanleuasenseer..... 58
275 ATTTCGCGCGCGCGAGCAANAATCTGCGCGCAKATCTCACTACGTGATGAAG 324
59 .....AsduasapaYgliephaspIyafTr 67
325 GATCGAGGCGGAAGAACCTCGACATGCGCTCGACAGACAGACGCC 363

seq_name:= qb-gss:N0656777

seq documentation block:
LOCUS      N0656777                570 bp            DNA                 GSS
DEFINITION Sheared DNA-27MY3 -TR Sheared dna Trypanosoma brucei genomic clone
ACCESSION  N0656777
VERSION    N0656777.1 GI:5164525
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei.
ORGANISM   Trypanosoma brucei
           Eukaryotes; Excystozoa; Kinetoplastida; Trypanosomatidae;
```

```
REFERENCE      1 (bases 1 to 570)
AUTHORS        El-Sayed,N.Y., Zhao,H., Gill,S., Sub,E., Malek,J., Fujili,C.,
               Gerrard,C., Leeoh,Y., de Jong P., Ullu E., Melville.S., Doneilson.J.C.,
               Fraser,C. and Adams M.
```

[illegible]


```

seq_name: gb-gss:A0950848
seq_documentation_block: 572 bp DNA GSS 27-JAN-2000
LOCUS A0950848
DEFINITION Sheared DNA-51M3.TF.Shaered DNA Trypanosoma brucei genomic clone
ACCESSION A0950848
VERSION A0950848.1 GI:6774113
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei.
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 572)
El-Sayed,N., Zhao,S., Zhao,H., Gull,S., Sub,E., Malek,J., Fujii,C.,
Gerard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
Fraser,C. and Adams,M.,
Determination of clone end sequences from Trypanosoma brucei cDNA
library.
JOURNAL Unpublished (1999)
COMMENT Other GSS: Sheared DNA-51M3.TF
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: nelson@tigr.org
Clones are derived from the Trypanosoma brucei cDNA 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tldb/tldb/.
Seq primer: M13-Forward
Class: Shotgun
FEATURES
source
1..572
location/Qualifiers
/organism="Trypanosoma brucei"
/strain="TREU927/4 cDNA 10.1"
/db_xref="taxon:5691"
/clone_lib="Sheared DNA-51M3"
/molecule="Vector: pUC18; Site1: Sma1; Constructed at the
Institute for Genomic Research, The Institute for Genomic Research,
9712 Medical Center Dr., Rockville, MD.
Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 cDNA 10.1) was mechanically
sheared to give a light size distribution (approx 2 kb).
The v + i method used for the library construction is
described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A Practical
Approach, Eds. M. Yandl and B. Barrell, Oxford University
Press, 1999)."
BASE COUNT 115 a 118 c 180 g 159 t
ORIGIN

```

```

alignment_scores:
  Quality: 68.00 Length: 31
  Ratio: 2.519 Gaps: 0
Percent Similarity: 87.097 Percent Identity: 38.710

```

```

alignment_block:
US-09-289-346a-5 x A0950848
Align seg 1/1 to: A0950848 from: 1 to: 572

```

```

11 G1ATGCGTCTCCGACATCTCCGACACGACGTCATGTGGA 27
|||||
291 GCTGCTCTCCGACATCTCCGACACGACGTCATGTGGA 340
|||||
27 uAlaLeuAnaIaSer:SerTyrSgluGluAlaGlnIle 41
|||||
341 AGTGTGCTGCGACATCTCCGACACGACGTCATGTGGA 383
|||||

```

```

seq_name: gb-gss:A0947513
seq_documentation_block: 587 bp DNA GSS 27-JAN-2000
LOCUS A0947513
DEFINITION Sheared DNA-49M17.TF.Shaered DNA Trypanosoma brucei genomic clone
ACCESSION A0947513
VERSION A0947513.1 GI:6770778
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei.
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 587)
El-Sayed,N., Zhao,S., Zhao,H., Gull,S., Sub,E., Malek,J., Fujii,C.,
Gerard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
Fraser,C. and Adams,M.,
Determination of clone end sequences from Trypanosoma brucei cDNA
library.
JOURNAL Unpublished (1999)
COMMENT Other GSS: Sheared DNA-49M17.TF
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: nelson@tigr.org
Clones are derived from the Trypanosoma brucei cDNA 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tldb/tldb/.
Seq primer: M13-Forward
Class: Shotgun
FEATURES
source
1..587
location/Qualifiers
/organism="Trypanosoma brucei"
/strain="TREU927/4 cDNA 10.1"
/db_xref="taxon:5691"
/clone_lib="Sheared DNA-49M17"
/molecule="Vector: pUC18; Site1: Sma1; Constructed at the
Institute for Genomic Research, The Institute for Genomic Research,
9712 Medical Center Dr., Rockville, MD.
Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 cDNA 10.1) was mechanically
sheared to give a light size distribution (approx 2 kb).
The v + i method used for the library construction is
described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A Practical
Approach, Eds. M. Yandl and B. Barrell, Oxford University
Press, 1999)."
BASE COUNT 176 a 175 c 128 g 108 t
ORIGIN

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alignment_scores:
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  Ratio: 2.519 Gaps: 0
Percent Similarity: 87.097 Percent Identity: 38.710

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497 GCTGCTCTCCGACATCTCCGACACGACGTCATGTGGA 448
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27 uAlaLeuAnaIaSer:SerTyrSgluGluAlaGlnIle 41
|||||

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9447 AGCTGTGTCGCAGACATCCCAAGCGCATTCAGAGTGAATG 405
seq_name: gb|est1:A1533218
seq_description: block: 608 bp mRNA EST 19-APR-2001
LOCUS A1533218 608 bp mRNA EST 19-APR-2001
DEFINITION SD04968 SpHrme sc Drosophila melanogaster Schneider L2 cell culture
SD04968 SpHrme sc Drosophila melanogaster cDNA clone SD04968 SpHrme, mRNA
sequence.
ACCESSION A1533218
VERSION A1533218.1 GI:4447353
KEYWORDS EST, fly, fruit fly, Drosophila melanogaster
ORGANISM Drosophila melanogaster
BUTRYOTA; MEZAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PLEYROKOTA; NEOPLATEA; ENDOPTERYGOATA; DIPTERA; BRACHYCERA;
Muscomorpha; Ephydroptera; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 608)
AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holin,M., Su,C., Tseng,G.,
Leary,S., and Rubin,G.M.
TITLE FlyBase release 4.0: The Drosophila genome project database
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: flybase@fruitfly.org/EST, est@fruitfly.berkeley.edu
Phone: 415 947 7700 column 8
High quality sequence stop: 515.
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Location/Qualifiers
1..608
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/collection="SD04968"
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/culture="pot2"
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culture pot2"
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/note="Vector: pot2; Site_1: EcoRI; Site_2: XhoI; sized
fractionated cDNAs were directly ligated into pot2.
Plasmid cDNA library."
BASE COUNT 172 a 170 c 137 g 129 t
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Ratio: 1.467 Percent Identity: 32.000
Percent Similarity: 61.333
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1 TTTTleValTPP gLgVlplheInAlaApSlAArSeeAlaArgLy. 16
||||||| ||| :||||||| ||| ||||| ||||| |||||
322 ACCCtCACtGGcAGAACACrCAACAGTAgTGATGACAGACCACAC 371
||||||| ||| :||||||| ||| ||||| ||||| |||||
17 ..... cLgCcagCaITTerSerSenAuAALaAGlUllleuan 30
||||||| ||| :||||||| ||| ||||| ||||| |||||
372 ACCTTCTGGCCrTCACCAATTCACACAGACAGACACTAGGGCT... 418
||||||| ||| :||||||| ||| ||||| ||||| |||||
31 AlAtSerLySLglUGlAlaIueGlnGlleIArGIuLylSlAPoAl 47
||||||| ||| :||||||| ||| ||||| ||||| |||||
419 ..... CTTCACATTAcrTGCCTCCAGACGCCACAC 447
||||||| ||| :||||||| ||| ||||| ||||| |||||
47 aAlAlaIleuphe cLlPhelIsenIeuaISerSenIeuaPaSIle 63
||||||| ||| :||||||| ||| ||||| ||||| |||||
448 GAATCCCrCTTCrCTTCCTTCAACAACATCCACACACACATAGrAcTc 497
||||||| ||| :||||||| ||| ||||| ||||| |||||
64 PhaaPlaySTPrProGLUpTo 70
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498 CTGAAGTGAAGCAACACCCCT 518
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  accession BE977193 mRNA
  description b660g11.y1 Drosophila melanogaster adult testis library drosophila
  melanogaster cdna clone b660g11 5', mRNA sequence.
  version BE977193
  keywords BE977193.1 GI:10607423
  source EST
  organism Drosophila
  trait fly
  tissue melanogaster
  project Drosophila melanogaster, Tracheata; Hexapoda; Insecta;
  pteroptera; Neoptera; Endopterygota; Diptera; Brachycera;
  muscomorpha; Ephyridiata; Drosophilidae; Drosophila.
  reference 1 (bases 1 to 612)
  authors Andrews, J., Bouffard, G. and Oliver, B.
  title Drosophila melanogaster testis expressed sequence tags
  journal Unpublished (1999)
  comment Laboratory of Celluluar and Developmental Biology
  NIDDK, National Institutes of Health
  6 Center Drive MSC 2715, Bldg 6, Rm. B1-13, Bethesda, MD 20892 USA
  fax: (301) 496 5239
  email: oliver@helix.nih.gov,
  http://www.niddk.nih.gov/intran/people/boliver.htm
  tissue Isolation and library construction performed at the National
  Institutes of Health, Bethesda, Maryland, USA.
  url http://www.niddk.nih.gov/intran/people/boliver.htm
  analyses and annotation performed by National Institutes of Health Intramural
  Sequencing Center (NISC; see http://www.nisc.nih.gov).
  plates: 60 rows: 6 columns: 11
  seq primer: M13p1 reverse primer (AMB).
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source
  /organism="Drosophila melanogaster"
  /strain="Y1" w167c1/Y"
  /db_xref="taxon:7227"
  /clone="b660g11"
  /clone_1lb="Drosophila melanogaster adult testis library"
  /sex="male"
  /dev_stage="1-5 day adult"
  /mol_method="PCR (polymerase)"
  /mol_reagent="primuscript sx (Stratagene)"
  /site_1: Ecoh I; site_2: Xho I;
  /site_1b: Ecoh I; site_2b: Xho I;
  /notes="1-5 day adult Y1" w167c1/Y males raised at 25oc. RNA
  isolated using RNeasy (Life Technologies) and a single
  round of Poly(A+) selection using Oligotex (Qiagen). cDNA
  library constructed using Stratagene ZAP-cDNA synthesis
  kit. Oligo of primed, size fractionated -1-6 kb, and
  size selected cDNA was ligated into Stratagene ZAP-cDNA
  polynucleotide phosphorylation (PNK) treated and amplified
  phageids were mass excised. A distribution channel for
  clones is being sought, but not currently available.
  Requests for clones cannot be honored."
BASE COUNT
  164 a 170 c 136 g 140 t
ORIGIN
alignment_scores:
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Percent Similarity: 61.333 Percent Identity: 32.000
alignment_block:
  US-09-2893-346A-5 x BE977193
Align seq 1/1 to: BE977193 from: 1 to: 612
1 ThTleValTTPr gTgYlpeGlnGlnAlaGp1VAcgeTAlaTgG1y. 16
||||| 111 :|||||:|||||:|||||:|||||:|||||:|||||:|||||
340 ACCCTGACGCTGCTGGAACGTCACAGTGGATGTCGACGATGTCACGACCC 369

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17 ..... GLYCGlnthSerAsnAPalaalagUALeuan 30
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390 ACCTCTTGCCCTTCACACACACACACACACCTC... 436
31 AlabSerIySglUgUaLndLleIleIySglUlyAlePAl 47
      ||| ||| .....
437 ..... CTACATTCACCTCGCCACACACCCACAC 465
47 AAlaAlaLeuPhe.GlnPheHIsaLnLeuAsnSerAsnLysPAl 63
      ||| ||| .....
466 GACGCGCTTCCTCGCTTCACACACACACACACACCTC... 515
64 PheAspLysThrProGluPro 70
      ||| .....
516 CTGACGACGATCACACACCCCT 536

seq_name: qb_esc2:B1366217
seq_documentation_block:
LOCUS B1366217 645 bp mRNA EST 01-AUG-2001
DEFINITION B55173.1 sprine RE Drosophila melanogaster normalized embryo p1/c-1
Drosophila melanogaster cDNA clone B55173.5 similar to C01245.1
Pha0001245 'transcription factor binding' located on: 3R 8387-8387
: 05/14/2001, mRNA sequence.
ACCESSION B1366217
VERSION B1366217.1 GI:15062245
KEYWORDS EST
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 645)
Stap J, Wang, S., Bock, J., P., Hong L., Tyler D., Bernan B., Carlson
J., Champa M., Chavez C., Bockel V., Farfan D., Friesz E., Geisler
R., Gonzalez M., Guarin H., Harris N., Li P., Liao G., Mista S.,
Mungai C.J., Nuno, J., Pacleb J., Paragas V., Park S.,
Phouanavong S., Wan K., Yu C., Lewis S.E., Celniker S. and Rubin
G.M.
BGEF/HMT RE Drosophila EST Project
COMMENT: B1366217 (2001)
CONTACT: Stapleton, M.
BDDP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST\_est/fruitfly\_berkeley.edu
B1366217.1 (2001)
Estimated-GenBank: 15062245
Plate: RE-517 row: B column: 1
High quality sequence stop: 608.
Location/Qualifiers
1..645
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/acc="B1366217"
/cdate="B55173"
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p1/c-1"
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/seq-stage="0-24 hours mixed stage embryonic".
/lab_host="DBS-alpha TONA"
/note="Organ: embryo; Vector: p1/c1; Site:1; XhoI; Site:2;
the RIKEN fly library is kindly generated by Piero Carninci at
the RIKEN fly library and excluded using
Cce recombinase. Plasmid cDNA library."
BASE COUNT 185 a 175 c 147 g 138 t
ORIGIN

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alignment_scores: 67.50 Length: 75
Quality: 1.46 Gaps: 4
Ratio: 1.46

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Percent Similarity: 61.333 Percent Identity: 32.000
alignment_block:
US-09-289-346a-5 x B1366217
Align seg 1/1 to: B1366217 from: 1 to: 645
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      ||| ||| .....
339 ACCTCGACCTCGCTTCACACACACACACACACCTC... 435
17 ..... GLYCGlnthSerAsnAPalaalagUALeuan 30
      ||| ||| .....
389 ACCTCTTGCCCTTCACACACACACACACACCTC... 435
31 AlabSerIySglUgUaLndLleIleIySglUlyAlePAl 47
      ||| ||| .....
436 ..... CTACATTCACCTCGCCACACACCCACAC 464
47 AAlaAlaLeuPhe.GlnPheHIsaLnLeuAsnSerAsnLysPAl 63
      ||| ||| .....
465 GACGCGCTTCCTCGCTTCACACACACACACACACCTC... 514
64 PheAspLysThrProGluPro 70
      ||| .....
515 CTGACGACGATCACACACCCCT 535

seq_name: qb_esc2:BF256735
seq_documentation_block:
LOCUS BF256735 844 bp mRNA EST 23-FEB-2001
DEFINITION HVSMEF0010N17f Hordeum vulgare seedling root EST library HVCNMA0007
(etiolated and unstressed) Hordeum vulgare cDNA clone
HVSMEF0010N17f, mRNA sequence.
ACCESSION BF256735
VERSION BF256735.2 GI:13118403
KEYWORDS EST
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
1 (bases 1 to 844)
Kleinbofs A., Wise R., Begum D., Fritsch D., Yu
T., Anderson H., Dale J., Henry D., Kerdouk S., Palmer M., Rambo
T., Saski C., Schwartzbeck J., Simons J., Choi D.W., Main D. and
Wood T.
Development of a genetically and physically anchored EST resource
for barley genomics
on Nov 16 2000 this sequence version replaced gi:11185848.
COMMENT:
JOURNAL:
Contact: Wang R.
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 7288
Email: rlwang@clemson.edu
Seq primer: ATTACACCTCCACACACG
High quality sequence stop: 752.
Location/Qualifiers
1..844
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/clone.lib="Hordeum
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/lab_host="TUC121"
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more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To

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order a clone see http://www.genome.clemson.edu/orders
BASE COUNT      209 a      181 c      240 g      214 t
ORIGIN

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BASE COUNT	209 a	181 c	240 g
ORIGIN			

ORIGIN

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Length: 55

Ratio: 2.109

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Percent Similarity: 58.182

Percent Identity: 38.182

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2116 ACCTATGATCTCCGCCGAGGACCTTAAGACAGCTTCAGTCAGAGCAG 21157
37 lalcauGlnlleltauglulyslelproAlaAlaAlaIleuPhaGlnPhe 53
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2116 CTTTACGAAATTAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAAT 2117
54 HlssAlaIleuAsnSerAsnIleuAsnParGlllePhaSplysPho 68
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2116 CAAATTAATTAATTAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAAT 2117
seq_name: /cgnl_7/prodata/1/ins/6b_COMB.seq:US-08-838-151A-1
seq_documentation_block:
; Sequence 1, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Hanson, Steve
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milwaukee & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Sequin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; ADDRESS: 1162 base patts
; REFERENCE/DOCKET NUMBER: US/83801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5460
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1162 base patts
; STRANDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Tomato Mottle Geminal Virus
; VECTORIAL ISOLATE: F10C10B
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 44..1127
; PUBLICATION INFORMATION:
; AUTHORS: Gilbertson, RL
; AUTHORS: Hidayat, SH
; AUTHORS: Regier, MA
; AUTHORS: Hou, YN
; AUTHORS: Maxwell, DP
; TITLE: Pseudorecombination between the infectious
; TITLE: cloned DNA components of tomato mottle and bean
; TITLE: dwarf mosaic geminiviruses.
; JOURNAL: Jour. General Virol.

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; PAGES: 23-31
; DATE: 1993
; US-08-838-151A-1
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; Ratio: 3.729 Gaps: 0
; Percent Similarity: 84.286 Percent Identity: 58.571
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; US-09-289-346a-5 x US-08-838-151A-1
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; Align seg 1/1 to: US-08-838-151A-1 from: 1 to: 1162
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; |||||
; 371 ACATGCAATGAGGAGATTTTCAGTCAGGAGGAGGAGGAGGAGGAGGAGG 420
; |||||
; 17 GCysGlnTrpSerAsnAspAlaIleuAsnParGlllePhaSplysPho 34
; |||||
; 421 CCACGATCGCTTACGATTCATATTCAGGAAAGGCTTAATTCAGATTGG 470
; |||||
; 34 YSGlnuAlaIleuGlnlleltauglulyslelproAlaAlaAlaIleu 50
; |||||
; 471 TTTCATCTCGCTTACGATTCAGGAGGAGGAGGAGGAGGAGGAGGAGG 520
; |||||
; 51 PhaeGlnPhaIleuAsnSerAsnIleuAsnParGlllePhaSplysPho 67
; |||||
; 521 TTACAAATATCATTAACATTCGCTTCATACCTTAACAGCATTCGCCAAGC 570
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; 67 TrpGlnuPro 70
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; seq_documentation_block:
; Sequence 3, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Hanson, Steve
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milwaukee & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; ADDRESS: 1162 base patts
; REFERENCE/DOCKET NUMBER: US/83801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5460
; TELEFAX: 312-616-5460

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? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? HYPOTHEetical: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Tomato Mottle Gemini Virus
? STRAIN: Florida
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1127
? PUBLICATION INFORMATION:
? AUTHORS: Gilbertson, R.L. et al.
? TITLE: Pseudorecombination between the infectious
? TITLE: Cloned DNA components of tomato mottle and bean
? TITLE: Dwarf mosaic geminiviruses.
? JOURNAL: Journal of General Virology
? PAGES: 23-31
? DATE: 1993
? US-08-838-151A-3

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? Quality: 220.00 Length: 70
? Ratio: 3.729 Gaps: 0
? Percent Similarity: 84.286 Percent Identity: 58.571

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? 17 ycygGlnThrSerAspAlaAlaIspGlyAqrsrAlaTgTgT 34
? | ||||| ||||| ||||| ||||| ||||| ||||| |||||
? 421 CCACGACGTCGCTTAATGATCATATGCAAGCAAGCGTTAAATGCAAGTTCG 470
? 34 ysgGlnAlaLeuGlnIleIleAlaGlyIstIleProAlaAlaLeu 50
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? 471 TTCACATCGCTTACGACGCTTACAGGAGAACCAACCAAGATTTCGA 520
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? ||||| ||||| ||||| ||||| ||||| ||||| |||||
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? 67 rProGlnPro 70
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? seq_name: /cgnl_7/prodata/1/lna/6b_COMB.seq:US-08-838-151A
? Patent No. 6291743
? GENERAL INFORMATION:
? APPLICANT: Stout, John T
? APPLICANT: Liu, Hang T
? APPLICANT: Maxwell, Douglas
? APPLICANT: Hanson, Steve
? APPLICANT: Anagnostis, George
? TITLE OF INVENTION: Geminiviruses
? NUMBER OF SEQUENCES: 63
? CORRESPONDENCE ADDRESS:
? ADDRESSER: Dressler, Rocky, Milnamov & Katz

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? STREET: Two Prudential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE:
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460
? INFORMATION FOR SEQ ID NO: 5:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1169 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? HYPOTHEtical: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Tomato Mottle Gemini Virus
? STRAIN: Florida
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 44..1127
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? Quality: 220.00 Length: 70
? Ratio: 3.729 Gaps: 0
? Percent Similarity: 84.286 Percent Identity: 58.571

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? 371 ACATGCAATGGAGGAGATTTCAGATCGACGCGCATCTCCCAAGSAG 420
? 17 ycygGlnThrSerAspAlaAlaIspGlyAqrsrAlaTgTgT 34
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? Sequence 7, Application US/0883151A

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1 Patent No. 6291743
2 GENERAL INFORMATION:
3 APPLICANT: Stout, John T
4 APPLICANT: Mawell, Mary
5 APPLICANT: Mawell, Douglas
6 APPLICANT: Atholust, Paul
7 APPLICANT: Hanson, Steve
8 TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
9 TITLE OF INVENTION: Genes
10 NUMBER OF SEQUENCES: 63
11 CORRESPONDENCE ADDRESS:
12 STREET: 1000 N. Lincolnway E, Katz
13 CITY: Chicago
14 STATE: Illinois
15 COUNTRY: U.S.A.
16 ZIP: 60601
17 COMPUTER READABLE FORM:
18 FILED: 1993-01-14
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: Patent Release #1.0, Version #1.30
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/838,151A
24 FILING DATE:
25 PRIORITY DATE: 800
26 CROSS-REFERENCE:
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Mueller, Lisa V
29 REGISTRATION NUMBER: 38,578
30 REFERENCE/DOCKET NUMBER: SYS801P0260
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: 312-616-5400
33 TELEFAX: 312-616-5460
34 INFORMATION: 303
35 SEQUENCE CHARACTERISTICS: 7:
36 LENGTH: 1169 base pairs
37 TYPE: nucleic acid
38 STRANDEDNESS: single
39 TOPOLOGY: circular
40 MOLECULE TYPE: DNA (genomic)
41 RECOMBINATION: NO
42 ANTI-SENSE: NO
43 ORIGINAL SOURCE:
44 ORGANISM: Tomato Mottle Gemini Virus
45 STRAIN: Florida
46 FEATURE:
47 NAME/KEY: CDS
48 LOCATION: 44..1127
49 US-08-838-151A-7
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52 Quality: 220.00 Length: 70
53 Ratio: 3.729 Gaps: 0
54 Percent Similarity: 84.286 Percent Identity: 58.571
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59 Align seq 1/1 to: US-08-838-151A-7 from: 1 to: 1169

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Patent No. 6291743
INVENTOR:
APPLICANT INFORMATION:
APPLICANT: John T
APPLICANT: Luu, Hong T
APPLICANT: Maxwell, Douglas
APPLICANT: Aniquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiviruses
TITLE OR INVENTION: Genes
NUMBER OF SEQUENCES: 63
COMPLETION DATES:
ADDRESS: Rockey, Milwaukee & Katz
SPRINT: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM compatible operating systems-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: B00
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
TELEPHONE: 312-615-5400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-615-5400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2602 base pairs
STRATEGIC ACID
TOPOLGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Geminivirus
STRAIN: Florida
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Quality: 220.00 Length: 70
Ratio: 3.729 Gaps: 0
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seq_documentation_block:
? Sequence 7, Application US/08809103b
? Patent No. 6135505
? GENERAL INFORMATION:
? APPLICANT: GROENBORN, Bruno
? TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
? TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
? NUMBER OF SEQUENCES: 17
? CORRESPONDENCE ADDRESS:
? ADDRESS: YOUNG & THOMPSON
? NUMBER: 445 South 23rd Street
? CITY: Arlington
? STATE: Virginia
? COUNTRY: U.S.A.
? ZIP: 22202
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? FILING DATE: 17-MAR-1997
? CLASSIFICATION: 800
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: FR 94.11040
? FILING DATE: 15-SEP-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: NO PCT/FR95/01192
? FILING DATE: 15-SEP-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: PATCH, Andrew J.
? REGISTRATION NUMBER: 32,925
? REFERENCE/DOCKET NUMBER: US94AL CNR TOM
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 521-2297
? TELEFAX: (703) 685-0573
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1145 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1077
? US-08-809-103b-7

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? Quality: 219.00 Length: 69
? Ratio: 3.842 Gaps: 0
? Percent Similarity: 82.609 Percent Identity: 57.971

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? Patent No. 6135505
? GENERAL INFORMATION:
? APPLICANT: GROENBORN, Bruno
? TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
? TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
? NUMBER OF SEQUENCES: 17
? CORRESPONDENCE ADDRESS:
? ADDRESS: YOUNG & THOMPSON
? NUMBER: 445 South 23rd Street
? CITY: Arlington
? STATE: Virginia
? COUNTRY: U.S.A.
? ZIP: 22202
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? FILING DATE: 17-MAR-1997
? CLASSIFICATION: 800
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: FR 94.11040
? FILING DATE: 15-SEP-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: NO PCT/FR95/01192
? FILING DATE: 15-SEP-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: PATCH, Andrew J.
? REGISTRATION NUMBER: 32,925
? REFERENCE/DOCKET NUMBER: US94AL CNR TOM
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 521-2297
? TELEFAX: (703) 685-0573
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1148 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)

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CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMMON AVAILABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentL Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/83#_151A
FILING DATE:
CLASSIFICATION: 800
ATOMIC INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38_978
REFERENCE/DOCKET NUMBER: SYS801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE INFORMATION:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGIN: GenBank
ORGANISM: Human
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
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? Patent No. 6291743
? GENERAL INFORMATION:
? APPLICANT: Stout, John T
? APPLICANT: Liu, Hang T
? APPLICANT: Maxwell, Douglas
? APPLICANT: Ahlquist, Paul
? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
? NUMBER OF SEQUENCES: 63
? CORRESPONDENCE ADDRESS: Rocky, Milnamov & Katz
? STREET: Two Prudential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: Patent Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460
? INVENTION FOR SEQ ID NO: 51:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1062 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? HYPOHETICAL: NO
? ORIGINAL SOURCE:
? ORGANISM: Bean Golden Mosaic Gemlinivirus
? STRAIN: Type II
? INDIVIDUAL ISOLATE: Guatemala
? FEATURE:
? NAME/KEY: CDS
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? Patent No. 6291743
? GENERAL INFORMATION:
? APPLICANT: Stout, John T
? APPLICANT: Liu, Hang T
? APPLICANT: Maxwell, Douglas
? APPLICANT: Ahlquist, Paul
? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
? NUMBER OF SEQUENCES: 63
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Dressler, Rocky, Milnamov & Katz
? STREET: Two Prudential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: Patent Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460
? INFORMATION FOR SEQ ID NO: 54:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1062 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? HYPOHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Bean Golden Mosaic Gemlinivirus
? STRAIN: Type II
? INDIVIDUAL ISOLATE: Guatemala
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1059
? US-08-838-151A-54

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? Quality: 218.00 Length: 70
? Ratio: 3.695 Gaps: 0
? Percent Similarity: 84.286 Percent Identity: 60.000

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Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Maxwell, Douglas

APPLICANT: Alquist, Paul

TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus

TITLE OF INVENTION: Genes

ADDRESS: 63

ADDRESS: 63

STREET: Two Prudential Plaza, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60601

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838-151A

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V

REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: SVS380LP0260

TELEPHONE: 312-616-5400

TELEPHONE: 312-616-5400

SEQUENCE CHARACTERISTICS:

LENGTH: 1183 base pairs

STRANDEDNESS: single

TOPOLOGY: circular

MODIFIED: YES (genomic)

HYPERMUTATED: NO

ANTI-SENSE: NO

ORGANISM: Bean Golden Mosaic Gemlinivirus

STRAIN: Type II Isolates

INDIVIDUAL ISOLATE: Guatemala

FEATURE:

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? NAME/KEY: CDS
? LOCATION: 1..1059
? PUBLICATION INFORMATION:
? AUTHORS: Farfa, JC
? AUTHORS: Gilbertson, RL
? AUTHORS: Morales, SJ
? AUTHORS: Alquist, P
? AUTHORS: Iontello, AO
? TITLE: Bean Golden Mosaic Gemlinivirus Type II
? TITLE: Isolates from the Dominican Republic and
? TITLE: Guatemala: Nucleotide Sequences, Infections
? JOURNAL: Phytopathology
? VOLUME: 84
? ISSUE: 3
? PAGES: 321-329
? DATE: 1994
? US-08-838-151A-43

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alignment_scores:

Quality: 218.00

Ratio: 3.695

Percent Similarity: 84.286

Percent Identity: 60.000

alignment_block:

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Sequence 45, Application US/08838151A

Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Maxwell, Douglas

APPLICANT: Alquist, Paul

TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus

TITLE OF INVENTION: Genes

ADDRESS: 63

ADDRESS: 63

STREET: Two Prudential Plaza, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60601

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.03/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: [REDACTED]
ADDRESS: [REDACTED]
REFERENCE/DOCKET NUMBER: SVS3801P0250
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 1183 base pairs
TOPLOGY: circular
STRANDEDNESS: single
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Cominivirus
CONTAINER TYPE:
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-45

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alignment_scores:
Quality: 218.00      Length: 70
Ratio: 3.695         Gaps: 0
Percent Similarity: 84.286   Percent Identity: 60.000

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alignment_block:

US-09-289-346a-5 x US-08-838-151A-45

Align seg 1/1 to: US-08-838-151A-45 from: 1 to: 1183

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1 ThrLeuValTrpGlyLysPheGlnValAspGlyArgSerAlaArgGly1 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
328 ACAATGCAATGCGAGCAATTCACACTCGACGCGATCTCCAGAGAGG 377
17 YCysGlnThrSerAsnAspAlaAlaGlnAlaLeuAsnAlaSerSerL 34
||||| ||||||| ||||||| ||||||| ||||||| |||||||
378 TCAGCAAGTCGCGACACGCTCATATGACAGAGCAACGCGATTCAGAA 427
34 YGlnGluAlaLeuGlnIleIleArgGluLysGlyIleProAlaAlaLeu 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
428 TTGAAATCTGCTTACACATATGACAGCAACGCGATTCAGAA 477
51 PheGlnPheIleAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
||||| ||||||| ||||||| ||||||| ||||||| |||||||
478 CTTCAACATCAACACATCCGTTATATCTCAACGATCTTCGTAAGT 527
67 PProGluPro 70
||||| |||||||
528 GCCGAAACCA 537

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34 ysglqiaialeandjilteileakrgiluyisllereoglulytytlan 50
|||||
2171 AAGAAAGACCCGCAATATTNAGSAGAAAATCCCAGAAATAATTA 2122
|||||
51 phealiphealialaleusnsersanleaspaaylllebaspystfh 67
|||||
87 pfecglupro 70
|||||
2071 TCCTGAACCA 2062
seq_name: gb_vl:AY029750

Loc doc documentation block:
LOCUS AY029750 2588 bp DNA circular VRL 08-MAY-2001
DEFINITION Tomato severe rugose virus DNA-A, complete sequence.
ACCESSION AY029750
VERSION AY029750.1 GI:14009278
KEYWORDS
SOURCE ORGANISM
Tomato severe rugose virus.
Tomato severe rugose virus
Virus; Eukaryota; Viridiplantae; Gemmatritidae; Begomovirus.
REFERENCE
1 (bases 1 to 2588)
Rezendez,W.L., Coulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
The full-length DNA-A nucleotide sequence of a novel
Tomato-Infecting Begomovirus, Tomato severe rugose virus, in Brazil]]
JOURNAL
TITILE Direct Submission
AUTHOR 2 (bases 1 to 2588)
Parreira,K.S. and Figueiredo,J.E.F.
Submitted (03-APR-2001) Instituto de Genetica e Biogenimica,
Universidade Federal de Uberlandia, Av. Amazonas s/n, Bloco 2E,
Salta 24, Campus Umuatema, Uberlandia, Minas Gerais 38.400-000,
Brazil]]

FEATURES
source Location/Qualifiers
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location=Tomato severe rugose virus"
/strain="Minas Gerais"
/db_xref="taxon:158463"
/country="Brazil]"
/note="Segment: DNA-A"
305..1060
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305..1060
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1060..2588
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/protein_id="AKS0360.1"
/db_xref="gi:14009282"
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YRPRIPTLRLDWDPRGCPSCQSVESRDIVSHVCYGVCSOTPKNCI THRGVG
RCVMSYLILCKNMHSEIKLNINTNSVAFVLRDRPGDPMDGNPNMPNEBPSRY
AKVKDDLRDRVMEHFPAKVGGVANSIDGLVAKPMKNNVVYRHQEGACKENHTF
EKMLLMKCHTHSNVAIETILRTFDSTN"
1060..2588
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complement(1057..1455)
/gene="AC1"
complement(1057..1455)
/gene="AC3"
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/protein_id="AKS0358.1"
/db_xref="gi:14009280"
/tranlation="MKSNTGGTLTRQAQENGNYIHEISPLRFKIINVEDPPITSRY
VYVDFVADKSLVSRVSGVSSVDSVSDVSGVSSVDSVSDVSGVSSVDSVSDVSGV
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/product="trpA"

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CD8      complement(153). .2588)
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/protein_id="AAK0361.1"
/db_xref="GI:14009283"
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SISVSGDGLTSLQDSGGSDSVHMGSLPRTNIVYQFDBE
complement(153). .2588)
/gene="AC1"
/complement(153). .2588)
/gene="AC1"
/proton_start=1
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/db_xref="GI:14009279"
/translation="MPSNRTRPOFKANKNYLVIYPKGSLSKEALSQKLMTPTCKKF
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SYVDKDIETEMEEQIDLGSGRGCGOTANDAMALNAAPSKDALI1RKLPKRL
FOHMNSMLRIFAFABERMAPPLFSSTTVWPRMONADPDYGRGAAPRPRI1ST
I1GOSRQTKRMARAGAHNI1SGHLHPNVYSNHV1NDVIDIAPY1KIKIME
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complement(217). .2434)
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/complement(217). .2434)
/gene="AC4"
/codon_start=1
/product="AC4 protein"
/protein_id="AAK0362.1"
/protein_accession="GI:14009281"
/translation="MKNGSLISTCFPNASKATPAKINOSTNSPOGOQDISITRELE
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/note="common region"

rep_origin
BASE COUNT    660 a   525 c   598 g   805 t
ORIGIN

alignment_scores:
Quality: 291.00          length: 70
Ratio: 4.619            gaps: 0
Percent Similarity: 90.000 Percent Identity: 78.571

alignment_block:
US-09-289-346A-6 x AN029150/rev ...

Align seg 1/1 to reverse of: AN029150 from: 1 to: 2588

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2258 ACTATGCAATTSGGGGCATATTCACAAACGACAGCAGACTGTCCADAGGGCG 2209
17 yChgInrThSerGaaATTCACAAACGACAGCAGACTGTCCADAGGGCG 34
2208 TTGGCAGACAGCTAACGATGCTGCCGCAGACAGCCTTGAAACGACCTTCCA 2159
34 yAgJugJuaLaLeuMD1le1laArgGluYu1a1erProGJu1yTYrIeu 50
|||||
2158 AAGAAGTGCCTCTGCAATAATATCCGGGACAACCTACGGAAAAATTYYTA 2108
51 PhcAlaPhcAlaAlaLeuInsSerAlaLeuAspArgIlePhcAspTrf 67
|||||
2108 TTTCATTTACACAACTTAATAGTATTATTTAGATATGATATTTACAGGCG 2059

seq_name: qb.v1:AF291705
seq_documentation_block:
LOCUS       AF291705        2622 bp    DNA    circular    VRL
DEFINITION  Tomato Etquose mosaic virus DNA-A, complete sequence.
ACCESSION   AF291705
VERSION     AF291705.1 GI:10281644

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SOURCE	Tomato rugose mosaic virus.
ORGANISM	Tomato rugose mosaic virus.
REFERENCE	1. Ueda, S.H.N. 2622.
AUTHORS	Fernandes,J.J., Fontes,E.P.B., Brommannchenkel,S.H., Carvalho,M.G., Zambolim E.M. and Zerbini,F.M.
TITLE	Molecular Cloning and Characterization of Tomato rugose mosaic virus (TRMV), a Begomovirus Isolated from Tomatoes at Triangulo Mineiro, Minas Gerais, Brazil
JOURNAL	Unpublished
RAPID COMMUNICAT	9 (bases 1 to 2622)
REMARKS	Recombinant virus used by Cecchini,F.M.
AUTHOR'S ADDRESS	direct submission
JOURNAL TITLE	Submitted (31-Jul-2000) Dept. de Fitopatologia, Universidade Federal de Viçosa, Av. P.H. Rolfs, s/n - Centro, Viçosa, MG 36571-000, Brazil
FEATURES	
source	Location/Organism 1..2622 /organism="Tomato rugose mosaic virus" /db_xref="taxon 134599"
gene	/country="Brazil": Uberlandia, Triangulo Mineiro, Minas Gerais".
CDS	/note="Previously referred to as Tomato geminivirus Uberlandia TRMV" 1..227 common region" complement(240..392) /gene="AC4" complement(240..392) /gene="AC4" /codon_start=1 /product="putative AC4 protein" protein_id="AGI5548.1" /db_xref="GI 10281645" /translation="MIVPSFSLIKVWVDMMVIDLPKRLILAVCYLSDLSIEHPI DLKTITVEIFSGCAEYIAEHNLKAKHGHTISITVPDQEGGVNVLOLVLIHP VLONHIAMNETETIHVCNWTTCIGADNHLLTSMKDVIETLKTSIPFMFTNNPNI GGSHIRPYTGCPGHNGVYPSGLGWPMNSCTMRINMAPALRCKSHVAPMGIALRHRT ELKYTVALLTYSVAWLSSVSSNAS" 342..1097 virus" length=1097 /gene="AV1" /note="CP" /codon_start=1 /product="capsid protein" protein_id="AGI5545.1" /db_xref="GI 10281645" translation="MKPKDIPIMASTSKISGVYNVSRAECGRSRNKATDWNPRI YKDAKKDKPPSPSTPTDPSTPLPDPEPVTPSTPTDPPDTPTDPRPTDPPDMGTENPDEPST RFCSYSTLIKIMDEDIELKHNTSNMAWLYPRDRPGTMDQSGVFNMKNPESST AYTKDAIPRGVRYEPAAVKVGQVANSDELAKRPKNVVNNHVYHQEGKYENHT ENMLILVMCHASNNPVATLETITFYFDISTN" complement(1094..1492) /gene="AC3" complement(1094..1492) /note="RNA" /codon_start=1 /product="replication-enhancer protein" protein_id="AGI5548.1" /db_xref="GI 10281648" translation="MSRSPTTELTAHQENGVTMETISNPLPFKNWEDLTITRRVR NYTLAFAARALKRKALNDLQWITSIPASSMTYLNFMTILLTIIDLGAVISY NNVLAFAARALKRKALNDLQWITSIPASSMTYLNFMTILLTIIDLGAVISY complement(11239..1628) /gene="AC2" complement(1239..1628) /gene="AC2" /note="rTAP"
gene	
CDS	

[illegible]

[illegible]

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seq_documentation_block:      17-JUN-1999
LOCUS               AF131071    1345 bp        DNA                VRL
DEFINITION          Tomato mild mottle geminivirus segment A replication-associated
ACCESSION            AF131071
VERSION              AF131071.1
KEYWORDS             tomato mild mottle geminiviruses; ssDNA viruses; Geminiviridae; unclassified Geminiviridae.
REFERENCE            1 (bases 1 to 1345)
AUTHORS             Nakhla M.K., Mejia-Ll., Ramirez, P., Karakashian, J.P., Doyle, M.M. and
TITLE               Molecular characterization and DNA-based detection methods for
                    vegetable-infecting geminiviruses in Central America
JOURNAL             Unpublished
AUTHORSHIP           2 (bases 1 to 1345)
PUBLISHED           Nakhla M.K., Mejias-G., Kamal,S. and Maxwell,D.P.
FEATURES             Submitted (25-FEB-1999) Plant Pathology, University of Wisconsin-Madison, 1830 Linden Dr., Madison, WI 53706-1598, USA
SOURCE              1. Genbank/Qualifiers
                    /organism="tomato mild mottle geminivirus"
                    /isolate="IH96-IH5K"
                    /specimen_voucher="HS"
                    /db_xref="taxon:92943"
                    /chromosome="segment_A"
                    /clone="PHN15A"
                    /country="Jordan"
                    /notes="Obtained from a Jordan plant collected in Dec. 1996 by M.K. Nakhla and D.P. Maxwell."
                    complement<1..(678)
gene                /gene="rep"
                    /note="ac1"
CDS                 complement<1..(678)
                    /gene="rep"
                    /note="rep protein"
                    /codon_start=location-associated protein"
                    /protein_id="AA033471.1"
                    /db_xref="GI:4928224"
                    /translation="MPLPKRKLINSKYVLPYIPGSLSKRETELKQLLRLLNPTRNKTK
IKIAELHEDEGVYLIVLDPFGKFQTNREFDLYVSRTHTPRPWCAKSSTDVNW
XNDGDGTIDTBEGRFDIGDKSRGGCGQTANDMAALANSSKEEMRIKKLPKSFY
FOVMKSSNNIRIFAKAEAPRPPEFLPSFTVPDEMWDITDFGKAVAAPRRIS
IITHEDSNR"
rep_origin          678..692
gene                1001..11345
                    /gene="cp"
                    /note="av1"
CDS                 1001..11345
                    /gene="cp"
                    /note="cp"
                    /note="capsid protein"
                    /codon_start=1
                    /product="coat protein"
                    /db_xref="GI:4928225"
                    /db_xref="GI:4928225"
                    /translation="MKKDADWIRMLSATPVYSRSSNSVPPDGCKARFSSSMANBPM
VRPFETFRVTSAGDVRCRGKPCQCTSPQRBDLSHTCKVCISTDYRNCRNGTHRVGR
RFQSVSYLVICW"
BASE COUNT         329 a       289 c       313 g       414 t
ORIGIN
alignment_scores:
Quality:   272.00     Length:   70
Ratio:     4.250      Gaps:    0
Percent Similarity:  91.429     Percent Identity:  72.857

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         APMSPSTIRPGIDSPGVNSRADLLEENSRLLTTPQRL"

BASE COUNT      359 a      296 c      327 g      401 t

ORIGIN

alignment_scores:
  Quality: 268.00      Length: 68
  Ratio: 4.467      Gaps: 0
  Percent Similarity: 88.235      Percent Identity: 79.412

alignment_block:
  us-09-289-346a-6 x AF288227/rev ..

Align seg 1/1 to reverse of: AF288227 from: 1 to: 1383

1  ThlaaValTRPGIYGLuphegiInValaIpdlYARGSerAlaAqGLYGL 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
902 ACCATCACCTGGGGGTGAATTCACAGCTGCAGCGGCAATCTCTACAGCAC 853
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 YCYGSLINThSerASpApAlaAlaIaIaIaIaIaIaIaIaIaIaIaIa 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
852 CGACGACGCTGTACAGACGACGACGACGACGCTGTACAGACGACGCTGTAC 803
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 YSGIUGIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
802 AAGAGACCTGCTTCCAAATATATACAGGAGGAGAACTCCTCAAAATATTTA 753
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 PhaaIaIaPhaaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
752 TTTCATTTCATTAATTTAGCTTGAATTTAATTAATTAATTTATTTCTCTCC 703
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 PPO 68
   |||
702 ACCT 699

seq_name: gb_v1:AF104036
seq_documentation_block:
  LOCUS      AF104036      2828 bp      DNA      circular      VR1      05-AUG-1999
  DEFINITION  Sweet potato leaf curl virus DNA A, complete sequence.
  ACCESSION  AF104036
  VERSION    AF104036.1 GI:5702158
  KEYWORDS   sweet potato leaf curl virus.
  ORGANISM   sweet potato leaf curl virus; geminiviridae; Begomovirus.
  AUTHORS    Lotrakul,P., Valverde,R.A., Clark,C.A., Sim,J. and De la Torre,R.
  TITLE      Detection of a geminivirus infecting sweet potato in the United
  States
  JOURNAL    Plant Dis. 82, 1253-1257 (1998)
  REFERENCES 1 (bases 1 to 2828)
             Lotrakul,P. and Valverde,R.A.
             Cloning of a DNA-A-like genomic component of sweet potato leaf curl
             virus: nucleotide sequence and phylogenetic relationships
  JOURNAL    Molecular Plant Pathology On-Line (1999)
  REMARK     http://www.bppp.org.uk/mpool/1999/04210trkul/
  AUTHORS    Lotrakul,P. and Valverde,R.A.
  TITLE      Detection of a geminivirus infecting sweet potato in the United
             States
  JOURNAL    Plant Pathology and Crop Physiology, 1998
             Lotrakul,P. and Valverde,R.A.
             Louisiana State University, 302 Life Sciences Bldg., LSU, Baton
             Rouge, LA 70803, USA
  FEATURES   Location/Qualifiers
             source
               1..2828

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CDS      /organism="sweet potato leaf curl virus"
         /db_xref="taxon:100755"
         /chromosome="DNA A"
         /country="USA"
         /gene="AC4"
         /note="AL4"
         /product="AC4"
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         /protein_id="AA047169.1"
         /db_xref="GI:5702159"
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         VPSRSGVRKRRKGRDIPKGCVCGRVDYERKMDHPHTGCVASDPTKSTGLHL
         GRACVKSNGIDKRWMDADNARKHGHNTITWLLIKDRNRKGLPLNGDITPDYER
         TTRALIKDRNRKGLKSTKSTSGPTSKKQALLKFFKGLTINHTYINRKEATKE
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         /complement(1232..1678)
         /note="AC2"
         /codon_start=1
         /product="AC2"
         /db_xref="GI:5702162"
         /translation="MSNPISGVRKRCRKTOTPIPRBAKAKKRVPEORTIYWKCCGCS
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         /note="AC1"
         /product="AC1"
         /db_xref="GI:5702163"
         /translation="MAMPKRRIDAKNPPTTPGCSISRENCIAOLLITQPSNKKRYI
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         YVDKDDGTITWGFQVQGRSARGGQOTANAAADALNMGSKENALQIIEKLYPKYLL
         OPHIN.VSNLDITWGFQVQGRSARGGQOTANAAADALNMGSKENALQIIEKLYPKYLL
         IGGSRIGVYKRSKIDPINTYICRHLDSKYSNSMNTVTDVNTOLKRNKPKG
         AAGTITKQNGTSTKINLSTHSTESSRIHQHQCSSDVTYPSQANCCPRHNGEN
         AAGTITKQNGTSTKINLSTHSTESSRIHQHQCSSDVTYPSQANCCPRHNGEN"
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BASE COUNT      741 a
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alignment_scores:
    Quality: 268.00      Length: 68
    Ratio: 4.467         Gaps: 0
    Percent Similarity: 88.235      Percent Identity: 79.412

alignment_block:
US-09-289-346A-6 x AF104036/rev ...
Align seq 1/1 to reverse of: AF104036 from: 1 to: 2828

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|||||
2354  ACCATCACCTGGGGGCAATTCACGTCGACGGCGCATCTGCTACGACGACG
17  ycySGIrtHserNarSPdAlaAlaIaIaIaLaaAlaIaSerGrl 34
|||||
2304  CCACCAAGTCTACACACACACACACACACACACACACACACACACACAC
34  ySLIGLIALaLeuAlaLeIaIaIaArgSLuLySLaIlePGGtLySLyTLau 50
|||||
2254  AGAAGCTGCTCTGGCAAAATATACGACGAAAGAAATCCCTGAGAAATATTA
51  PhealPheAlaAlaLeuAlaSerNarLeuAlaPgrTlPheASpLySth 67
|||||
2204  TTTTCATTTCATATTTATTTATTTATTTATTTATTTATTTATTTATTTTCCTC
67  rPTro 68
|||||
2154  ACCT 2151      1

seq_name: gb_vl:SG067926
seq_documentation_block:
LOCUS      SG067926          554 bp      DNA           VRL          28-JAN-1996
DEFINITION slide golden mosaic geminivirus Rep protein (AC1) gene, partial cds
ACCESSION  U67926.1 GI:1546801
VERSION    U67926.1 GI:1546801
KEYWORDS   slide golden mosaic virus,
SOURCE     slide golden mosaic virus,
ORGANISM   slide golden mosaic virus.
REFERENCE  1 (bases 1 to 554)
AUTHORS    Roye M.E., McLaughlin W.A., Naktha, N.K. and Maxwell, D.P.
TITLE      Genetic diversity among geminiviruses associated with the weed
          Commelina sp. Macropodium laticyroides, and Wissadula
          plumiflora (Plant Dis. 81, 1251-1258 (1997))
          2 (bases 1 to 554)
AUTHORS    Roye M.E., McLaughlin W.A. and Maxwell, D.P.
TITLE      Direct Submissions
JOURNAL    Submitted (23-AUG-1996) Plant Pathology, University of Wisconsin,
          1630 Linden Drive, Madison, WI 53706-1598, USA
FEATURES
SOURCE
location/Qualifiers
    /organism="slide golden mosaic virus"
    /strain="Jamaica"
    /isolate="Jamaica, May 1993"
    /db_xref="taxon:51034"
    /note="DNA A component"
    complement(1..554)
    /gene="AC1"
gene

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[illegible]


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protein_id=AB082606.1
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464 PDS_1165
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/db_xref="gi:2583074"
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RICREHLENGEPIHYILOEKRCCTNNELDLWPTSGTHHNGLQASSDIKS
KIDRIENGEPIHYILOEKRCCTNNELDLWPTSGTHHNGLQASSDIKS
DYNLSNPSMADPMKPMPNRPPLTSSTTNPHNQEMSHSDIFOSKANIGHIISIIL
IEDSRCTGMNAKR".
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BASE COUNT 350 a 264 c 256 g 295 t

ORIGIN

alignment_scores:

	Quality:	251.00	Length:	70
Percent Similarity:	90.000	Percentage Identity:	67.143	

alignment_block:
US-09-289-346A-x AF026553 ..

Align seq 1/1 to: AF026553 from: 1 to: 1165

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1   TTTGGTAATTCGTGTCUAGCCTCAATAAGCCGTCATCATAGTGCGT 17
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
791 ACCATGGAATTGGGGATGTTGCCCATGATGACCAGAAGACTCTCGAGATGG 840

17   YCSGIoThTerAsanSpAlaAlaAlaAlaAlaAlaAlaAlaAlaSeSertc 34
     | | | | | | | | | | | | | | | | | | | | | | | | | | | |
841 GCACAGAACCCCAAGACGACGCCTCGCGAGCCCTTAAACATCTGSAACA 890

34   YSGLUGLIAnonchItleIEtArgSIUYgJyleprocihiySYrTLen 50
     ||| | | | | | | | | | | | | | | | | | | | | | | | | |
891 AGGAAGAACCCCAAGAAACNTAAAAGAGXGACTTCGCCGAAACATTTCYT 940

51   PhaeAlaPhaeAlaAlaIsauSnSerAsnLeuAlaSPArTILEpheaspysth 67
     || | :: | : | : | : | : | : | : | : | : | : | : | : |
941 TTTCAGTATCTCAATCACATTCACAGTAGCTCGATGAGATTTCATCAAGAGC 950

67   rProGUptro 70
     |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
991 TTCGAATTCG 1000
```

seq_name: qb.v1.AB001315

seq_documentation_block:
LOCUS AB001315.1 gb1 300 bp DNA
DEFINITION Tobacco leaf curl virus CI and CA genes, clone YOKOHAMA3-1, partial
and complete cds.
ACCESSION AB001315
VERSION AB001315.1 GI:3798714
KEYWORDS
SOURCE ORGANISM Ool.K.

Tobacco leaf curl virus [isolate,YOKOHMA3,
SPECIES:Tobacco ripidictum mikiroot] DNA, clone:YOKOHAMA3-1,
partial sequence.
VINUSES: sgNM viruses; Geminiviridae; Begomovirus.

1 (bases 1 to 570)
ool.k.

Direct submissions
Submitted (19-FEB-1997) to the DDBJ/EMBL/Genbank databases.
Accession No.: Kyushu University, Department of Biology: 6-10-1
E-mail:koshi@kshu.ac.jp
(E-mail:koshi@kshu.ac.jp; Tel:+81-92-642-2624,
Fax:+81-92-642-2645)
2 (bases 1 to 570)
ool.k., Ohshima,S., Ishii,T. and Yahara,T.
Molecular phylogeny of geminivirus infecting wild plants in Japan

JOURNAL	J. Plant Res.	110,	247-257	(1997)
FEATURES				
Source	Location/Qualifiers			
	1..570			
	/organism="Eubacterium coli curl virus"			
	/db_xref="taxon:"YOKOHAMA3-1"			
	/specific_host="Escherichia coli"			
	/db_xref="taxon:67762"			
	/clone="YOKOHAMA3-1"			
gene	complement(1..570)			
	/gene="C1"			
CDS	complement(<1..>570)			
	/cds_start=1			
	/protein_id="BAA34033.1"			
	/db_xref="gi:4456541"			
	/translation="EPALSLQININTPNKLYIKITRELFHEDSPHLAVLADGPKRYK KNMFFPDLSTRTRAKSHIFNFGARSSSDVSTIDDDTETWGTQIDRNSKGSG DNNNAICAFKSSSKSAVALATIKELFKLPDIPDYHNIAINSMDIRFAPLVLCPTP VAGASAKSSANAKSNWEM"			
gene	complement(231..488)			
	/gene="C4"			
CDS	complement(231..488)			
	/gene="C4"			
	/cds_start=1			
	/protein_id="BAA34034.1"			
	/db_xref="gi:4788715"			
	/translation="MEALLISMPFCSSKANNTKNDTSWTGPDPQHLSIRTFRELNE APPSSTPISTRTNSGGHSRRTEVLDEMAKRLTHTVQR"			
BASE COUNT	141 a	121 c	126 g	182 t
ORIGIN				

```

Alignment scores:
Query ID: 248_00 Length: 85
Accession: Q96780.1 Gaps: 1
Percent Similarity: 71.765 Percent Identity: 58.824

Alignment block:
US-09-285-346A-6 x AB001315/rev ...

Align seg 1/1 to reverse of: AB001315 from: 1 to: 570

      1   ThrlcvalvtppdglvuplgiwspicgltvgrserAlargsglyel 17
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
     318 ACGETCAATGGGAAACATTCCAGAACCTCACCAGGAAGTGTCTGAGGAG 269
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
     17 yrcslntlrstsrAmaspAlalalagualAlcamaAlaserSerL 34
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
     268 CTGCAGAAATCTTCACAGACCATCTCGAGGCCCTTAATCGAAATCTCA 219
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
     34 yscIguAlaleugdllellrArggilulyllrProglutryIdau 50
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
     218 AGCGAMAGCATTGCMATMTATVGGGMAAACCTCCCTMAAGATTATA 169
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
     51 PhealPhealAlalaAsASerAsnIle..... 63
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
     168 TTTCATATCATATTMTATATGATTTGATGGATTTTTTCTCTCC 119
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
     64 .....Phesplysrhp 68
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
     118 GTTGAGAGCTTTTGTTCCTTCCTTCACAGGCTACCTCTGATCAAGTTC 69
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
     68 roslu 69
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
     68 CAGA 64

```

```

2216 ACCTAATGATGCTCCGAGGAGCCCTTAATGACAGTTCACGTGACGAC 2167
37 lalenclnlllellaarglulysileptcglulysyltylcphealaape 53
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
2166 CTTTACGATATATGAGAACACCCCAATGAAATTTATTTTCAATXT 2117
54 AAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspIysrthPro 68
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
2116 CATATTATTAATGTATTTATGATGATTTT.....ACACCT 2078

seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NAL1995.DAT:AA084371
seq_documentation_block:
ID: AA084371 standard; DNA: 434 BP.
XX
XX AA084371:
XX
XX 19-AUG-1995 (first entry)
XX
XX Gemini virus-specific polyribozyme-E target sequence.
XX
XX polyzyme target sequence: polyribozyme-F:
XX tomato leaf curl virus: Rm1 cleavage; tomato transgenic plant;
XX virus disease-resistance: ss.
XX
XX Tomato leaf curl virus.
XX
XX Key location/Qualifiers
XX misc_feature 13..43
XX /note= "R1 cleavage site"
XX misc_feature 26..28
XX /tag= b
XX /note= "R1 cleavage site"
XX misc_feature 312..342
XX /note= "R2 cleavage site"
XX misc_feature 325..327
XX /note= "R2 cleavage site"
XX /tag= d
XX /note= "R2 cleavage site"
XX misc_feature 384..414
XX /tag= e
XX /note= "R3 target sequence"
XX misc_feature 397..398
XX /tag= c
XX /note= "R3 cleavage site"
XX
XX W05030404-A.
XX
XX 02-FEB-1995.
XX
XX 22-JUL-1993: 93W0-EP01946.
XX
XX 22-JUL-1993: 93AU-0047014.
XX
XX 22-JUL-1993: 93W0-EP01946.
XX
XX (BIOC-) BIOCEN SA
XX (GSK-) COMOKOMKALTH SCT 6 IND RES ORG.
XX
XX Baudino S, Comeau D, Dry IB, Gruber V, Lence P;
XX Mason J, Rezaiian MA, Ridsden JE, Rezaiian MA:
XX
XX WPI: 1995-075232/10.
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX and disease caused by cleaving target virus sequence,
XX useful for preparing resistant plants; esp tomatoes.
XX
XX Example 10: Fig 11b: 90pp: English.
XX
XX The sequence is a tomato leaf curl virus target sequence for
XX polyribozyme-E, which hybridizes to and cleaves the sequence and
XX thereby reduces replication, infection and/or assembly of the virus

```

```

CC substantially. The ribozyme may be expressed in a transgenic plant,
CC e.g. tomato, to confer virus disease-resistance.
XX
XX Sequence 434 BP: 126 A; 86 G; 91 G; 131 T; 0 other:
XX
XX alignment_scores:
XX      Quality: 220.00      length: 65
XX      Ratio: 3.667
XX      Percent similarity: 70.588      Percent identity: 52.941
XX
XX alignment_block:
XX US-09-289-346a-6 x AA084371
XX
XX Align seg 1/1 to: AA084371 from: 1 to: 434
XX
XX      1 ThrlenuValrTrrGlyGlnPhaGlnValAspGlyYAsrSerAlaArgGlyG 17
XX      ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
XX      95 ACCCTCGAATGGGAGGAGTTTCAGATCGATGACATGCTCAGAAAGGCGG 144
XX
XX      17 YGSGlInrThSerAsnAspAlaAlaIaGlnAlaLeuAsnAsrSrl 34
XX      ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
XX      145 AACACATGCGCATGACAGCTTACGCCGCGCTTACACTGGAATGA 124
XX
XX      34 YSGlInclAlaLeuGlnlIlelAargGlnLysIleProGlnIysrYrleu 50
XX      ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
XX      195 ACTCAGAGCTCTTACAGCTTCCTTAGGAGATTAAGCCCTCAGAGATTATGTT 244
XX
XX      51 PheAlaPheAlaAlaLeuAsnSerPheAlaAspThrIle 63
XX      ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
XX      245 TTACATTTCATATTTAACTAATGATTAAGATTTTACAGCTTC 294
XX
XX      64 .....PheAspIysrThp 68
XX
XX      295 GTTSGAGCTTATGCTTCTCCTTTTATCTTCTTCTTGTGATGAGATTC 344
XX
XX      68 rGcln 69
XX      |||||
XX      345 CAGAA 349
XX
XX seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NAL1995.DAT:AA084372
XX seq_documentation_block:
XX ID: AA084372 standard; DNA: 479 BP.
XX
XX AA084372:
XX
XX 19-AUG-1995 (first entry)
XX
XX Gemini virus-specific polyribozyme-F target sequence.
XX
XX polyzyme target sequence: polyribozyme-F:
XX tomato leaf curl virus: Rm1 cleavage; tomato transgenic plant;
XX virus disease-resistance: ss.
XX
XX Tomato leaf curl virus.
XX
XX Key location/Qualifiers
XX misc_feature 13..46
XX /tag= a
XX /note= "R4-R5 target sequence"
XX misc_feature 58..60
XX /tag= b
XX /note= "R4 cleavage site"
XX misc_feature 81..83
XX /tag= c
XX /note= "R5 cleavage site"
XX misc_feature 356..366
XX /tag= d
XX /note= "R2 target sequence"
XX misc_feature 370..372
XX /tag= c
XX /note= "R2 cleavage site"

```



```

401 TCCGTTGAGGCTTATGTTCTCTCTTTTATGCTTCTTTGATCGAG 450
67 hProcln 69
|||||
451 TTCCAGGA 458
seq_name: /cgnl_8/gcdata/geneseq/geneseq/NA1996.DAT:AA12904
seq_documentation_block:
ID: AA12904 standard; DNA: 1080 BP.
XX AA12904:
XX
XX 07-NOV-1996 (first entry)
XX
XX Sardinian tomato yellow leaf curl virus mutated CI gene (K227A).
XX
XX Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
XX modification; mutation; viral replication; deficient; inhibition;
XX Sardinian isolate; SYVICV; transgenic plant; P-loop; CI gene;
XX All gene; dominant negative phenotype; ss.
XX
XX Sardinian tomato yellow leaf curl virus.
XX
XX Key Location/Qualifiers
XX CDS 1..1080
XX /tag= a
XX /product= Rep (K227A)
XX /note= "encodes Rep protein in which wild-type Lys
XX at position 227, i.e. within the NTP-
XX binding site, is replaced by Ala"
XX
XX M09608573-A1.
XX
XX 21-MAR-1996.
XX
XX 15-SEP-1995: 95MO-FR01192.
XX
XX 15-SEP-1994: 94FR-0011040.
XX
XX (CNRS ) CENT NAT RECH SCI.
XX
XX Gronenborn B:
XX
XX WPI: 1996-179947/18.
XX
XX P-PSDB: AAR88870.
XX
XX Procd. of virus-resistant transgenic plants - using mutated genomic
XX sequence from phytopathogenic DNA virus
XX
XX Disclosure: Fig 13; 93pp; French.
XX
XX
XX Mutation of consensus amino acids in the NTP-binding site of
XX geminivirus Rep protein is used to produce replication deficient
XX viruses. The mutated viral nucleic acid is used for producing
XX transgenic plants that are resistant to, or tolerant of, the native
XX virus. The present invention provides a method for producing such
XX protein from the Sardinian isolate of tomato yellow leaf curl virus
XX (SYVICV) in which the wild-type Lys227 residue has been changed to an
XX Ala residue; transgenic Nicotiana benthamiana plants generated by a
XX transformation with the mutated virus were found to be resistant to
XX SYVICV, i.e the mutation results in a dominant negative phenotype.
XX
XX Sequence 1080 BP; 355 A; 248 C; 210 G; 267 T; 0 other:
XX
XX
XX Alignment_scores:
XX Quality: 210.00 Length: 69
XX Ratio: 3.750 Gaps: 0
XX Percent Similarity: 81.159 Percent Identity: 56.522
XX
XX

```

```

Alignment_block:
us-09-289-346a-6 x AA12904
Align seg 1/1 to: AA12904 from: 1 to: 1080
2 LeuValTrgcluphoclunylasgclyvargserAlaAragclxlycy 18
|||||
331 CTTCGATGCGGTACTTTCGACATCCAGCGCAGATCTGCTAGCGGACACA 380
18 scliThrSerAsnspAlaAlaAlaGluAlaLeuAsnAlaSerSerLyg 35
|||||
381 ACAGACAGCCACAGACGCTTACGCAAGACGATTAACGAGGAGTAACT 430
35 lnguAlaLeuGlnlletlAArgGluysrleProclnlySTYTLAmphe 51
|||||
431 GCGAGCGCTTCATGTAAATTAAGATAGAGCGCTTAGAGATTACGTTCTA 480
52 AlaPheAlaAlaLeuAsnSerAsnLeuAspArglePheAspLystrPr 68
|||||
481 CATTTTCATTAATATTAATTAATTAATTAATTAATTAATTAATTAATTA 530
68 ocLupro 70
|||||
531 GCGACCT 537
seq_name: /cgnl_8/gcdata/geneseq/geneseq/NA1996.DAT:AA12905
seq_documentation_block:
ID: AA12905 standard; DNA: 1080 BP.
XX AA12905:
XX
XX 07-NOV-1996 (first entry)
XX
XX Sardinian tomato yellow leaf curl virus mutated CI gene (K227H).
XX
XX Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
XX modification; mutation; viral replication; deficient; inhibition;
XX viral resistance; geminivirus; tomato yellow leaf curl virus;
XX Sardinian isolate; SYVICV; transgenic plant; P-loop; CI gene;
XX All gene; ss.
XX
XX Sardinian tomato yellow leaf curl virus.
XX
XX Key Location/Qualifiers
XX CDS 1..1080
XX /tag= a
XX /product= Rep (K227H)
XX /note= "encodes Rep protein in which wild-type Lys
XX at position 227, i.e. within the NTP-
XX binding site, is replaced by His"
XX
XX M09608573-A1.
XX
XX 21-MAR-1996.
XX
XX 15-SEP-1995: 95MO-FR01192.
XX
XX 15-SEP-1994: 94FR-0011040.
XX
XX (CNRS ) CENT NAT RECH SCI.
XX
XX Gronenborn B:
XX
XX WPI: 1996-179947/18.
XX
XX P-PSDB: AAR88871.
XX
XX Procd. of virus-resistant transgenic plants - using mutated genomic
XX sequence from phytopathogenic DNA virus
XX
XX Disclosure: Fig 13; 93pp; French.
XX
XX Mutation of consensus amino acids in the NTP-binding site of
XX

```

```

FD 21-MAR-1996.
xx
PF 15-SEP-1995: 95WC-FR01192.
xx
xx 15-SEP-1994; 94FR-0011040.
xx
PA (CNRS ) CENT NAT RECH SCL.
xx
PI Gromehorn B:
xx
DR WPI: 1996-179947/18.
xx
DR P-PSDB: AAO8072.
xx
PF Proba. of virus-resistant transgenic plants - using mutated genomic
sequence from phytopathogenic DNA virus
xx
PS
PS Disclosure: Fig 13: 93pp. French.
xx
xx
CC Mutation of consensus amino acids in the NTP-binding site of
CC geminivirus Rep protein is used to produce replication deficient
CC viruses. The mutated viral nucleic acid is used for producing
CC transgenic plants resistant to the virus. The resulting transgenic
CC virus. The present invention encodes a mutant form of the Rep (or CI)
CC protein from the sardinian isolate of tomato yellow leaf curl virus
CC (STYLCV) in which the wild-type Lys227 residue has been changed to an
CC Arg residue; transgenic Nicotiana benthamiana plants generated by
CC transformation with the mutated virus were not resistant to STYLCV.
CC In contrast, plants transformed with a virus in which Lys227 had been
CC replaced by Ala were found to be resistant.
xx
xx
SO Sequence 1080 BP; 356 A; 247 C; 210 G; 267 T; 0 other:

alignment_scores:
Quality: 210.00 Length: 69
Ratio: 3.750 Gaps: 0
Percent Similarity: 81.159 Percent Identity: 56.522

alignment_block:
US-09-289-346A-6 x AMT12906 ..

Align seq 1/1 to: AAT12906 from: 1 to: 1080

2 LeuValaIreGluGluIuphGhisIuValaSpIyATsSerAlaIArgIyelycy 18
   ||| ||||| |||||
331 CTTGAAATGAGGGGATCTTCACAGATCGACGACGACATCTCTAGGAGGAGCA 380
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
18 sGIrThsSerGAGGAPAlaAlaAlaAlaAlaAlaAlaAlaAlaSerLysd 35
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
381 ACAGACGACGACGACGACCTTACCGGACGACGACATTAACGACGACGACG 430
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
35 IuGluAlaIreGluIuIleIleIleArgIduIyIleIreGluIuIyryrLeuphe 51
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 GCGAGGCGCTTTGATGTATATTAAGATATTAACGCGCTCTAGGACATTAAC 480
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52 AlaPheAlaIleAlaAlaSerSerLysAlaSpArgIleIleAlaSpLyGthr 68
   ||| :||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTCATTAATATTAATTAAGTATTAATTAAGATTAAGGTTTCACGCGCC 530
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

seq_name: /cgnl_8/gcugata/gemiseq/gemiseq/MAL1995.DMT-AAO84378
seq_documentation_block:
ID AAO84378 standard: DNA; 1695 BP.
xx
xx AAO84378.
xx
xx
xx 19-AUG-1995 (first entry)
xx
xx Tomato yellow leaf curl virus DNA sequence.
xx

```



```

2236 GGAGGTTCCTTGGTTGCTCCATTTTCATTACCTCATATGCATCAATTCCTCG 2187
        69      11
        II     69
2186 NA 2185

seq_name: /cgnl_B/gcgdata/geneseq/geneseq/NM1997.DNF:AA793291
seq_documentation_block:
ID   AA793291 standard; DNA; 1062 bp.
AC   AA793291;
CD   ;
XX   27-Apr-1998 (first entry)
DE   Bean golden mosaic geminivirus CI mutant ORF BGAC221.
XX   ;
XX   Geminivirus; BGWV; CI gene; transposant mutation;
XX   RW transgenic plant; disease resistance; ss: cyclic; circular.
XX   ;
XX   Bean golden mosaic virus type II isolate Guatemala.
XX   ;
XX   KM09739110.AL.
XX   ;
XX   23-Oct-1997.
PD   ;
PE   15-Apr-1997; 97MO-US06300.
XX   ;
XX   16-Apr-1996; 96US-0015517.
XX   ;
PA   (SEMI-) SEMINIS VEGETABLE SEEDS INC.
PA   (MISC.) WISCONSIN ALUMNI RRS FOUNO.
PI   ;
PI   Ahlquist PC, Hanson SF, Liu HT, Maxwell DP, Strout JT;
DR   P-FSDB; AAM34333.
XX   ;
PT   Transgenic plants expressing geminivirus ACI and CI wild-type and
PT   mutant genes - have increased resistance to geminivirus infection
PT   e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
PT   golden mosaic geminivirus
XX   ;
XX   ;
XX   Claim 13: Page 107-109; 132pp; English.
XX   ;
XX   This DNA sequence comprises construct BGAC221 that codes for a
XX   C transdominant lethal mutant (see AAM34333) of the CI protein (see
XX   AAM34338) of bean golden mosaic virus (BGWV). It was obtained by
XX   Kunzel mutagenesis of the wild-type CI gene (see AA793314). CI is
XX   required for replication. The invention involves production of
XX   transgenic plants containing DNA that negatively interfere in trans
XX   wild-type or mutant sequences that negatively interfere in trans
XX   with the function of the CI gene product. These transgenic plants are
XX   resistant to BGWV, tomato mottle virus or tomato yellow leaf
XX   curl virus (see AA793282-93) and encode polypeptides (see AAM34324-35)
XX   that have mutations in the highly conserved polyprotein(s) and/or the
XX   NTP-binding domains.
XX   ;
SQ   Sequence 1062 bp; 339 A; 245 C; 219 G; 259 T; 0 other; *

alignment_scores:
Quality: 206.00          Length: 70
Ratio: 3.552             Gaps: 0
Percent Similarity: 82.857 Percent Identity: 57.143

alignment_block:
US-09-289-346A-6 x AA793291 ..
Align seg 1/I to: AA793291 from: 1 to: 1062

1 ThrtleValTrtpdlyGtlupheGclValAspcglvArSseAlargrglcyol 17

```

[illegible]

```
CC AA04338) of bean golden mosaic virus (BGWV). It was obtained by  
CC kinet mutagenesis of the wild-type CI gene (see AAT93314). CI is  
CC required for replication. The invention involves production of  
CC transgenic plants containing DNA comprising genomes viruses CI or ACI  
CC with specific deletions in the coat protein coding region. Such transgenic  
CC plants are resistant to viral infection. The ACI/C1 genes are  
CC especially from BGWV, tomato mottle virus or tomato yellow leaf  
CC curl virus (see AAT93282-93) and encode polypeptides (see AA04324-35)  
CC that have mutations in the highly conserved DNA-binding and/or the  
CC NIP-binding domains.  
XX  
XX Sequence 1062 BP; 340 A; 245 C; 219 G; 258 T; 0 other:  
XQ  
XN  
  
alignment_scores:  
Quality: 206.00 Length: 70  
Ratio: 3.552 gaps: 0  
Percent Similarity: 82.857 Percent Identity: 57.143  
  
alignment_block:  
US-09-289-346v.6 x AAT93293 ...  
  
Align seg 1/I to: AAT93293 From: 1 to: 1062  
  
1 ThrLeuValTrrpDlGtUpHscGlnAlaAspCylArSserAlaArgLysl 17  
|||||  
328 ACAATCGAATGGAGCAATTTCACAGCTGCAGCGCACATCTCGAAAGAGGCG 377  
|||  
17 CygGluInTrbSerAsnMetAlaAlaIleGluAlaMetAsnGlySerThr 34  
| |||||  
378 TCAGCGACTCTCCACACACTCATATTCGAAGAAGCATTAACGCCAGATTTCAA 427  
|||  
34 YsgGlucIuAlaIleAndGllTelLeArgGJulysIIleProSluArgTyrlleu 50  
|||||  
428 TTGAATCTTGCTGTGGCAAAATTTGAGAGGAAACAACGCAAGAATTAGCGTC 477  
|||||  
51 PheAlaPheAlaIleAlaMetSerAsnMetAlaAspArgIllePheAspArgTh 67  
::: |||||  
478 CTTCACACATCCACACATCACTCTTAACTTCGACAGCGATCTCTCCAAAGT 527  
|||||  
67 rProGIuPro 70  
528 GCCGCAACCA 537  
  
seq_name:=cogn_L8/gsgodola/geneseq/geneseq/NM1997.DMT.AAT93314  
seq_documentation_block:  
ID AAT93314 standard: DNA; 1183 BP.  
XX  
XX AAT93314;  
AC  
XX 27-APR-1998 (first entry)  
XX  
XX Bean golden mosaic geminivirus CI open reading frame.  
DE  
XX  
XX Geminivirus: BGWV; CI gene: transdominant mutation.  
KW transgenic plant; disease resistance; ss; cyclic; circular.  
XX  
XX Bean golden mosaic virus type II isolate Guatemala.  
XX  
XX  
XX Key location/Qualifiers  
PI 1..1062  
FT CDS /*tag= a  
XX  
XX MO9739110-AI.  
XX  
XX 23-OCT-1997.  
XX  
XX 15-APR-1997; 97NM-US06300.  
XX  
XX 16-APR-1996; 96US-C015517.  
XX
```


PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
 PA (MISC.) WISCONSIN ALUMNI RES FOUND.
 XX
 XX Abiquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT.
 XX MPI: 1997-526447/48.
 XX P-PSDB: AAM34338.
 XX
 XX Transgenic plants expressing geminivirus AC1 and CI wild-type and
 XX mutant genes - have increased resistance to geminivirus infection
 XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
 XX golden mosaic geminivirus
 XX
 XX Example 5; Page 100-102; 132pp; English.
 XX
 XX This genomic DNA sequence includes the open reading frame (ORF) of
 XX the wild-type CI gene of bean golden mosaic virus (BGWV), a
 XX geminivirus that has a monopartite genome. The CI protein (see
 XX AAM34338) is required for replication. The wild-type CI ORF was
 XX subjected to Kunkel mutagenesis (see AAT93290-93). The invention
 XX comprises a set of transgenic plants that have been created using
 XX CI or AC1 wild-type or mutant sequences that negatively interfere
 XX in trans with geminiviral replication during infection. Such
 XX transgenic plants are resistant to viral infection. The AC1/CI
 XX genes are especially from BGWV, tomato mottle virus or tomato
 XX yellow leaf curl virus (see AAT93282-93) and encode polypeptides
 XX (see AAM34324-35) that have mutations in the highly conserved
 XX DNA-nicking domain and/or the NTP-binding domains.
 XX
 XX Sequence 1183 BP; 372 A; 276 C; 248 G; 287 T; 0 other;

alignment_scores:
 Quality: 206.00 Length: 70
 Ratio: 3.352 Gaps: 0
 Percent Similarity: 82.857 Percent Identity: 57.143

alignment_block:
 US-09-289-346a-6 x AAT93314

Align seg 1/1 to: AAT93314 from: 1 to: 1183

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1 1ThleuvalITGCIYCIUpheGlnValaApGlyAAGSerAlaATGtGtC 17
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  17 CYGGINthSerAspAlaAlaGtAlaAlaLeuAspAlaSeS 34
  | |||||
378 TCAGCAGTCTGCCAAGCATCATGCAAGCAAGCATTTAAAGCAATTC 427
  34 YGCIuGlnAlaLeuGlnIleLeaGtGluYgIIlePGGtGtYtLeu 50
  |||||
428 TTGAATCTGCTTCACATATGGAAGAGAACCCAAAGATTTACGTC 477
  51 PheAlaPheAlaAlaLeuAspSerAspArgIIlePheAspArg 67
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478 CTTCAACATCCACATCCGTTCTTAATTCGAGACGATCTCGTCAAG 527
  67 PheGluGlu 70
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528 GCGGAAACCA 537
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seq_name: /cgnl_8/gcdata/geneseq/geneseq/NA1997.DAT:AAT93290

seq_documentation_block:
 ID AAT93290 standard: DNA: 1183 BP.

AC AAT93290:

DT 27-APR-1998 (first entry)

DE Bean golden mosaic geminivirus CI mutant gene.

KW Geminiviruses: BGWV, CI gene; transdominant mutation;
 KW transgenic plant; disease resistance; ss: cyclic; circular.
 XX
 XX Bean golden mosaic virus type II isolate Guatemala.
 XX
 XX Key Location/Qualifiers
 XX CDS 1:1062
 XX FT //tag- a

W09739110-AI.

23-OCT-1997.

15-APR-1997; 97NO-US06500.

16-APR-1996; 9605-0015517.

PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
 PA (MISC.) WISCONSIN ALUMNI RES FOUND.

XX Abiquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT.
 XX MPI: 1997-526447/48.
 XX P-PSDB: AAM34332.

DR Transgenic plants expressing geminivirus AC1 and CI wild-type and
 DR mutant genes - have increased resistance to geminivirus infection
 DR e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
 DR golden mosaic geminivirus
 DR
 DR Claim 13; Page 103-105; 132pp; English.

XX This DNA sequence comprises construct BGAC190 that codes for a
 XX control mutant (see AAM34332) of the CI protein (see AAM34338) of bean
 XX golden mosaic virus (BGWV). It was obtained by Kunkel mutagenesis
 XX of the wild-type CI gene (see AAT93314). CIs are required for
 XX replication of geminiviruses. CIs of geminiviruses that infect
 XX plants containing geminiviruses CI or AC1 wild-type or
 XX mutant sequences that negatively interfere in trans with
 XX geminiviral replication during infection. Such transgenic plants
 XX are resistant to viral infection. The AC1/CI genes are especially
 XX from BGWV, tomato mottle virus or tomato yellow leaf curl virus (see
 XX AAT93282-93) and encode polypeptides (see AAM34324-35) that have
 XX mutations in the highly conserved DNA-nicking and/or the NTP-binding
 XX domains.
 XX
 XX Sequence 1183 BP; 371 A; 277 C; 249 G; 286 T; 0 other;

alignment_scores:

Quality: 206.00 Length: 70
 Ratio: 3.352 Gaps: 0
 Percent Similarity: 82.857 Percent Identity: 57.143

alignment_block:
 US-09-289-346a-6 x AAT93290

Align seg 1/1 to: AAT93290 from: 1 to: 1183

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1 1ThleuvalITGCIYCIUpheGlnValaApGlyAAGSerAlaATGtGtC 17
  |||||
328 ACATGCAATGGGGCAATTCAGATCGACGCCAGATCGCAAGAGAG 377
  17 CYGGINthSerAspAlaAlaGtAlaAlaLeuAspAlaSeS 34
  | |||||
378 TCAGCAGTCTGCCAAGCATCATGCAAGCAAGCATTTAAAGCAATTC 427
  34 YGCIuGlnAlaLeuGlnIleLeaGtGluYgIIlePGGtGtYtLeu 50
  |||||
428 TTGAATCTGCTTCACATATGGAAGAGAACCCAAAGATTTACGTC 477
  51 PheAlaPheAlaAlaLeuAspSerAspArgIIlePheAspArg 67
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478 CTTCAACATCAGACATCCGTTCTATCTCGAACGGATCTCTCAAGT 527
 67 FPGCJupro 70
 528 GCCGAAACA 537

seq_name: /cqn1_8/gcgdata/geneseq/geneseq/NA2000.DAT:AAA94700

seq_documentation_block:
 ID AAA94700 standard: DNA: 1651 bp.

AAA94700:

15-JAN-2001 (first entry)

PMRG 2288 35S-rep gene cassette.

XX Gemlinivirus: DNA-A: gemlinivirus replication inhibitor; ac3 gene;
 XX transgenic plant; antiviral; gene therapy; bean golden mosaic virus;
 KM BGMY; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CMV; ds.
 OS Bean golden mosaic virus.
 OS Cauliflower mosaic virus.
 OS Alfalfa mosaic virus.
 OS Synthetic.

US6118048-A.

12-SEP-2000.

PF 24-APR-1998: 98US-0065999.

PR 25-APR-1997: 97US-0044925.

XX (WISC) WISCONSIN ALUMNI RES FOUND.

XX WPI: 2000-610861/58.

XX Genetic construct comprising a mutant gemliniviral rep gene, useful for
 PT producing a plant resistant to gemliniviral infection -

XX Example: Column 15-16; 14pp: English.

XX The present sequence is a 35S-rep gene cassette comprising the rep gene
 CC of bean golden mosaic virus (BGMY)-GA cloned downstream of the CMV
 CC 35S promoter and an alfalfa mosaic virus (AMV) leader sequence. The
 CC sequence was integrated into pBSII-KS+ to produce a rep gene expression
 CC vector. DNA-nicking domain mutations may be incorporated into rep gene
 CC to produce a genetic construct that acts as a trans-dominant inhibitor
 CC of gemlinivirus replication. When expressed in a plant cell, this
 CC inhibitory construct inhibits gemlinivirus replication and gemlinivirus
 CC genetic constructs that include sequences containing a portion of the
 CC ac3 gene in addition to the trans-dominant inhibitor exhibit increased
 CC efficiency and broadened specificity of inhibition of gemliniviral
 CC replication. gemliniviruses are one of the greatest constraints on
 CC production of important crops, including cassava, beans, cowpeas,
 CC peppers, tomatoes and cotton. The effects of the virus can be overcome
 CC by using the genetic construct.

XX Sequence 1651 bp; 517 A; 393 C; 342 G; 399 T; 0 other:

alignment_scores:

Quality:	206.00	Length:	70
Gap:	2.85310		
Percent Similarity:	82.857	Percent Identity:	57.143

alignment_block:

US-09-289-346a-6 x AAA94700

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 17 TCGGCTThSerAaSPAlAlaAGlAlaLeuAaSPAlaSer 34
 ||||:||||:|||||||||||||||||||||||||||||||||
 846 TCAACAGTCTGCCAAGCTCTCATATGCAAAAGCATTTAAAGCAATTCCA 895
 34 YSGlGAlaLeuGlnlleleAAGgluYslllePrgGluYsTYrleu 50
 ||||:||||:|||||||||||||||||||||||||||||||||
 896 TTGAATCTGCTTCAACAAATTGAAGAAACAAACGCAAAAGATTACGTC 945
 51 PheAlaPheAlaAlaLeuAaSPAlaLeuAaSPAlaLeuAaSPAlaLeu 67
 ||||:||||:|||||||||||||||||||||||||||||||||
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 67 TPGCJupro 70
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 996 GCCGAAACA 1005

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142 AACATCAT 150

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seq_documentation_block: 414 bp mRNA EST 17-OCT-2000
DEFINITION AV741296 CB Homo sapiens CDNA clone CBCCJ06 5', mRNA sequence.
ACCESSION AV741296
VERSION AV741296.1 GI:10858877
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 414)
AUTHORS Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
Chen,S., Mao,M. and Chen,Z.
Homo sapiens CB library cDNA clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: mbsnl@ms.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Shanghai Hi-Tech Park, Pudong.
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1. 414
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BASE COUNT 109 a 100 c 119 g 84 t 2 others
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Ratio: 1.892 Gaps: 2
Percent Similarity: 69.811 Percent Identity: 32.075

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US-09-289-346a-6 x AV741296 ..
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1 AATTCGCGCGCGCTGCAGTACGCTGCAGAAAGCAGACAGCGCTTC 50
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25 AAlaGluAlaLeuAsnAlaSerGtGluGluAlaLeuGlnIleTaa 42
|||||
51 CACAGAGGCGCTACACCGCGCGCTCCGCTGCAGCAGTCTCTAGTG 99
|||||
42 TgGluGlyAlleProGluTyrLeuPheAlaPheAlaAlaLeuAsn 56
|||||
100 .....ATCCCTGAAAGTTCCAGCATATTTTGGAGTACTCAGCACGC 141
59 AsnLeuAsp 61
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142 AACATCAT 150

seq_name: gb-est1:AV739224

seq_documentation_block: 525 bp mRNA EST 17-OCT-2000
DEFINITION AV739224 CB Homo sapiens CDNA clone CBRR04 5', mRNA sequence.
ACCESSION AV739224
VERSION AV739224.1 GI:10856805
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 525)
AUTHORS Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
Chen,S., Mao,M. and Chen,Z.
Homo sapiens CB library cDNA clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: mbsnl@ms.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Shanghai Hi-Tech Park, Pudong.
FEATURES
source
1. 525
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/clone_id="CB"
/lisue_type="cord blood"
/lab_host="BW25.8"
/note="Vector: plasmid; site:1; EcoRI: The insert is
cloned randomly with the EcoRI digestion"
BASE COUNT 135 a 135 c 157 g 96 t 2 others
ORIGIN

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Quality: 68.50 Length: 64
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Percent Similarity: 59.375 Percent Identity: 28.125

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US-09-289-346a-6 x AV739224 ..
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9 GCGCTGACCGCGCGCTGCAGCAGCTGCAGAAAGCAGACAGAG 58
|||||
20 .....ThsrsrAspAlaAlaAlaGluAlaLeuAana 31
|||||
59 GACAGCGCTGCAGAAAGCAGACAGACGCGCTCCACAGAGGCGCTTACG 108
|||||
31 TAsrSerGtGluGluAlaLeuGlnIleTleArgIcGlyTyr 47
|||||
109 CCGCGCGCTTCTGTCGACGCACTCTCTAGTG.....ATCCCTGA 149
|||||
48 TAsrTyrLeuPheAlaPheAlaAlaLeuAsnSerAlaLeuAsn 61
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seq_name: gb-est1:AV731422

seq_documentation_block:

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[illegible]

KEYWORDS CSS.

SOURCE Trypanosoma brucei.

ORGANISM Trypanosoma brucei.
Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1) Besser, N., To 572).

AUTHORS Gerard, C., Leech, V., de Jong, P., Ollivier, M., Melville, S., Donelson, J., Fraser, C. & Adams, M.

TITLE Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library

JOURNAL Other:GSSS: Sheared DNA-51M3-TR

COMMENT Other:GSSS: No. 1999-06-18
Department of Biomedical Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel.: 301 838 0200
Fax: 301 838 0208
Email: nelsayed@tigr.org

FEATURES Locations:
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared DNA library. The clones were sequenced by PCR using primers distributed through ATCC. Sheared DNA end sequences search page: <http://www.tigr.org/db/bdb/tbdb/>.
Seq primer: M3-forward
Class: shotgun.

FEATURES Location/Qualifiers
1..572
/organism="Trypanosoma brucei"
/strain="Pep027/GUTat 10.1"
/db_xref="taxon:5693"
/clone="Sheared DNA-51M3"
/clove.lib="Sheared DNA"
/note="vector: pUC18; site:1: SmaI; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (Pep027/4) was mechanically digested with SmaI (100bp fragments). The v + l method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999)." Press. 1999."

RANGE COUNT 115 a 118 c 180 g 159 t

ORIGIN

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Ratio: 2.513 Gaps: 0
Percent Similarity: 87.097 Percent Identity: 38.710

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US-09-285-346A-x AQ950848 ..

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11 GYAGrserAlAAgClyGCyGciThrsSeruaaspAlAAaAgcI 27
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341 AGCGTGTCCTCGACACTCTCCGACGACGACCATGCAAGTCATG 383

seq_name: qb_gss:AQ947513

seq_documentation_block:
587 bp DNA
LOCUS AQ947513
DEFINITION Sheared DNA-49M17.TF Sheared DNA Trypanosoma brucei genomic clone
Accession Number: AF0947513

Accession AF0947513

Fri Jan 4 09:38:57 2002

us-09-289-346a-6.p2n.rst

Page 9

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1 2 LeuValTrpGlyGlyJuphGcInAlaIAspGlyArgSerAlaArgGlyGlyC 18
2 331 CTTGAATGGGGCTACTTTCCAGTGCAGGAGGAGCTCCTGATGGGAGGCA 380
3 18 sGltThrSerAspAlaAlaIaGAlaAlaIleuAsnAlaSerSerLeu 35
4 381 ACAGACACCGACGACCTTACGACGAAAGGACATTTAGCCGACGAGATGT 430
5 35 LucIAlaIeugInIleIleArgGlyValIleProGluValSerIleuPhe 51
6 431 CCGAGCGCTCTTGATGCTAAATTAAAGATACGGCTCTAGAGATTACGTTCA 480
7 52 AlaPheAlaIaIeuaSerAsnLeuAspArgIlePheAspValThrP 68
8 481 CATTTCATATATTAATTAATGATTATTAAATTAAGCTTTTTCACAGCGCTCC 530
9 68 ocLupro 70
10 531 GGCACCT 537
11
12 seq_name: /cgnl_7/prodate/1/ins/6A_COMB_seq-US-08-809-103B-1
13
14 seq_documentation_block:
15 1. Sequence 1, Application US/080809103B
16 2. Patent No. 6133505
17
18 GENERAL INFORMATION:
19 1. APPLICANT: GRONENBORN, Bruno
20 2. TITLE OF INVENTION: PHOTOPHOTOCENIC DNA VIRUS RESISTANT
21 3. NUMBER OF INVENTIONS: 17
22 4. ADDRESS: YOUNG & THOMPSON
23 STREET: 745 South 23rd Street
24 CITY: Arlington
25 STATE: Virginia
26 COUNTRY: U.S.A.
27
28 ZIP: 22202
29
30 COMPUTER READABLE FORM:
31 1. OPERATING SYSTEM: IBM PC/XT/AT/PS/486
32 2. SOFTWARE: Patentin Release #1.0, Version #1.30
33
34 CURRENT APPLICATION DATA:
35 1. APPLICATION NUMBER: US/08/809,103B
36 2. FILING DATE: 17-MAR-1997
37
38 CLASSIFICATION: 800
39 1. PRIOR APPLICATION DATA:
40 2. APPLICATION NUMBER: FR 94,11040
41 3. FILING DATE: 15-SEP-1994
42
43 PRIOR APPLICATION NUMBER: WO PCT/FR95/01192
44 1. APPLICATION NUMBER: WO PCT/FR95/01192
45 2. FILING DATE: 15-SEP-1995
46
47 ATTORNEY/AGENT INFORMATION:
48 1. NAME: PATCH, Andrew J.
49 2. REGISTRATION NUMBER: 32,925
50 3. REFERENCE/DOCKET NUMBER: US94AL CNR TOM
51 4. TELEPHONE: (703) 521-2295
52 5. TELEFAX: (703) 685-0573
53
54 INFORMATION FOR SEQ ID NO: 1:
55 1. SEQUENCE CHARACTERISTICS:
56 LENGTH: 1148 base pairs
57 TYPE: nucleic acid
58 STRANDEDNESS: double
59 2. SOURCE: Linear
60 3. MOLECULE TYPE: DNA (genomic)
61
62 NAME/KEY: CDS
63
64 LOCATION: 1..1077
65
66 US-08-809-103B-1

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 Quality: 210.00 Length: 69
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 Percent Similarity: 81.159 Percent Identity: 56.522

US-09-289-346a-6 x US-08-809-103B-1

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seq_documentation_block:
? Sequence 3, Application US/08809103B
? Patent NO. 6133505
? GENERAL INFORMATION:
? APPLICANT: GROWNBORN, Bruno
? TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
? NUMBER OF SEQUENCES: 17
? CORRESPONDENCE ADDRESS:
? ADDRESSER: YOUNG & THOMPSON
? STREET: 745 South 23rd Street
? CITY: Arlington
? STATE: Virginia
? COUNTRY: U.S.A.
? ZIP: 22202
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentio Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? FILING DATE: 17-MAR-1997
? CLASSIFICATION: 800
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: FR 94.11040
? PRIORITY DATE: 15-SEP-1994
? PRIOR APPLICATION NUMBER: NO PCT/FR95/01192
? FILING DATE: 15-SEP-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: PATCH, Andrew J.
? REGISTRATION NUMBER: 32,925
? REFERENCE/DOCKET NUMBER: US94AL CNR TOM
? TELEPHONE: (703) 521-2297
? TELEFAX: (703) 685-0573
? TELEX: 248425 EMBON
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1150 base pairs

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TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE: CDS
 LOCATION: 1..1077
 US-08-809-103B-3

alignment_scores:
 Quality: 210.00 Length: 69
 Ratio: 3.750 Gaps: 0
 Percent Similarity: 81.159 Percent Identity: 56.522

US-09-289-346a-6 x US-08-809-103B-3

Align seg 1/1 to: US-08-809-103B-3 from: 1 to: 1150

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52 AlaPheAlaIleuAsnSerAsnLeuAspArgIlePheAspLysThr 68
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481 CATTTTCATATAATATGATTAATTTAGATTAAGTTCCTCCAGTCCCTCC 530
68 scLupPro 70
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531 GGCACCT 537

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? APPLICANT: GROWNBORN, Bruno
? TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
? NUMBER OF SEQUENCES: 17
? CORRESPONDENCE ADDRESS:
? ADDRESSER: YOUNG & THOMPSON
? STREET: 745 South 23rd Street
? CITY: Arlington
? STATE: Virginia
? COUNTRY: U.S.A.
? ZIP: 22202
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentio Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? FILING DATE: 17-MAR-1997
? CLASSIFICATION: 800
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: FR 94.11040
? PRIORITY DATE: 15-SEP-1994
? PRIOR APPLICATION NUMBER: NO PCT/FR95/01192
? FILING DATE: 15-SEP-1995
? ATTORNEY/AGENT INFORMATION:

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```

? NAME: PATCH, Andrew J.
? REGISTRATION NUMBER: 32,925
? REFERENCE/DOCKET INFORMATION: US94AL CNR TOM
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 248425 EMBON
? TELEFAX: (703) 685-0573
? FILING DATE: 09/08/93
? INFORMATION FOR SEQ ID NO: 5:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1150 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1077
? US-08-809-103b-5

alignment_scores:
? Quality: 210.00 length: 69
? Ratio: 3.750 gaps: 0
? Percent Similarity: 81.159 Percent Identity: 56.522

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US-09-289-346a-6 x US-08-809-103b-5 ..
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381 acnagacgacacgcttgcgacgacacgcttgcgacgacgacgacgac 430
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||||| ||||| ||||| ||||| ||||| ||||| |||||
431 ccgagcgtcttgatgtaattaaagattagccctgcagattcgtctca 480
52 alphealalaleuanaserasnleuaspargylepheasplysthrp 68
481 ctttctcaataatataatgtaatttgattgattgatttcagagcgctcc 530
68 oclupro 70
|||
531 gccacgt 537

seq_name: /cgnl_7/prodata/1/lna/6b_CONB.seq:US-08-838-151A-48
seq_documentation_block:
? Sequence 48, Application US/08838151A
? Patent No. 6291743
? GENERAL INFORMATION:
? APPLICANT: Scout, John T
? APPLICANT: Liu, Hang T
? APPLICANT: New, Douglas
? APPLICANT: Ahlquist, Paul
? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
? NUMBER OF SEQUENCES: 63
? CORRESPONDENCE ADDRESSES:
? ADDRESS: Dressler, Rocky, Milinow & Katz
? STREET: 400 Prudential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk

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? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? FILING DATE: 09/08/93
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5460
? TELEFAX: 312-616-5460
? INFORMATION FOR SEQ ID NO: 48:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1062 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Bean Golden Mosaic Geminivirus
? STRAIN: Type II
? INDIVIDUAL ISOLATE: Guatemala
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1059
? US-08-838-151A-48

alignment_scores:
? Quality: 206.00 length: 70
? Ratio: 3.582 gaps: 0
? Percent Similarity: 82.857 Percent Identity: 57.143

alignment_block:
US-09-289-346a-6 x US-08-838-151A-48 ..
Align seq 1/1 to: US-08-838-151A-48 from: 1 to: 1062

1 thleuvaltrpqluphcdlnvalaspolyatgseralagrglycyl 17
||||| ||||| ||||| ||||| ||||| ||||| |||||
328 acaatcgatgggacattccatcgatcgacgacgacgacgacgacgag 377
17 cygscinttserasnspalalalagialaleuanalaserseet 34
||||| ||||| ||||| ||||| ||||| ||||| |||||
378 tgcacgctgcgacgacgacgacgacgacgacgacgacgacgacgac 427
34 vsgulalalaleuglnleilearglnlysllpepoglulystyleau 50
||||| ||||| ||||| ||||| ||||| ||||| |||||
428 ttgaaatcgccctgcacatvttsaagcaagacacgacgacgacgac 477
51 phealphealaleuanaserasnleuaspargylepheasplysthrp 67
||| :||| :||| :||| :||| :||| :||| :|||
478 cttcagacacgacacgacgacgacgacgacgacgacgacgacgac 527
67 ptcgclupro 70
|||||
528 gccgacgac 537

seq_name: /cgnl_7/prodata/1/lna/6b_CONB.seq:US-08-838-151A-51
seq_documentation_block:
? Sequence 51, Application US/08838151A
? Patent No. 6291743
? GENERAL INFORMATION:
? APPLICANT: Scout, John T
? APPLICANT: Liu, Hang T
? APPLICANT: New, Douglas
? APPLICANT: Ahlquist, Paul

```

```

? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
? TITLE OF INVENTION: Genes
? NUMBER OF SEQUENCES: 63
? CORRESPONDENCE ADDRESSES: Rocky, Milamov & Katz
? ADDRESS: 200 Prudential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460
? INFORMATION FOR SEQ ID NO: 51:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1062 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? RECOMBINATION: NO
? HYPOTHEetical: NO
? ORIGINAL SOURCE:
? ORGANISM: Bean Golden Mosaic Geminivirus
? STRAIN: Type II
? INDIVIDUAL ISOLATE: Guatemala
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1059
? US-08-838-151A-51

alignment_scores:
? Quality: 206.00 Length: 70
? Ratio: 3.552 Gaps: 0
? Percent Similarity: 82.857 Percent Identity: 57.143

alignment_block:
US-09-289-346a-6 x US-08-838-151A-51 ..
Align seq 1/1 to: US-08-838-151A-51 from: 1 to: 1062

1 ThTLeuValTPrGtYgIuPhGnInValAaSpGtIYAgsSerAlaArgGtIgcI 17
|||||
328 ACATGCAATGGGAGCAATTCGATGAGCAAGGCGATTCGCAAGAGAGAG 377
17 YCysGtInThSerAsnAspAlaAlaGtInAlaAlaLeuAsnAlaSerGtL 34
|||||
378 TCAGCAGTCCGACAGCAGCATATGCAAGAGGCAATTAAAGCGAGATTCCA 427
34 YsGtInGtAlaLeuGnInTlGtIeaArgIaYsTlIeProGtYuYsTylEu 50
|||||
428 TTGAGATCTGCTTGCACATATGTAAGAGAGAACACGACGAAAGATTACGTC 477
53 PhAlaAlaPhAlaAlaLeuAsnSerGtInLeuAsnGtAlaTlIePhaAspTlYTh 67
|||||
478 CTCACATGACACATACGCTTCTATCTCCAGCGAGATTCGTCACAAAGT 527
67 rProGtUpPro 70

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528 GCCGAGACCA 537
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seq_name: /cgn1_7/ptodata/1/lna/66.COMB.seq:US-08-838-151A-54
seq_documentation_block:
? Sequence 54 Application US/088380151A
? Patent No. 6291743
? GENERAL INFORMATION:
? APPLICANT: Stout, John T
? APPLICANT: Liu, Hang T
? APPLICANT: Maxwell, Douglas
? APPLICANT: Arizqust, Paul
? CORRESPONDENCE ADDRESSES: Transgenic Plants Expressing Geminivirus
? TITLE OF INVENTION: Genes
? NUMBER OF SEQUENCES: 63
? CORRESPONDENCE ADDRESS:
? ADDRESSER: Dressler, Rocky, Milamov & Katz
? STREET: Two Prudential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460
? INFORMATION FOR SEQ ID NO: 54:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1062 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? HYPOTHEtical: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Bean Golden Mosaic Geminivirus
? STRAIN: Type II
? INDIVIDUAL ISOLATE: Guatemala
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1059
? US-08-838-151A-54

alignment_scores:
? Quality: 206.00 Length: 70
? Ratio: 3.552 Gaps: 0
? Percent Similarity: 82.857 Percent Identity: 57.143

alignment_block:
US-09-289-346a-6 x US-08-838-151A-54 ..
Align seq 1/1 to: US-08-838-151A-54 from: 1 to: 1062

1 ThTLeuValTPrGtYgIuPhGnInValAaSpGtIYAgsSerAlaArgGtIgcI 17
|||||
328 ACATGCAATGGGAGCAATTCGATGAGCAAGGCGATTCGCAAGAGAGAG 377

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17 YCYGcInThrSerAsnAspAlaAlaIaGlnAlaLeuAsnAlaSecSerL 34
1  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
378 TCACACATCTGCACACACATCTATTCAGACAGCATTAACCAAGATTCA 427
34 YGcInGlnAlaLeuGlnIleIleAlaGlnAlaGlyIleProGluYrTyrLeu 50
1  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
428 TTAGATCTCCCTTGACATATTCAGACAGGAGAACCAACCAAGATTTCGTC 477
51 PheAlaPheAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspYrTyr 67
1  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
478 CTTCAACATCAACACATCCGCTCTATATCTCGACAGCATTCCTGCACAACT 527
67 PTCGAGUPro 70
1  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
528 GCCGAGACCA 537

seq_name: /cogn1_7/ptodata/1/lna/68_COMB.seq:US-08-838-151A-43

seq_documentation_block:
/ Sequence 43, Application: US/08838151A
/ Feature: 1, 2, 3, 4
/ INTERNAL INFORMATION:
/ APPLICANT: Scout, John T
/ APPLICANT: Luu, Hang T
/ APPLICANT: Maxwell, Douglas
/ APPLICANT: Ahlquist, Paul
/ APPLICANT: Hanson, Steve
/ TITLE OF INVENTION: Transgenic Plants Expressing GeminiInflavirus
/ NUMBER OF SEQUENCES: 63
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Dressler, Rocky, Milomov & Katz
/ STREET: Two Prudential Plaza, Suite 4700
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: U.S.A.
/ ZIP: 60601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/838-151A
/ FILING DATE:
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mueller, Lisa V
/ REGISTRATION NUMBER: 38,978
/ REGISTRATION/DOCKET NUMBER: SV63801P0260
/ TELEPHONE: 312-616-5400
/ TELEFAX: 312-616-5400
/ INFORMATION FOR SEQ ID NO: 43:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1183 base pairs
/ TYPE: nucleic acid
/ TOPOLOGY: single
/ RECOMBINATION: none
/ MOLECULE TYPE: DNA (genomic)
/ HYDROTHERMAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Bean Golden Mosaic GeminiInflavirus
/ STRAIN: Type 11 Isolates
/ TISSUE: Individual Isolates: Guatemala
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..1059
/ PUBLICATION INFORMATION:
/ AUTHORS: Faria, JC
/ AUTHORS: Gilbertson, RL
/ AUTHORS: Hanson, SP

```

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/ AUTHORS: Morales, RJ
/ AUTHORS: Ahlquist, P
/ AUTHORS: Iomello, AO
/ AUTHORS: Maxwell, D
/ TITLE: Bean Golden Mosaic GeminiInflavirus Type 11
/ TITLE: Guatemala: Nucleotide Sequences, Infections
/ TITLE: Pseudorecombinants, and Phylogenetic Relationships
/ JOURNAL: Phycopathology
/ VOLUME: 84
/ ISSUE: 3
/ PAGES: 321-329
/ DATE: 1984
/ US-08-838-151A-43

alignment_scores:
Quality: 206.00 Length: 70
Ratio: 3.552 Gaps: 0
Percent Similarity: 82.857 Percent Identity: 57.143

alignement_block:
US-09-289-346a-6 x US-08-838-151A-43 ..
Align seq 1/1 to: US-08-838-151A-43 from: 1 to: 1183

1 PThLeuValTyrGlyGlnPheGlnAlaAspGlyArgSerAlaArgGlyGyl 17
1  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
328 ACATATCGAATGCGACATCTCAATCGACATCGACATCTCGACAGAGAG 377
17 YCYGcInThrSerAsnAspAlaAlaIaGlnAlaLeuAsnAlaSecSerL 34
1  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
378 TCACACATCTGCACACACATCTATTCAGACAGCATTAACCAAGATTCA 427
34 YGcInGlnAlaLeuGlnIleIleAlaGlnAlaGlyIleProGluYrTyrLeu 50
1  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
428 TTAGATCTCCCTTGACATATTCAGACAGGAGAACCAACCAAGATTTCGTC 477
51 PheAlaPheAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspYrTyr 67
1  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
478 CTTCAACATCAACACATCCGCTCTATATCTCGACAGCATTCCTGCACAACT 527
67 PTCGAGUPro 70
1  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
528 GCCGAGACCA 537

seq_name: /cogn1_7/ptodata/1/lna/68_COMB.seq:US-08-838-151A-45

seq_documentation_block:
/ Sequence 45, Application: US/08838151A
/ Feature: 1, 2, 3, 4
/ INTERNAL INFORMATION:
/ APPLICANT: Scout, John T
/ APPLICANT: Luu, Hang T
/ APPLICANT: Maxwell, Douglas
/ APPLICANT: Ahlquist, Paul
/ APPLICANT: Hanson, Steve
/ TITLE OF INVENTION: Transgenic Plants Expressing GeminiInflavirus
/ NUMBER OF SEQUENCES: 63
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Dressler, Rocky, Milomov & Katz
/ STREET: Two Prudential Plaza, Suite 4700
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: U.S.A.
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:

```


STREET: One South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/065,999
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27,386
 REFERENCE/DOCKET NUMBER: 950296,94754
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-251-5000
 TELEFAX: 608-251-9180
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1651 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOTIF TYPE: DNA (genomic)
 US-09-065-999-6

alignment_scores:
 Quality: 206.00 Length: 70
 Ratio: 3.552 Gaps: 0
 Percent Similarity: 82.857 Percent Identity: 57.143

alignment_block:

US-09-289-346a-6 x US-09-065-999-6 ..

Align seq 1/1 to: US-09-065-999-6 from: 1 to: 1651

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1 1Thleuvaltrfgyclupheginalapqlyavgsrslatarglycl 17
   |||
796 ACATCGATGGGACATTCGATCGGACATTCGACAGGAG 845
   |||
17 ycgslnthserasnaspalalalaculalaleuasnalaser 34
   |||
846 TCAGCAGCTGGCCACGACATCATGCAACAGCCATTAAAGCAGATTC 895
   |||
34 ycgslnualaleugdlialalagqluysileptoculuytytleu 50
   |||
896 TTGATCTGCTTCACATATTCGAGGACAGACACGAAAGATTACCTC 945
   |||
51 Phealaphelialaleuasnserasnleuaspavgllephaaplysth 67
   |||
946 CTTCAACATCAACATCTCGTCTTAATCTGACGAGCATCTTCGCAAGT 995
   |||
67 pfcgclupro 70
   |||
996 GCCGGACCA 1005
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seq_name: /cgnl_7/prodata/1/lna/6a.COMB.seq:US-09-065-999-8

seq_documentation_block:

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? Sequence 8, Application US/09065999
? Sequence 17, Application US/09065999
? GENERAL INFORMATION:
? APPLICANT: Hanson, Stephen F.
? APPLICANT: Maxwell, Douglas P.
? TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
? TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
```

ADDRESSER: Charles & Brady
 STREET: One South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/065,999
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27,386
 REFERENCE/DOCKET NUMBER: 950296,94754
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-251-5000
 TELEFAX: 608-251-9180
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1894 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOTIF TYPE: DNA (genomic)
 US-09-065-999-8

alignment_scores:
 Quality: 206.00 Length: 70
 Ratio: 3.552 Gaps: 0
 Percent Similarity: 82.857 Percent Identity: 57.143

alignment_block:

US-09-289-346a-6 x US-09-065-999-8 ..

Align seq 1/1 to: US-09-065-999-8 from: 1 to: 1894

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1 1Thleuvaltrfgyclupheginalapqlyavgsrslatarglycl 17
   |||
796 ACATCGATGGGACATTCGATCGGACATTCGACAGGAG 845
   |||
17 ycgslnthserasnaspalalalaculalaleuasnalaser 34
   |||
846 TCAGCAGCTGGCCACGACATCATGCAACAGCCATTAAAGCAGATTC 895
   |||
34 ycgslnualaleugdlialalagqluysileptoculuytytleu 50
   |||
896 TTGATCTGCTTCACATATTCGAGGACAGACACGAAAGATTACCTC 945
   |||
51 Phealaphelialaleuasnserasnleuaspavgllephaaplysth 67
   |||
946 CTTCAACATCAACATCTCGTCTTAATCTGACGAGCATCTTCGCAAGT 995
   |||
67 pfcgclupro 70
   |||
996 GCCGGACCA 1005
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seq_name: /cgnl_7/prodata/1/lna/6a.COMB.seq:US-09-065-999-7

seq_documentation_block:

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? Sequence 17, Application US/09065999
? Sequence 8, Application US/09065999
? GENERAL INFORMATION:
? APPLICANT: Hanson, Stephen F.
? APPLICANT: Maxwell, Douglas P.
? TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
? TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
```

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: One South Plinckney Street
 CITY: Madison
 STATE: INDIANA
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/065,999
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Seely, Nicholas J.
 REGISTRATION NUMBER: 27,386
 TELEPHONE: 608-251-5000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-251-5000
 TELEFAX: 608-251-9166
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2072 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-065-999-7

alignment_scores:
 Quality: 206.00 Length: 70
 Ratio: 0.532 Gaps: 0
 Percent Similarity: 82.857 Percent Identity: 57.143

alignment_block:
 US-09-289-346a-6 x US-09-065-999-7 ..

Align seg 1/1 to: US-09-065-999-7 from: 1 to: 2072

1 Thleuvaltrpglygubhcglnvalaspglyarsgerlaatsgylcl 17
 |||||
 796 ACATGCAATGGCGCAACATTCACATCGACCGCAATCTGCAGAGAGG 845
 17 YCYSGlnThSerAspAlaIaIngluAlaLeuAsnAlaSerSetL 34
 |||||
 846 TCGACGAGTCGCGACAGCTCATATGCAAGAGCAATTAAGCAATTTC 895
 34 psglunlAlaLeuGlnInlAlaIaGlygylstleptrogluylcu 50
 |||||
 896 TTGATCTGCCTTCGACATATGAGAGAGAACACCAAGCAATTAAGTC 945
 51 PheAlaPheAlaAlaLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
 |||||
 946 CTTTCACATCAACACATCCGCTTCATATCTCGAAGGATCTCGTCAAGT 995
 67 pProgluGlu 70
 |||||
 996 GCGGAGACCA 1005

seq_name: /cgnl_7/plodata/1/lna/6b_COMB.seq:US-08-838-151A-1

seq_documentation_block:
 Sequence 1: application US/08838151A
 General Information:
 APPLICANT: Stout, John T
 APPLICANT: Lau, Heng T
 APPLICANT: Maxwell, Douglas
 APPLICANT: Ahlquist, Paul

APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing Gemlativrus
 NUMBER OF INVENTION: Genes
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Rocky, Milamov & Katz
 STREET: Two Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838,151A
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2072 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 BIOTHERETICAL: NO
 ANTI-SENSE: NO
 ORIGIN: GenBank
 ORGANISM: Tomato Mottle Geminal Virus
 INDIVIDUAL ISOLATE: Florida
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 44..1127
 PUBLICATION INFORMATION:
 AUTHORS: Gilbertson, RL
 AUTHORS: Hildebrand, JH
 AUTHORS: Paplomatas, EJ
 AUTHORS: Rojas, WR
 AUTHORS: Hou, YW
 TITLE: Pseudorecombination between the infectious
 TITLE: cloned DNA components of tomato mottle and bean
 TITLE: mottle virus.
 JOURNAL: J. Gen. Virol.
 VOLUME: 74
 PAGES: 23-31
 DATE: 1993
 US-08-838-151A-1

alignment_scores:
 Quality: 204.00 Length: 70
 Ratio: 3.517 Gaps: 0
 Percent Similarity: 82.857 Percent Identity: 54.286

alignment_block:
 US-09-289-346a-6 x US-08-838-151A-1 ..

Align seg 1/1 to: US-08-838-151A-1 from: 1 to: 1162

1 Thleuvaltrpglygubhcglnvalaspglyarsgerlaatsgylcl 17
 |||||
 371 ACATGCAATGGCGAGATTTCACATGATCGAGCGCAAGATCTGCAGAGAGG 420

seq_name	gb_vl:AF188708	2105 G	2105	70	0	70
seq_documentation_block:						
LOCUS	AF188708	1365 bp	DNA			
DEFINITION	Cowpea golden mosaic geminivirus replication associated protein (rep) and coat protein (cp) genes, partial cds.					
ACCESSION	AF188708					
KEYWORDS	AF188708.1	GI:6273115				
SOURCE	cowpea golden mosaic geminivirus.					
ORGANISM	cowpea golden mosaic geminivirus					
REFERENCE	Ylviser, SPNA viruses: geminiviridae: Begomovirus.					
AUTHORS	1 (bases 1 to 1365)					
TITLE	Partial nucleotide sequence of cowpea golden mosaic geminivirus					
JOURNAL	Partia.J.C.					
REFERENCE	2 (bases 1 to 1365)					
AUTHORS	Paria.J.C.					
TITLE	Direct Submission					
JOURNAL	Submitted (21-SEP-1999) Biotechnology Laboratory, EMBRAPA, Caixa Postal 179, Goiania, GO 75375, Brazil					
FEATURES	1 localities					
source	1 localities					
gene	1 localities					
cds	1 localities					
rep_origin	1 localities					
gene	1 localities					
cds	1 localities					
rep_origin	1 localities					
gene	1 localities					
cds	1 localities					
rep_origin	1 localities					
gene	1 localities					
cds	1 localities					
rep_origin	1 localities					
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cds	1 localities					
rep_origin	1 localities					
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gene	1 localities					
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rep_origin	1 localities					

[illegible]

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CDS      complement(815..1072)
         /gene="AC4"
         /note="A14"
         /codon_start=1
         /product="A14"
         /db_xref="GI:985127"
         /translation="MNLISMCMSCSSKANSNOADSSVSHRTDRITFTPTRELAP
         /APMSPTSTICITDPSPCVSRSSVADLLLEASRLTLTOPQRL"

BASE COUNT      359 a      296 c      327 g      401 t

Alignment_scores:
      Quality: 270.00      Length: 68
      Ratio: 4.500      Gaps: 0
      Percent similarity: 88.235      Percent identity: 79.412

alignment:
us-09-269-346a-7 x AF288227/rev ..

Align seg 1/1 to reverse of: AF288227 from: 1 to: 1383

1  ThleuValTrpGlyGluPheGlnValAspIleArgSerAlaArgIYGI 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
902 ACCATCACCTGGSGTGATATTCACGTCGACCGCAATCTGCTGAGAGAG 853
17 YCYGlnTrpSerAsnAPaAlaAlaAlaGluAlaLeuAsnAlaSerG 34
852 CCAGCAACTGCTTAAAGCCACGCGAGAGAGGCTCTTAAAGAGG 803
34 YSGlGluAlaLeuGlnGlnIleArgGluIleProGluIleYrIleu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
802 AAGAGAGCTGCTTGCATATATACAGSGAGAAACTCCTGAAATATTTA 753
51 PhcGlnPheHisAsnLeuAsnSerAlaAlaGluAlaIlePheAspIle 67
752 TTTCATTTCATCATTTTGATGTGATATTTAGATAGAGATTTTTCCTCC 703
67 rPro 68
   |||
702 ACCT 699

seq_name: gb_v1:AF104036
seq documentation block:
LOCUS      AF104036      2828 bp      DNA      circular      VRL      05-AUG-1999
DEFINITION Sweet potato leaf curl virus DNA A, complete sequence.
ACCESSION  AF104036
VERSION    AF104036.1 GI:5702158
KEYWORDS   Sweet potato leaf curl virus.
SOURCE     Sweet potato leaf curl virus.
ORGANISM   Viruses; ssDNA viruses; Gemniviridae; Begomovirus.
REFERENCE  1 (bases 1 to 2828)
AUTHORS    Lotrakul,P., Valverde,R.A., Clark,C.A., Slim,J. and De la Torre,R.
TITLE      Detection of a geminivirus infecting sweet potato in the United
           States
JOURNAL    Plant Dis. 82, 1253-1257 (1998)
REFERENCE  2 (bases 1 to 2828)
AUTHORS    Lotrakul,P. and Valverde,R.A.
TITLE      Cloning of a DNA-A-like genomic component of sweet potato leaf curl
           virus : nucleotide sequence and phylogenetic relationships
JOURNAL    Molecular Plant Pathology on-line (1999)
REFERENCE  3 (bases 1 to 2828)
AUTHORS    Lotrakul,P. and Valverde,R.A.
TITLE      Submitted (02-Nov-1998) Plant Pathology and Crop Physiology,
           Louisiana State University, 302 Life Sciences Bldg., LSU, Baton
           Rouge, LA 70803, USA
FEATURES   source
           1..2828
           Location/Qualifiers
CDS      complement(1267..2524)
         /organism="sweet potato leaf curl virus"
         /db_xref="taxon:100755"
         /chromosome="DNA A"
         /country="USA"
         /size=476
         /size=476
         /size=476
         /gene="AV2"
         /note="AV2"
         /codon_start=1
         /product="precoat protein AV2"
         /protein_id="AAD47169.1"
         /db_xref="GI:5702159.1"
         /translation="MPLNPLNDPLDPLTNGPFCMLSNVYLGSTIKKYEGLTREL
         /GSELIIRPRVROYDEANRAPELISIMWETGKATLALBDSYRALHMMCCPCCKKICP
         /GPKRRDDEKGE"
         /size=301..1065
         /gene="AV1"
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         /note="AV1"
         /codon_start=1
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         /protein_id="AAD47170.1"
         /db_xref="GI:5702160"
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         /VVSRSVKNRRKRCORIPKCGVSGKVDYERKMDKVPHTGCVASDFKSTGLTHRL
         /GRVCRVSGIDKQVMDNANRSDHTIITWLLIDRRNRKDPALNGDILPTMDPEP
         /KQNDRLVKSQSLKSNISVYSGPFSKRLQIKAFKFGILINHTINRKEANTE
         /complement(1081..1515)
         /gene="AC3"
         /note="AC3"
         /size=1081..1515
         /gene="AC3"
         /note="AC3"
         /codon_start=1
         /product="coat protein AC3"
         /protein_id="AAD47171.1"
         /db_xref="GI:5702161"
         /translation="MDSRTGISTSHAQTPFAVEEDTNPMSYGRFAPHLRIYVHEST
         /QERTILKPOLRVNVERROLGFKIFIOFRLITLRLTGLAIHSPTGILERLAKRLCNEL
         /ANICFSLVNIQVIRYLPVCSVIMDELTPDCNDVDKYLTY"
         /complement(1232..1678)
         /gene="AC2"
         /note="AC2"
         /size=1232..1678
         /gene="AC2"
         /note="AC2"
         /codon_start=1
         /product="transactivator protein AC2"
         /protein_id="AAD47172.1"
         /db_xref="GI:5702162"
         /translation="MNSPPLSGSKRRCYGGPIPLPRKAKRKKPQDRTIYWGCGCS
         /MNSPPLSGSKRRCYGGPIPLPRKAKRKKPQDRTIYWGCGCS
         /HOIIPAEKFLKRGATGRTIDPLPIPLDIDPSNCTNSOLDMYGTF"
         /complement(1587..2681)
         /gene="AC1"
         /note="AC1"
         /size=1587..2681
         /gene="AC1"
         /note="AC1"
         /codon_start=1
         /product="initiation protein AC1"
         /protein_id="AAD47173.1"
         /db_xref="GI:5702163"
         /translation="MAAPKRRIOANFTYTPGCSISEKEDCAQLANTIQPSNKKYK
         /HYARELHEGEGPLIVIVDFRKYVTASFPDPLVSPNSHHHFNIGASSDYKS
         /HYARELHEGEGPLIVIVDFRKYVTASFPDPLVSPNSHHHFNIGASSDYKS
         /OHRMLVSNLIDTFSPSPSSSPSSSPSSFPAAVPIISMALENVMSADRPRLISV
         /IGESKRTKQVWKLQDPLNLCGLDLSKYSNSMTNITDITNPOYKAKRHEKG
         /KAKRHEKGKAKRHEKGKAKRHEKGKAKRHEKGKAKRHEKGKAKRHEKGKAKRHEKG
         /DQSPRPVQDEYSHSGKAKRHEKGKAKRHEKGKAKRHEKGKAKRHEKGKAKRHEKG
         /complement(2267..2524)
         /gene="AC4"
         /note="AC4"
         /size=2267..2524

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/gene="AC4"
/note="AC4"
/organism="Homo sapiens"
/protein_id="AA047174.1"
/db_xref="gi:5702164"
/translation="MGMTSCMKSSKANSNAOIAOSINSHTDRTITPTSTREUN
ARMSPTSTRTGTPSPVSNSTADLFEPSRLTTPQORL"
BASE COUNT      741 a      606 c      675 g      806 t
ORIGIN

alignment_scores:
  Quality: 270.00      Length: 68
  Ratio: 4.500      Gaps: 0
  Percent Similarity: 88.235      Percent Identity: 79.412

alignment_block:
US-09-289-346a-7 x AF104036/rev

Align seg 1/1 to reverse of: AF104036 from: 1 to: 2828

1 ThleuValTrpGlyGluPheGlnValAspGlyAysSerAlaArgGlyGly 17
|||||
2354 ACATCACTACCTGGGCTGATTCAGATCGACGACGACATCTCTCTACAGAG 2305
|||||
17 YCYSGLIThrSerAsnAPhAlaAlaGluAlaLeuAsnAlaSerSerL 34
2304 CCAGACAGCTGACAGCCAGCCAGCCAGGAGCTCTCAAGAGAGTTCTA 2255
|||||
34 YSGIuGlAlaLeuGlnAlaLeuArgGlyLysLeuProGlyLysTyrLeu 50
|||||
2254 AAGAAGCTGGGCTGCAATTAATCAGGAGAAACCTCCCGAAATATTTA 2205
|||||
51 PhocIaPheIaAsnLeuAsnSerAlaLeuAlaAlaIlePheAspLysTh 67
|||||
2204 TTTCATTTCTATTAATTGTTAGTATTAATTAAGCATTTTTCCTCC 2155
|||||
67 PPro 68
|||||
2154 ACCT 2151
seq_name: gb_v1:SCU67926

seq_documentation_block:
LOCUS SCU67926 554 bp DNA VRL 28-JAN-1998
DEFINITION Sida golden mosaic geminivirus Rep protein (AC1) gene, partial cds.
ACCESSION U67926
VERSION 067926.1 GI:1346801
KEYWORDS
SOURCE Sida golden mosaic virus.
ORGANISM Sida golden mosaic virus.
VIRUSES: ssDNA, viroases; Geminiviridae; Begomovirus.
1 (bases 1 to 554)
Royce, M.E., McLaughlin, M.A., Nekhla, N.K. and Maxwell, D.P.
Genetic diversity among geminiviruses associated with the weed
species Sida spp. Macropodium lathyroides, and Mistaquula
pinnatifida from Jamaica.
Plant Dis 81: 151-158 (1997)
2 (bases 1 to 554)
Royce, M.E., McLaughlin, M.A. and Maxwell, D.P.
Direct Submission
Submitted (23-AUG-1996) Plant Pathology, University of Wisconsin,
1690 Linden Drive, Madison, WI 53706-1598, USA
JOURNAL
FEATURES
Location/Qualifiers
/organism="Sida golden mosaic virus"
/strain="Jamaica"
/isolate="Jamaica, May 1993"
/db_xref="taxon:51034"
/note="DNA A component"
complement(1..554)
/gene="AC1"

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CDS
complement(<1..>554)
/gene="AC1"
/note="replication-associated protein"
/organism="Homo sapiens"
/protein_id="AA047174.1"
/db_xref="gi:5702164"
/translation="SISKREALISQLOTLTTPVKKKIKICREIHNCEPHILVLOPE
GKYNCTNNKFEIDVYPTKRSVHPNIGGASSSSVSVKEDGDTILMKVQVLDGRSA
KRCOOTANDMAALANSCKRCKDAKILREKLEERYLEQYHNSSNIDRIFSRPEPMS
HPEFESPTAVPQDMQMDKGRFR"
BASE COUNT      121 a      127 c      135 g      167 t
ORIGIN

alignment_scores:
  Quality: 267.00      Length: 70
  Ratio: 4.238      Gaps: 0
  Percent Similarity: 90.000      Percent Identity: 70.000

alignment_block:
US-09-289-346a-7 x SCU67926/rev

Align seg 1/1 to reverse of: SCU67926 from: 1 to: 554

1 ThleuValTrpGlyGluPheGlnValAspGlyAysSerAlaArgGlyGly 17
|||||
290 ACATCACTACCTGGGCTGATTCAGATCGACGACGACATCTCTCTACAGAG 241
|||||
17 YCYSGLIThrSerAsnAPhAlaAlaGluAlaLeuAsnAlaSerSerL 34
240 TCAGCAACAGCTACAGCCAGCCAGCCAGCAGCTTGATTCGTGACAA 191
|||||
34 YSGIuGlAlaLeuGlnAlaLeuArgGlyLysLeuProGlyLysTyrLeu 50
|||||
190 AAGAGATGCTGCTGAATCATCTACAGAGAACTTTCAGAGATATCTC 141
|||||
51 PhocIaPheIaAsnLeuAsnSerAlaLeuAlaAlaIlePheAspLysTh 67
|||||
140 TTTCATTTCTATTAATTGTTAGTATTAATTAAGCATTTTTCCTCC 91
|||||
67 PProGPro 70
|||||
90 TCCTCAACCTC 81
seq_name: gb_v1:YE132548

seq_documentation_block:
LOCUS YE132548 2763 bp DNA circular VRL 01-FEB-1999
DEFINITION Ipomoea yellow vein virus V2, VI, C3 and C2 genes.
ACCESSION AY132548
VERSION AY132548.1 GI:4210720
KEYWORDS
SOURCE Ipomoea yellow vein virus.
ORGANISM Ipomoea yellow vein virus.
VIRUSES: ssDNA, viroases; Geminiviridae; Begomovirus.
1 (bases 1 to 2763)
Banks, G.K., Bedford, I.D., Belski, F.J., Corezo, E.R. and Markham, P.G.
Direct Submission
Submitted (26-JUN-1999) Banks G.K., Virus Research, John Innes
Centre, Norwich Research Park, Colney Lane, Norwich, NR4 6JL, UK
2 (bases 1 to 2763)
Banks, G.K., Bedford, I.D., Belski, F.J., Corezo, E.R. and Markham, P.G.
A novel geminivirus of Ipomoea indica (Convolvulaceae) from southern
Spain
Unpublished
JOURNAL
FEATURES
Location/Qualifiers
/organism="Ipomoea yellow vein virus"
/virion
/specific_host="Ipomoea indica"
/db_xref="taxon:87832"

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34 ysglgluialaenglnlllearglulysllepoglutyltyrlu 50
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194 AGAGAGCGCCATGAGATAGCTAAGAGAGAGTCCGCAAAAGTTCTC 145
53 Phgclnphehlaenleuanserlaialaialaialephaplyrth 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
144 TTTCATATCCACACTCCAGTACGATGATGATTTTCATGAGGA 95
67 rProgiupro 70
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
94 TCCGGAACA 85
seq_name: gb_v1:AF098940
seq_documentation_block:
LOCUS AF098940 1405 bp DNA VRL 04-MAR-1999
DEFINITION Macropitium golden mosaic geminivirus strain Jamaica 1
partial cds.
ACCESSION AF098940.1 GI:4336584
VERSION AF098940.1
KEYWORDS Macropitium golden mosaic geminivirus.
SOURCE Macropitium golden mosaic geminivirus.
ORGANISM Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE 1 (bases 1 to 1405)
AUTHORS Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
TITLES Molecular characterization of two distinct geminiviruses infecting M. latifolius from Jamaica
JOURNAL 2 (bases 1 to 1405)
REFERENCE 3 (bases 1 to 1405)
AUTHORS Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
TITLES Direct Submission
JOURNAL Submitted (14-OCT-1998) Biotechnology Centre, University of the West Indies, Mona, Kingston 7, Jamaica
FEATURES
source
Location/Qualifiers
/organism="Macropitium golden mosaic geminivirus"
/strain="Jamaica strain 1"
/specific_host="Macropitium latifolius"
/db_xref="taxon:51676"
/country="Jamaica"
/clone="pK042; pMGJ3"
/complement(<1..701)
/gene="rep"
/complement(<1..701)
/codon_start=1
/product="replication associated protein"
/protein_id="AA017850.1"
/db_xref="GI:4336586"
/translation="MSTKAKKATPTTGGCTGKSPALISQTLNAPNPKKRT
KICRPHDPDPIIVLIDRGKGTNNRLFDLVSPPRSNRIKRNALICASSSSQYS
YVERDDITTEGVIQDASRGQSTNDMAALNASTKRNARIVKLETFEFLF
OYHNLSDNLTDPKDEPPAPPPPLSTFNVDEQHMADYDFGNSAARPRMST
IWEDESRCKTKMAC"
misc_feature
702..1030
/note="intergenic region"
gene
1031..51405
/translation="
1031..51405
/gene="cp"
/codon_start=1
/product="coat protein"
/protein_id="AA017849.1"
/db_xref="GI:4336585"
/translation="WPAKRSWMTTPGVAKSRRLNVSPPKQIGPSRKAQEWKRP"

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YKRPRIYRTLSPDVPGCEGRCQVSGEQRDHSVQKWCISDSTRGVYTHRWCK
RFQVKEVYLGKIMNDENINSC*
alignment_scores:
BASE COUNT 328 a 333 c 357 g 386 t 1 others
Origin
alignment_scores:
Quality: 259.00 Length: 70
Ratio: 4.246 Gaps: 0
Percent Similarity: 87.143 Percent Identity: 68.571
alignment_block:
US-09-289-346a-7 x AF098940/rev
Align seg 1/1 to reverse of: AF098940 from: 1 to: 1405
1 Thrlaenvaltrfglyglupheglnaiaapojvaygsrslaeaaygl 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
374 ACCTATGAGATGGAGATGTCGATGACGACGAAAGTCTCCAGCG 325
17 PCYgclnphehlaenleuanserlaialaialaialephaplyrth 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
324 TCACCAACATCTTACCATGACGACCGCCGCAAGCATTTAATTCGGAACA 275
34 ysglgluialaenglnlllearglulysllepoglutyltyrlu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
274 AGAGAGCGCCATGAGATAGCTAAGAGAGAGTCCGCAAAAGTTCTC 225
53 Phgclnphehlaenleuanserlaialaialaialephaplyrth 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
224 TTTCATATCCACACTCCAGTACGATGATGATTTTCATGAGGA 175
67 rProgiupro 70
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
174 TCCGGAACA 165
seq_name: gb_v1:AF026553
seq_documentation_block:
LOCUS AF026553 1165 bp DNA VRL 03-NOV-1997
DEFINITION Potlato yellow mosaic virus Tomato strain AV1 and AC1 genes, partial cds.
ACCESSION AF026553.1 GI:2583073
VERSION AF026553.1
KEYWORDS Geminiviridae.
ORGANISM Geminiviridae.
REFERENCE 1 (bases 1 to 1165)
AUTHORS Guzman,P., Arredondo,C.R., Esmaty,D., Portillo,R.J. and
TITLES Partial characterization of two whitefly-transmitted Geminiviruses Infecting Tomatoes in Venezuela
JOURNAL Plant Dis. 81, 312-313 (1997)
2 (bases 1 to 1165)
AUTHORS Guzman,P., Arredondo,C.R., Esmaty,D., Portillo,R.J. and
TITLES Direct Submission
JOURNAL Submitted (1997) Plant Pathology, University of California-Davis, Department of Plant Pathology, Davis, CA 95616, USA
FEATURES
source
Location/Qualifiers
1..1165
/organism="Geminiviridae"
/strain="Tomato strain"
/db_xref="taxon:10811"
/translation="
1031..51405
/translation="whitefly-transmitted: DNA-A
Monongas (Venezuela)"
/complement(<1..153)
/note="capsid protein"
/codon_start=1
/product="AV1"

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401 TCGGTGAGGCTTATCTCTCTTTTATCTCTCTTTGATCGAG 450
67 hPrGolu 69
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451 TTCGAGAA 458

seq.name: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AA193291
seq.documentation_block:
AA193291 standard: DNA: 1062 bp.
AA193291:
AA193291:
27-APR-1998 (first entry)
Bean golden mosaic geminivirus CI mutant ORF BGAC221.
Geminivirus: BGWV: CI gene: transdominant mutation;
transgenic plant; disease resistance: ss; cyclic: circular.
Bean golden mosaic virus type II isolate Guatemala.
MO9739110-A1.
23-OCT-1997.
15-APR-1997: 97MO-US06300.
16-APR-1996: 9605-0015517.
(SEMI-) SEMINIS VEGETABLE SEEDS INC.
(MISC) WISCONSIN ALUMNI RES FOUND.
Ahlgquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT.
WPI: 1997-526447/48.
P-PSDB: AAW34333.
Transgenic plants expressing geminivirus AC1 and CI wild-type and
mutant genes - have increased resistance to geminivirus infection
e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
golden mosaic geminivirus
Claim 13: Page 107-109; 132pp: English.
This DNA sequence comprises construct BGAC221 that codes for a
transdominant lethal mutant (see AAW34333) of the CI protein (see
AAW34338) of bean golden mosaic virus (BGWV). It was obtained by
Kunkel mutagenesis of the wild-type CI gene (see AA193314). CI is
transgenic plants containing DNA comprising geminivirus CI or AC1
wild-type or mutant sequences that negatively interfere in trans
with geminiviral replication during infection. Such transgenic
plants are resistant to viral infection. The AC1/CI genes are
especially from BGWV, tomato mottle virus or tomato yellow leaf
curl virus (see AA193282-93) and encode polypeptides (see AAW34324-35)
that have mutations in the highly conserved DNA-nicking and/or the
NTP-binding domains.
Sequence 1062 bp: 339 A; 245 C; 219 G; 259 T; 0 other:

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Alignment scores:
Quality: 213.00 Length: 70
Ratio: 82.83 Gaps: 0
Percent Similarity: 82.83 Percent Identity: 50.571

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Alignment block:
US-09-289-346a-7 x AA193291
Align seg 1/1 to: AA193291 from: 1 to: 1062

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1 PhrLeuValTrpGlyGluPheGlnValaIaPglAArgSerAlaArgIgcI 17
|||||
328 ACATTCGAAATGGAGAACATTCACAGTCAAGTCAAGTCAAGTCAAGTCAAG 377
17 KCGATGThSerSerSerSerSerSerSerSerSerSerSerSerSerSer 34
|||||
378 TCACGACGTCCGACGACGACGACGACGACGACGACGACGACGACGACGAC 427
34 YAGIuGlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 50
|||||
428 TTGGAATCTGCTCTTCAAAATTCGAGGACCAACCAACCAATTCACGTC 477
51 PhcGlnPheIleAsnLeuAsnSerAlaIleuAlaIaIaIaIaIaIaIaIa 67
|||||
478 CTTCAACATCACAACATCCTGTTATCTGACGACGACGACGACGACGAC 527
67 PProGluPro 70
|||||
528 GCGGAGAACCA 537

seq.name: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AA193292
seq.documentation_block:
AA193292 standard: DNA: 1062 bp.
AA193292:
AA193292:
27-APR-1998 (first entry)
Bean golden mosaic geminivirus CI mutant ORF BGAC228.
Geminivirus: BGWV: CI gene: transdominant mutation;
transgenic plant; disease resistance: ss; cyclic: circular.
Bean golden mosaic virus type II isolate Guatemala.
MO9739110-A1.
23-OCT-1997.
15-APR-1997: 97MO-US06300.
16-APR-1996: 9605-0015517.
(SEMI-) SEMINIS VEGETABLE SEEDS INC.
(MISC) WISCONSIN ALUMNI RES FOUND.
Ahlgquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT.
WPI: 1997-526447/48.
P-PSDB: AAW34334.
Transgenic plants expressing geminivirus AC1 and CI wild-type and
mutant genes - have increased resistance to geminivirus infection
e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
golden mosaic geminivirus
Claim 13: Page 111-112; 132pp: English.
This DNA sequence comprises construct BGAC228 that codes for a
transdominant lethal mutant (see AAW34334) of the CI protein (see
AAW34338) of bean golden mosaic virus (BGWV). It was obtained by
Kunkel mutagenesis of the wild-type CI gene (see AA193314). CI is
transgenic plants containing DNA comprising geminivirus CI or AC1
wild-type or mutant sequences that negatively interfere in trans
with geminiviral replication during infection. Such transgenic
plants are resistant to viral infection. The AC1/CI genes are
especially from BGWV, tomato mottle virus or tomato yellow leaf
curl virus (see AA193282-93) and encode polypeptides (see AAW34324-35)
that have mutations in the highly conserved DNA-nicking and/or the
NTP-binding domains.

```



```
CC transdominant lethal mutant (see AAW3433) of the CI protein (see  
CC AAW3438) of bean golden mosaic virus (BGWV). It was obtained by  
CC kinase mutagenesis of the wild-type CI gene (see AA793314). CI is  
CC required for replication of the nontrans-activating particle (CI-  
CC RNP), which encodes the movement proteins (MPs) involved in trans-  
CC wide type of mutant sequences that negatively interfere in trans-  
CC with geminiviral replication during infection. Such transgenic  
CC plants are resistant to viral infection. The ACI/C1 genes are  
CC especially from BGWV, tomato mottle virus or tomato yellow leaf  
CC curly virus (see AA693282-93) and encode polypeptides (see AAW3432-35)  
CC that have mutations in the highly conserved DNA-nicking and/or the  
CC MP-binding domains.  
XX MF-binding domain.
```

```
SF Sequence 1062 BP; 340 A; 245 C; 219 G; 258 T; 0 other;  
SO
```

alignment_scores:

	Quality:	213.00	Length:	70
Percent Similarity:	Kello: 3.6%2	Gaps:	0	
	Percent Identity:	58.571		

Alignment Block:
US-09-289-346A-7 x AAT93293 ..

Align seq 1/I to: AAT93293 from: I to: 1062

```
1 ThrLeuValTrrPolYGlurPheGluVaIsppClvAr-gSerAlarAgcLygl 17  
   |||||.....  
328 NCMTAGCATGTGGCGACATTTCGAAGTGCCGCAGACTCTGCCAAAGAGAG 377  
       |||||.....  
    17 YCysLthrSerAsnApLaALAIalAGlualAjenuAnSLserSeft.. 34  
      | .....|||||...: ||:::||:|||||.....  
378 TCtGCAgtTTccCACgAcTCTCTACAAGScAtTAAGAACCgATTCOA 427  
  
34 ysgLiuaIAleacGIatllelaRgcLuaystleRpocIdyStyldeu 50  
     |||||.....  
428 TTGATAITDGTCTTGACAAATttGaAGaaBdAACAGOCaAAAgaATTAGCc 477  
           |||||.....  
51 PHeGlnrHemlsrAmJauasncERfalaEulaIALaiIEPRkspdySrh 67  
         |||||.....  
478 cPTTGAaATtCaCMAGactCGTctTAATCTCAAGCCGATCTTCGCAAMCr 527  
  
67 rPrGcuUpRo 70  
        :|||:|||||  
528 GCCGAGACCh 537
```

seq_name: /cpnl_8/gcgdata/geneseq/genesequ_NA1997.DAT.AAT93314

seq_documentation_block:

ID AAT93314 standard; DNA: 1183 BP.

AAT93314:

27-Apr-1998 (first entry)

DE Bean golden mosaic geminivirus Cl open reading frame.

XX

RN Gemlinivirus; BGWV; Cl gene; transdominant mutation;

KM Transgenic plant; disease resistance; ss; cylicic; circular.

XX

CX Bean golden mosaic virus type II isolate Guatemala.

XX

FT Key Location/Organisms

DT CDS 1..1062

FF *tag= a

PX MO9739110-AI.

DN 23-OCT-1997.

PF 15-Apr-1997; 97MO-USO6300.

XR 16-Apr-1996; 96OUS-0015517.


```

          :::::  |||||:::  |||  |||||  ||:::
          478 CTTCAACATCAACAACTCCCTTCAATCTCAACAGCATCTTCACAAAGT 527
          67 rProclupro 70
          :::::  |||||:::  |||  |||||  ||:::
          528 GCCGGAACCA 537

seq_name: /cgnl_8/9cgcdata/geneseq/geneseqn/NA2000.DAT:AAA94700

seq_documentation_block:
ID   AAA94700 standard: DNA: 1651 BP.
AC   AAA94700:
XX
XX   15-JAN-2001 (first entry)
DE
DE   pMRG 2288 35S-rep gene cassette.
KM   Geminivirus; DNA-A: geminivirus replication inhibition; ac3 gene:
KM   transgenic plant; antiviral; gene therapy; bean golden mosaic virus;
KM   BGWV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CMV; ds.
XX   Bean golden mosaic virus.
OS   Cauliflower mosaic virus.
XX   Alfalfa mosaic virus.
XX   Synthetic.
XX   US6118048-A.
XX
XX   12-SEP-2000.
PF   24-APR-1998: 98US-0065999.
XX
XX   25-APR-1997: 97US-0044925.
XX
XX   (WISC ) WISCONSIN ALDUNIT RES FOUND.
XX
XX   WPI: 2000-610861/58.
XX
XX   Genetic construct comprising a mutant geminiviral rep gene, useful for
XX   producing a plant resistant to geminiviral infection.
XX
XX   Example: Column 15-16; 14pp; English.
XX
XX   The present sequence is a 35S-rep gene cassette comprising the rep gene
XX   of bean golden mosaic virus (BGWV-GA cloned downstream of the CMV)
XX   35S promoter and an alfalfa mosaic virus (AMV) leader sequence. The
XX   sequence was integrated into pBSII-KS+ to produce a rep gene expression
XX   vector. DNA-nicking domain mutations may be incorporated into rep gene
XX   to produce a genetic construct that acts as a trans-dominant inhibitor
XX   of geminiviral replication. When expressed in a plant cell, this
XX   genetic construct can dramatically reduce replication of geminivirus.
XX   Geminiviruses are one of the greatest constraints on
XX   ac3 gene in addition to the trans-dominant inhibitor exhibit increased
XX   efficiency and broadened specificity of inhibition of geminiviral
XX   replication. Geminiviruses are one of the greatest constraints on
XX   production of important crops, including cassava, beans, cowpeas,
XX   peppers, tomatoes and cotton. The effects of the virus can be overcome
XX   by using the genetic construct.
XX
XX   Sequence 1651 BP: 517 A; 393 C; 342 G; 399 T; 0 other:

```

```

alignment_scores:
Quality: 213.00      Length: 70
Ratio: 3.672         Gaps: 0
Percent Similarity: 82.857 Percent Identity: 58.571

```

alignment_block:

us-09-289-346a-7 x AAA94700 ..

Align seg 1/1 to: AAA94700 from: 1 to: 1651

```

1 ThrLeuValTrpGlyIupheGluValaIaSpolyArGserAlaIaArgIyGL 17
   :::::  |||||:::  |||  |||||  ||:::
796 ACATCGAATGATGGGACATTCAGATCGCGGACATCTGCAMAGCAGAG 845
17 yCysGlnThrSerAsnAlaAlaAlaGluAlaLeuAsnAlaSerSerL 34
846 TCAGCAGTCTGCCACGATCATTCGAAAGCATTTAAACCGAGATTCAC 895
34 yGluGluValaLeuGlnIleIleArgIyLysIleProGluIyTYrIleu 50
896 TTGAATCTGGCTCTACCATATTTGAAGAGAAACACCAAGATATTCCTC 945
51 PheGlnPheIleAlaLeuAsnSerAlaLeuAlaAlaIlePheAspIyGth 67
946 CTTCAACATCAACAACTCCCTTCAATCTCAACAGCATCTTCGCAAAAGT 995
67 rProclupro 70
   :::::  |||||:::  |||  |||||  ||:::
996 GCCGGAACCA 1005

seq_name: /cgnl_8/9cgcdata/geneseq/geneseqn/NA2000.DAT:AAA94701

seq_documentation_block:
ID   AAA94701 standard: DNA: 1651 BP.
AC   AAA94701:
XX
XX   15-JAN-2001 (first entry)
DE
DE   PT-repN nucleotide sequence.
XX
XX   Geminivirus; DNA-A: geminivirus replication inhibition; ac3 gene:
XX   transgenic plant; antiviral; gene therapy; bean golden mosaic virus;
XX   BGWV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CMV; ds.
XX   Bean golden mosaic virus.
XX   Cauliflower mosaic virus.
XX   Alfalfa mosaic virus.
XX   Synthetic.
XX   US6118048-A.
XX
XX   12-SEP-2000.
PF   24-APR-1998: 98US-0065999.
XX
XX   25-APR-1997: 97US-0044925.
XX
XX   (WISC ) WISCONSIN ALDUNIT RES FOUND.
XX
XX   WPI: 2000-610861/58.
XX
XX   Genetic construct comprising a mutant geminiviral rep gene, useful for
XX   producing a plant resistant to geminiviral infection.
XX
XX   Example: Column 17-18; 14pp; English.
XX
XX   The present sequence is pRrepN, a vector containing a CMV-35S
XX   promoter-driven rep gene derived from bean golden mosaic virus (BGWV-GA.
XX   Site-directed mutagenesis was used to engineer an NcoI site in the start
XX   codon of the rep gene. The resulting genetic construct contains a trans-
XX   dominant inhibitor of geminiviral replication. When expressed in a plant cell,
XX   these inhibitors are able to dramatically reduce replication of
XX   geminiviruses. Genetic constructs that include sequences containing a
XX   portion of the ac3 gene in addition to the trans-dominant inhibiting
XX   exhibit increased efficiency and broadened specificity of inhibition of
XX   geminiviral replication. Geminiviruses are one of the greatest constraints
XX   on production of important crops, including cassava, beans, cowpeas,
XX   peppers, tomatoes and cotton. The effects of the virus can be
XX   overcome by using the genetic construct.
XX
XX   Sequence 1651 BP: 517 A; 392 C; 343 G; 399 T; 0 other:

```

alignment_scores:
 Quality: 213.00 Length: 70
 Ratio: 3.672 Gaps: 0
 Percent Similarity: 82.657 Percent Identity: 58.571

alignment_block:
 US-09-289-346a-7 x AAA94701 ..

Align seg 1/1 to: AAA94701 from: 1 to: 1651

```

1 ThrlcvaVlrrpGlyGlnpHeGlnVaInaSpGlyVAhYgSerAlaArgGlyCl 17
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
796 ACAATGGAATGGGACAAATCTCACTCAAGCGGACGATCTGCACAGACAG 845

17 YCYGlnfHrSerAsnApAlaAlaIaGlnAlaLeuAsnAlaSerSerL 34
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
846 TCACGACGCTGCCACACCTCATATGACACGACCATTAACGCAATTCAC 895

34 YSGlnGlnAlaIaGlnGlnIleIaArgGlnLysIleProGlnLysTyrLeu 50
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
896 TTGCATCTCCCTTCACAAATATTCAGACAGACACCGCAATATTCCTGC 945

51 PheGlnPheHisAsnLeuAsnSerAlaLeuAlaIaIlePheAspLysTrh 67
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
946 CTTCACATCTCACACATTCCTGTATCTCAACGCAATCTTGTCTCAAGT 995

67 PProGlnLPro 70
||||| |||||||
996 GCCGGAACCA 1005

seq_name: /cgnl_8/ycgdata/geneseq/geneseq/NA2000.DAT:AAA94703
seq_documentation_block:
ID AAA94703 standard: DNA: 1894 BP.
XX AAA94703:
XX
XX 15-JAN-2001 (first entry)
XX
XX pTrep23delta/CX nucleotide sequence.
XX
XX Geminivirus: DNA-A: geminivirus replication inhibition; ac3 gene;
XX transgenic plant; antiviral; gene therapy; ds.
XX
XX Synthetic.
XX
XX US6118048-A.
XX
XX 12-SRP-2000.
XX
XX 24-APR-1998: 9805-0065999.
XX
XX 25-APR-1997: 9705-0044925.
XX
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX WPI: 2000-610861/58.
XX
XX
XX Example: Column 19-22: 14pp: English.
XX
XX The present sequence is pTrep23delta/CX. It contains a mutated
XX geminivirus rep gene sequence. Genetic constructs containing
XX domain mutants in the rep gene may be used as trans-dominant inhibitors
XX of geminiviral replication. When expressed in a plant cell,
XX CC these inhibitors are able to dramatically reduce replication of
XX CC geminiviruses. Genetic constructs that include sequences containing a
XX CC portion of the ac3 gene in addition to the trans-dominant inhibitor
XX CC exhibit increased efficiency and broadened specificity of inhibition of

```

CC geminiviral replication. Geminiviruses are one of the greatest
 CC constraints on production of important crops, including cassava, beans,
 CC cowpeas, peppers, tomatoes and cotton. The effects of the virus can be
 CC overcome by using the genetic construct.

Sequence 1894 BP: 604 A; 421 C; 388 G; 481 T; 0 other;

alignment_scores:
 Quality: 213.00 Length: 70
 Ratio: 3.672 Gaps: 0
 Percent Similarity: 82.657 Percent Identity: 58.571

alignment_block:
 US-09-289-346a-7 x AAA94703 ..

Align seg 1/1 to: AAA94703 from: 1 to: 1894

```

1 ThrlcvaVlrrpGlyGlnpHeGlnVaInaSpGlyVAhYgSerAlaArgGlyCl 17
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
796 ACAATGGAATGGGACAAATCTCACTCAAGCGGACGATCTGCACAGACAG 845

17 YCYGlnfHrSerAsnApAlaAlaIaGlnAlaLeuAsnAlaSerSerL 34
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
846 TCACGACGCTGCCACACCTCATATGACACGACCATTAACGCAATTCAC 895

34 YSGlnGlnAlaIaGlnGlnIleIaArgGlnLysIleProGlnLysTyrLeu 50
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
896 TTGCATCTCCCTTCACAAATATTCAGACAGACACCGCAATATTCCTGC 945

51 PheGlnPheHisAsnLeuAsnSerAlaLeuAlaIaIlePheAspLysTrh 67
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
946 CTTCACATCTCACACATTCCTGTATCTCAACGCAATCTTGTCTCAAGT 995

67 PProGlnLPro 70
||||| |||||||
996 GCCGGAACCA 1005

seq_name: /cgnl_8/ycgdata/geneseq/geneseq/NA2000.DAT:AAA94702
seq_documentation_block:
ID AAA94702 standard: DNA: 2072 BP.
XX AAA94702:
XX
XX 15-JAN-2001 (first entry)
XX
XX pTrep23 nucleotide sequence.
XX
XX Geminivirus: DNA-A: geminivirus replication inhibition; ac3 gene;
XX transgenic plant; antiviral; gene therapy; ds.
XX
XX Synthetic.
XX
XX US6118048-A.
XX
XX 12-SEP-2000.
XX
XX 24-APR-1998: 9805-0065999.
XX
XX 25-APR-1997: 9705-0044925.
XX
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX WPI: 2000-610861/58.
XX
XX Genetic construct comprising a mutant geminiviral rep gene, useful for
XX producing a plant resistant to geminiviral infection.
XX
XX Example: Column 17-20: 14pp: English.
XX
XX The present sequence is pTrep23. It contains the wild type geminivirus
XX rep gene sequence. Genetic constructs containing DNA-nicking domain

```

CC mutants in the rep gene may be used as trans-dominant inhibitors of geminiviral replication. When expressed in a plant cell, these inhibitors are able to dramatically reduce replication of geminivirus. Genetic constructs that include sequences containing a geminivirus origin of replication and a trans-dominant inhibitor exhibit increased efficiency in inhibiting the replication of geminiviral replication. Geminiviruses are one of the greatest constraints on production of important crops, including cassava, beans, cowpeas, peppers, tomatoes and cotton. The effects of the virus can be overcome by using the genetic construct.

XX Sequence 2072 BP; 661 A; 467 C; 421 G; 523 T; 0 other:

alignment_scores:
Quality: 213.00 Length: 70
Ratio: 3.672 Gaps: 0
Percent Similarity: 82.857 Percent Identity: 58.571

alignment_block:

US-09-289-346a-7 x AAN94702 ..

Align seg 1/1 to: AAN94702 from: 1 to: 2072

```

1  ThrLeuValTrpGlyGluPheGlnValAspGlyValGserAlaArgGlyGcl 17
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
796  ACATGCGATGCGGCAATTCGACAGTCGACGCGATCTCGCAAGAGAG 845
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
17  YGSGGTPHrSerAspAlaAlaAlaGluAlaLeuAsnAspSerL 34
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
846  TCAGCGTCGCGACGACCTCATTCGCAAGCATTTAAGCGCATTTCA 895
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
34  YSGGGLuAlaLeuGlnIleLeuArgLysIleProGlyLysTyrLeu 50
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
896  TTGAATCTGCGCTGACATATTCAGAGAGAACACAGCAAAATTCGTC 945
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
51  PheGlnPheHisAsnLeuAsnSerAlaGluAlaAlaAlaIlePheAspYrth 67
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
946  CTTCAACATGACACATCCGCTCATATCTCGACAGCATCTTCGCAAGT 995
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
67  PProGluPro 70
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
996  GCGGAGACCA 1005

```

seq_name: /cgnl_8/gcgdata/geneseq/geneseq/MN1998.DAT:AAV29761

seq_documentation_block:

ID AAV29761 standard; DNA: 2766 BP.

AAV29761:

11-AUG-1998 (first entry)

XX Tobacco leaf curling virus gene.

DE Tobacco leaf curling virus gene; TICV; Promoter; ds.

XX Tobacco leaf curling virus.

OS JPI0070982-A.

XX 17-MAR-1998.

XX 30-AUG-1996; 96TP-0230394.

XX 30-AUG-1996; 96TP-0230394.

XX (NORO) NORINJUSANSNHO KXUSHU NOGYO SHIKENIYO.

XX MPI: 1998-233630/21.

DR Tobacco leaf curling virus gene - useful for inserting into vectors
XX for expression in, e.g. tomato plants
PT

XX Claim 1; Figs 1-3; 9pp; Japanese.

PS This sequence represents the tobacco leaf curling virus (TLCV) gene of
XX the invention. TLCV gene or its promoter can be inserted into a vector
XX for expression in a plant cell. The tobacco leaf curling virus is
XX believed to encode the TLCV proteins shown in AAM56493-W56498.

XX Sequence 2766 BP; 722 A; 576 C; 609 G; 859 T; 0 other:

alignment_scores:
Quality: 212.00 Length: 84
Ratio: 3.533 Gaps: 1
Percent Similarity: 71.429 Percent Identity: 52.381

alignment_block:
US-09-289-346a-7 x AAV29761/rev ..

Align seg 1/1 to reverse of: AAV29761 from: 1 to: 2766

```

2  LeuValTrpGlyGluPheGlnValAspGlyValGserAlaArgGlyGcl 18
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
2436  CTTGATTTTCGAGTTTTCGAGTCGATGAGCATGCTGAGGAGGAGTTG 2387
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
18  sGlnTrpSerAspAlaAlaAlaGluAlaLeuAsnAspSerLysG 35
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
2386  CCGAATCTGCCACAGCGCATTCGCGAGCATCAACATCGATCAAACT 2337
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
35  LUGLUAleuGlnIleLeuArgLysIleProGlyLysTyrLeuPhe 51
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
2336  CATTGCGCATCATATTTAAGAGGCAAAAGCTCCCAAGATTTGTTTA 2287
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
52  GlnPheHisAsnLeuAsnSerAlaLeuAlaAlaLeu..... 63
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
2286  CAAATTCATATTTAATTTAAATTTAGATAGCATGTTTCTCTCCCAT 2237
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
64  ..... PheAspLysYrth-ProG 69
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
2236  GCGAGCTTTGTTGCTCTTTTCAGATGCTTCATTCATCAAGTTCTCG 2187
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
69  || 69
2186  AA 2185

```

seq_name: /cgnl_8/gcgdata/geneseq/geneseq/MN1996.DAT:ANT12904

seq_documentation_block:

ID ANT12904 standard; DNA: 1080 BP.

ANT12904:

07-NOV-1996 (first entry)

XX Sardinian tomato leaf curl virus mutated CI gene (K227A).

XX Nucleotide triphosphate binding site; DNA helicase; RNA helicase;

XX modification; mutation; viral replication; deficient; inhibition;

XX viral resistance; geminivirus; tomato yellow leaf curl virus;

XX Sardinian isolate; STRICV; transgenic; P-loop; CI gene;

XX full gene; dominant negative phenotype; ss.

XX Sardinian tomato yellow leaf curl virus.

OS Sardinian tomato yellow leaf curl virus.

XX Key Location/Qualifiers
FT 1..1080
FT /tag= 3 Res.(K227A)
FT /product= encodes 826 protein in which wild-type Lys
FT at position 227, i.e. within the NTP-
FT binding site, is replaced by Ala*
PN

MO9608573-A1.

XX 21-MAR-1996.
 PD 15-SEP-1995: 95MO-FR01192.
 XX 15-SEP-1994: 94FR-001040.
 PR (CNRS) CENT NAT RECH SCI.
 PA
 XX Gronenborn B:
 PL WPI: 1996-179947/18.
 XX P-PSDB: AAR88870.
 DR
 XX Prodn. of virus-resistant transgenic plants - using mutated genomic
 PT sequence from phytopathogenic DNA virus
 XX
 XX Disclosure: Fig 13: 93pp: French.
 XX
 CC Mutation of consensus amino acids in the NRP-binding site of
 CC geminivirus Rep protein is used to produce replication deficient
 CC viruses. The mutated viral nucleic acid is used for producing
 CC transgenic plants that are resistant to, or tolerant of, the native
 CC virus. The present sequence encodes a mutant form of the Rep (or C1)
 CC protein from the Sardinian isolate of tomato yellow leaf curl virus
 CC (STRIDE) in which the wild-type lys227 residue has been changed to an
 CC Ala residue. This substitution results in a virus that is resistant to
 CC transformation with the mutated virus were found to be resistant to
 CC stylxv, i.e the mutation results in a dominant negative phenotype.
 XX
 SQ Sequence 1080 BP: 355 A; 248 C; 210 G; 267 T; 0 other;

Alignment-scores:
 Quality: 211.00 Length: 69
 Ratio: 3.768 Gaps: 0
 Percent Similarity: 81.159 Percent Identity: 56.522

Alignment_block:
 US-09-289-346a-7 x AAT12904

Align seq 1/1 to: AAT12904 from: 1 to: 1080

```

2 LeuValTrpGlyIuPheGlnValAspGlyArgSerAlaArgIglyIcy 18
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
331 CTTGAATCGCGTACTTCAGATCCAGCAGCATCTGCTAGCGAGGACGA 380
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
18 sGlnThrSerAsnAspAlaAlaIaGluAlaLeuAsnAlaSerSerIysc 35
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
361 ACAAAGACGACACGACCTTACGACAGCAATTCACGACGACGACGAC 430
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
35 IuGluAlaIaGlnIleIleArgIuLysIleProGluLysTyrLeuPhe 51
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTGTGATTAAGCAATAGCCCTAGACATTAAGCTTCTA 480
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52 GlnPheHisAsnLeuAsnSerAlaLeuAlaIaIlePheAspLysThr 68
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTCAGATTAAGTAAGTAATTAAGATTACAGATTTCAGATTCCTC 530
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
68 oGluPro 70
   ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
531 CGCACCT 537
```



```

FEATURES
  source
    Location/Qualifiers
      1..646
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone_lib="NCI-60"
        /clone_lib="NCI-60"
        /lab_host="DHI08 (71 phase-resistant)"
        /note="Organ: brain; Vector: PCMV-SPORE; Site:1; Note:
        Site:2; Salt: Cloned unidirectionally. Primer: oligo dr.
        Average insert size 1.57 kb. Constructed by Life
        Technologies, Note: this is a NCI-CoAP Library."
BASE COUNT      150 a 198 c 197 g 141 t
ORIGIN
Alignment_scores:
  Quality:      68.00      Length:      42
  Ratio:        2.345      Gaps:      2
  Percent Similarity: 69.048      Percent Identity: 42.857
Alignment_block:
  US-09-289-346a-7 x BR342302 ..
Align seq 1/1 to: BR342302 from: 1 to: 646
3 ValTTPGly...GlnPhgInValaSPGlyArgSerAlaArgGlyCly 18
|||||.....|
202 GTGTGGGCGGCTACGACGCTCTGCTGCGACGGGCGACCGGGGCGGCGAT 251
18 sginthrsrAsnAspAlaAlaAlaAlaAlaAlaAlaAlaSerSerCys 35
|||||.....|
252 TGAAGTCGGGAGCGGGCGACCGACAGAGGCTGACGGGCGCCAAACCCCTG 301
35 lncUaAlaLeuGlnInlIleTargGlu 43
|||||.....|
302 Ah.....ATCCCTGAA 312
seq_name: gb_est2: B1251979
seq_documentation_block:
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DEFINITION 602691947F1 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:5086779 5'.
ACCESSION  B1251979.1 GI:14801989
VERSION    B1251979.1 GI:14801989
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 677)
  AUTHORS  NIH_MGC http://mhc.nci.nih.gov/.
  TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL  Unpublished (1999)
  COMMENT  Contact: Robert Strausberg, Ph.D.
            Email: ccapbs-f@mail.nih.gov
            Tissue Procurement: CGAP (Stanford)
            CDNA Library Preparation: JING Hong/Rubin Laboratory
            CDNA Sequencing by: Inoue Genomex, Inc.
            DNA Sequencing by: Inoue Genomex, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LML at:
            http://image.jni.gov
            Plate: LMC1843 row: c column: 04
            High quality sequence stop: 676.
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                /db_xref="taxon:9606"
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                /clone_lib="NIH_MGC_100"
                /lab_host="NIH_MGC_100"
                /tissue_type="hepatocellular carcinoma, cell line"

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FEATURES
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        /clone_lib="NIH_MGC_97"
        /lab_host="DHI08"
        /note="Organ: testis; Vector: phiuescripTR (modified
            /lab_host="DHI08 (phage-resistant)"
            /note="Organ: liver; Vector: pOT87; Site:1; XhoI; Site:2;
            XhoI; cDNA made by oligo-dr priming. Directionally cloned
            into EcoRI/XhoI sites using the following 5' adaptor:
            size selected >500bp for average insert size
            of Gerald M. Rubin (University of California, Berkeley)
            using zap-cDNA synthesis kit (Stratagene) and Superscript
            II RT (Life Technologies). Note: this is a NIH_MGC
            Library."
BASE COUNT      162 a 197 c 198 g 120 t
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Alignment_scores:
  Quality:      68.00      Length:      49
  Ratio:        2.125      Gaps:      0
  Percent Similarity: 65.306      Percent Identity: 32.653
Alignment_block:
  US-09-289-346a-7 x B1251979 ..
Align seq 1/1 to: B1251979 from: 1 to: 677
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127 AGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 176
28 AlaAsnAlaSerSerCysGlnGlnAlaAlaAlaAlaAlaAlaAla 45
177 ATCTCGGATCTCAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 226
45 lncProGluTyrLeuPhgGlnPhgHisAsnLeuAlaSerAlaLeu 60
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seq_name: gb_est2: B6720738
seq_documentation_block:
LOCUS      B6720738          680 bp      mRNA      EST      08-MAY-2001
DEFINITION 602691947F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4824371 5'.
ACCESSION  B6720738
VERSION    B6720738.1 GI:13999925
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 680)
  AUTHORS  NIH_MGC http://mhc.nci.nih.gov/.
  TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL  Unpublished (1999)
  COMMENT  Contact: Robert Strausberg, Ph.D.
            Email: ccapbs-f@mail.nih.gov
            Tissue Procurement: Mikiros Palkovits, M.D., Ph.D.
            CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
            Toshiyuki and Piero Carninci (RIKEN)
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)
            CDNA Sequencing by: Inoue Genomex, Inc.
            DNA Sequencing by: Inoue Genomex, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LML at:
            http://image.jni.gov
            Plate: LML10735 row: m column: 12
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                /note="Organ: testis; Vector: phiuescripTR (modified

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Ratio: 2.125 Gaps: 0
Percent Similarity: 65.306 Percent Identity: 32.653

Alignment block:
US-09-289-346a-7 x BE304728

Align seg 1/1 to: BE304728 from: 1 to: 803

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144 AGGAGCGGCGCGCCGCCCTCCCAAAAGCAATGSGATTTCACCTGACAA 193
28 alaunhAlaSerSerLysGlnGluAlaLeuGlnIleIleArgGluLysI 45
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
194 ATCTCGCGATCCAGAGACACAAACAAATATACAGCGCATTCGAGAGCA 243
45 leProGluLysTyrLeuPheGlnPheIleAsenIleuAsnSerAlaLeu 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
244 AGCCTCAACACACACACTTCACCGCGCGCTCTGCTGCGACGCTCTG 290
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FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-51

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Quality: 213.00 Length: 70
Ratio: 3.672 Gaps: 0
Percent Similarity: 82.857 Percent Identity: 58.571

Alignment_block:
US-09-289-346a-7 x US-08-838-151A-51
Align seg 1/1 to: US-08-838-151A-51 from: 1 to: 1062

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|||||
328 ACAATCGAATGGGACAAATTCGCAATGCGACGCAATCTGCACAAAGG 377
17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
|||||
378 TCAGCAGTGTCCCAACGACATTCGCAATGCAAGCATTAAAGCAATTCA 427
34 ySGlGluAlaLeuGlnIleAlaLeuGluLysTrpGluLysTrpLeu 50
|||||
428 TTGAATCTGCTGTGACATATGAAAGAGAACACGGAAGATTCGTC 477
51 PheGlnPheIleAsnLeuAsnSerAlaLeuAlaIlePheAspLysTh 67
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478 CTCACATCGACACATCCGCTCTATCTGCAACGAGATCTTCGCAAGT 527
67 rProGluPro 70
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seq_documentation_block:
Sequence 54, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Scout, John T
APPLICANT: Liu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME/Address: Milnamow & Katz, 38 978
ROOSEVELT UNIVERSITY
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460

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INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDNESS: single
MOLECULAR TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic GeminiVirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
FEEDBACK:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-54

Alignment_scores:
Quality: 213.00 Length: 70
Ratio: 3.672 Gaps: 0
Percent Similarity: 82.857 Percent Identity: 58.571

Alignment_block:
US-09-289-346a-7 x US-08-838-151A-54
Align seg 1/1 to: US-08-838-151A-54 from: 1 to: 1062

1 ThrleuValTrpGlyIuphGlnValAspGlyAyrSerAlaLeuGlyL 17
|||||
328 ACAATCGAATGGGACAAATTCGCAATGCGACGCAATCTGCACAAAGG 377
17 yCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSerL 34
|||||
378 TCAGCAGTGTCCCAACGACATTCGCAATGCAAGCATTAAAGCAATTCA 427
34 ySGlGluAlaLeuGlnIleAlaLeuGluLysTrpGluLysTrpLeu 50
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428 TTGAATCTGCTGTGACATATGAAAGAGAACACGGAAGATTCGTC 477
478 CTCACATCGACACATCCGCTCTATCTGCAACGAGATCTTCGCAAGT 527
51 PheGlnPheIleAsnLeuAsnSerAlaLeuAlaIlePheAspLysTh 67
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528 GCCGACCA 537

seq_name: /cgnl_7/ctcdatg/1/lna/6b_CONB.seq:US-08-838-151A-43
seq_documentation_block:
Sequence 43, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Scout, John T
APPLICANT: Liu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1077
? US-08-809-103b-1

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381 ACAGACACCCACGACGCTTACGCAAGCAATTACGCAAGCACTAAC 430
35 LcGluAlaLeuGlnIleLeuArgGluGlyIleProGluGlySTyLeuPhe 51
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTGATGTAATTAAGAAATTACGCCCTAAGATACGTTCTA 480
52 GlnPheHisAsnLeuAsnSerAlaLeuAlaAlaIlePheAspGlySTyPr 68
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? Patent No. 6133505
? GENERAL INFORMATION:
? APPLICANT: GENEWORM, Bruno
? TITLE OF INVENTION: TRANSGENIC DNA VIRUS RESISTANT
? TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
? NUMBER OF SEQUENCES: 17
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: YOUNG & THOMPSON
? STREET: 745 South 23rd Street
? CITY: Arlington
? STATE: Virginia
? ZIP: 22202
? COUNTRY: U.S.A.
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? FILING DATE: 17-MAR-1997
? CLASSIFICATION: 800
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PR 94.11040
? FILING DATE: 15-SEP-1994
? PRIOR APPLICATION DATA:

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? APPLICATION NUMBER: WO PCT/FR95/01192
? FILING DATE: 15-SEP-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: PATCH, Andrew J.
? RESIDENTIAL NUMBER: 2, 925
? RESIDENTIAL ADDRESS: 521-2297
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 521-2297
? TELEFAX: (703) 685-0573
? TELEX: 248425 EMBON
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1148 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
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? LOCATION: 1..1077
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||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGGCTCTGATGTAATTAAGAAATTACGCCCTAAGATACGTTCTA 480
52 GlnPheHisAsnLeuAsnSerAlaLeuAlaAlaIlePheAspGlySTyPr 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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531 GGCACCT 537

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? Patent No. 6133505
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? APPLICANT: GENEWORM, Bruno
? TITLE OF INVENTION: TRANSGENIC DNA VIRUS RESISTANT
? TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
? NUMBER OF SEQUENCES: 17
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: YOUNG & THOMPSON
? STREET: 745 South 23rd Street
? CITY: Arlington
? STATE: Virginia
? ZIP: 22202
? COUNTRY: U.S.A.
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible

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? OPERATING SYSTEM: PC-DOS/MS-DOS
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? APPLICATION NUMBER: US/08/809,1038
? FILING DATE: 17-MAR-1997
? PRIORITY DATE: 17-MAR-1997
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: FR 94.11040
? FILING DATE: 15-SEP-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: WO PCT/FR95/01192
? FILING DATE: 15-SEP-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: [REDACTED]
? REGISTRATION NUMBER: 32,925
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 521-2297
? TELEFAX: (703) 685-0573
? ETELEX: 248425 EMDON
? INFO: 248425 EMDON
? SOURCE CHARACTERISTICS: 5:
? LENGTH: 1150 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
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? LOCATION: 1..1077
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? Patient No. 6291743
? GENERAL INFORMATION:
? APPLICANT: Seoul, John T
? APPLICANT: Liu, Hang T
? APPLICANT: Maxwell, Douglas
? APPLICANT: Ahlquist, Paul

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? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing GeminiViruses
? TITLE OF INVENTION: Genes
? NUMBER OF SEQUENCES: 63
? CORRESPONDENCE ADDRESS:
? CORRESPONDENCE: Dressler, Rocky, Millanow & Katz
? STREET: 400 Industrial Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: [REDACTED]
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5460
? TELEFAX: 312-616-5460
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1150 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGIN:
? ORGANISM: Tomato Mottle Gemini Virus
? INDIVIDUAL ISOLATE: Florida
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 44..1127
? PUBLICATION INFORMATION:
? AUTHORS: Gilbertson, RL
? AUTHORS: Gilbertson, SH
? AUTHORS: Paplomatas, EJ
? AUTHORS: Rojas, MR
? AUTHORS: Hou, YM
? AUTHORS: Maxwell, DP
? TITLE: Pseudorecombination between the infectious
? TITLE: cloned DNA components of tomato mottle and bean
? JOURNAL: Plant Disease
? VOLUME: 74
? PAGES: 23-31
? DATE: 1993
? US-08-838-151A-1

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? Ratio: 3.638 Gaps: 0
? Percent Similarity: 82.657 Percent Identity: 55.714

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LOCUS AF289227 1363 bp DNA VRL 20-AUG-2000
DEFINITION Sweet potato leaf curl virus replication association protein (ACI)
and AC4 (Ac4) genes; complete cds.
ACCESSION AF289227
KEYWORDS
SOURCE sweet potato leaf curl virus
ORGANISM sweet potato leaf curl virus
VIRUSES: ASPMA Viruses; Geminaliviridae; Begomovirus.
REFERENCE Lotnickal,P., Valverde,R.A., Clark,C.A., Sim,J. and De La Torre,R.
AUTHORS Detection of a geminivirus infecting sweet potato in the United
TITLE Plant Dis. 82, 1253-1257 (1998)
JOURNAL 2 (bases 1 to 1363)
RECORDS Lotnickal,P. and Valverde,R.A.
DIRECT SUBMISSION Submitted (18-JULY-2000) Plant pathology and Crop Physiology,
Louisiana State University, 302 Life Sciences Bldg., Baton Rouge,
LA 70803, USA
FEATURES
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location/Qualifiers
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/note="subgenomic DNA"
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/complement(285..1229)
/note="full"
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/translaton="MAMPKRKIDANNPTTPPCSLSRKEDCAQLNATITPNSKKIT
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OENLYNKTDITSPPSYSPPSSSFNNVAIPISDMALEWMDAARDPRTSY
IEDEPRGTGCVARSLGFPHNYTCGLHDIPLRVYSNNWNVDIVNPÖTLHKRPKMG
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complement(815..1072)
/gene="AC4"

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BASE COUNT      359 a       296 c       327 g       401 t
ORIGIN

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    Quality:   278.00          Length:           68
    Ratio:     4.557              gaps:         0
Percent Similarity: 89.706        Percent Identity: 80.882

alignment_block:
US-09-289-346A x AF288227/rev ..

Align seq 1/I to reverse of: AF288227 from: 1 to: 1383

1  TrrleavtAtPpDlyGluaAlaAlaAlaNGSVYVRSGSRrLAAGSGLY91 17
|||||.....|.....|.....|.....|.....|.....|.....|.....|
902 ACCMCACCTCGGGGGAATTCCAGGCGAGGCGAGGTCTGTAGAGGAG 853
17 ycygclnrThSerAmSpAlaAlaAlaAGUALAGUALaluaAlaSerSELT 34
|||||.....|.....|.....|.....|.....|.....|.....|.....|
852 CGAGGCAGTCGACAGCACGACGACGACGACGACGACGACGACGACGAC 803
34 ysglucAlaLeuChIetleAgGSluyvGIyIEpTGcUlySTYLau 50
|||||.....|.....|.....|.....|.....|.....|.....|.....|
802 AAGAAGCTCGCTGCCAAATAATCATCGSGAGAAATCCCAGAAAATATTTA 753
51 PhelInPherIsAnluAsnSerSasnuLeuAsPaRgllePhesApSynH 67
752 TTTCATTTCAATCAATTTATTTGATTTGATTTGATTTGATTTTTCCTCTC 703
67 rPro 68
|||
702 ACCT 699

seq_name: qb.v1:AF104036
seg documentation_block:
LOCUS                2828 bp    DNA    circular    VRL             05-AUG-1999
DEFINITION           AF104036
SOURCE               Sweet potato leaf curl virus DNA A, complete sequence.
ACCESSION            AF104036
VERSION              AF104036.1 GI:5702158
KEYWORDS
SOURCE ORGANISM
Okinawa
REFERENCE
AUTHORS              Lotrakul,P., Valverde,R.A., Clar,F.C.A., Sim,J., and De La Torre,R.
TITLE                Detection of geminiviruses infecting sweet potato in the United States
JOURNAL              Plant Dis.- 82, 1253-1257 (1998)
REFERENCE
REMARKS              1. (bases 1 to 2828)
                     Cloning of a DNA-RNA-like genomic component of sweet potato leaf curl
                     virus : nucleotide sequence and phylogenetic relationships
                     Molecular Plant Pathology: On-line (1999)
                     http://www.bppp.org.uk/mpap/1999/0422lotrakul/
                     3. (bases 1 to 2828)
                     Lotrakul,P. and Valverde,R.A.
                     Direct Submission
                     Submitted (Sep-1998), Plant Pathology and Crop Physiology,
                     Louisiana State University, 302 Life Sciences Bldg., LSU, Baton
                     Rouge, LA 70803, USA
FEATURES
source
Location/Qualifiers
1..2828

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[illegible]

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/ gene="AC4"
/ note="FL4"
/ codon_start=1
/ protein_id="A0047174.1"
/ db_xref="GI:5702164"
/ translation="MGULSMKCSKSNSSAQAIDSSISMRDRIITFTPSRELNP
APMSSTIRGIPSPSEVNSRSTADLEESHLITOPOL."
BASE COUNT      741 a      606 c      675 g      806 t
ORIGIN

Alignment_scores:
  Quality: 278.00      Length: 68
  Ratio: 4.557      Gaps: 0
  Percent Similarity: 89.706      Percent Identity: 80.882

Alignment_block:
  US-09-289-346a-8 x AF104036/rev

Align seg 1/1 to reverse of: AF104036 from: 1 to: 2828

1 ThleuValTrpGlyAlaAlaValaIaApolYAGseGalaAaglyG 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2354 ACATCATCGTGGGGGTATTCGACGCGCCAGCCGATCTCGTACAGGAG 2305
17 YCGSLThrSerAsnAPAlaAlaAclAlaLeuAsnAlaSerSerL 34
2304 CCAGCAGCTGCTACGACGCGCCAGCCGATCTCGTACAGGAGTCTA 2255
34 YGSLGAlaAlaLeuGlnTlleAaglyuylslePProGlyuylsleu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2254 AAGAGCTGCGCTTCGCAATATCATGAGGAGAACACTCCGAAAAATTTTA 2205
51 PhcGlnPhcHisAsnLeuAsnSerAsnLeuAspATGlllePhaSplyth 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2204 TTTCATTTCATAAATTTGATTGATTGATTGATTAAGAGATTTTTCCTCC 2155
67 PPro 68
|||||
2154 ACCT 2151

seq_name: gb_v1:SGU67926

seq_documentation_block:
  LOCUS      SGU67926      554 bp      DNA      VRL      28-JAN-1998
  DEFINITION  Sida golden mosaic geminivirus Rep protein (AC1) gene, partial cds.
  ACCESSION  U67926
  VERSION    U67926.1 GI:1546801
  KEYWORDS   Sida golden mosaic virus.
  SOURCE      Sida golden mosaic virus.
  ORGANISM    Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
  REFERENCE   1 (bases 1 to 554)
  AUTHORS     Roye,M.E., McLaughlin,W.A., Nakhlá,N.K. and Maxwell,D.P.
  TITLE       Genetic Diversity among geminiviruses associated with the weed
  species Sida spp. Macropitulum lathyroides, and Wissadula
  amplissima from Jamaica
  JOURNAL     2 (bases 1 to 554)
  JOURNAL     2 (bases 1 to 1258 (1997))
  REFERENCES  Roye,M.E., McLaughlin,W.A. and Maxwell,D.P.
  TITLE       Direct Submission
  AUTHORS     Submitted (23-AUG-1996) Plant Pathology, University of Wisconsin,
  1630 Linden Drive, Madison, WI 53706-1598, USA
  JOURNAL     Location/Qualifiers
  FEATURES    1. organism="Sida golden mosaic virus"
  /strain="Jamaica"
  /isolate="Jamaica, May 1993"
  /db_xref="taxon:51034"
  /note="DNA A component"
  /complement(1..554)
  /gene="AC1"

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```

CDS
  complement(1..>554)
  / gene="AC1"
  / note="replication-associated protein"
  / codon_start=1
  / protein_id="A0897865"
  / db_xref="GI:1546802"
  / translation="SISKEPALASQIOTLKTTPVKKFKTKICRLHLDSEPHVLIQPE
GKYNKNNRPFPLVSPRSVFHPIHPIGKASSDSVSYEKSCDTI ENQVQIDQSA
RGGQVANDAAEALNSGKTKMDLKIIRRLPERVLYFIHLNSNIDRLTSKPPSPS
HFFPLSTFANPQAGNSMADDTGCR"
BASE COUNT      121 a      127 c      139 g      167 t
ORIGIN

Alignment_scores:
  Quality: 275.00      Length: 70
  Ratio: 4.297      Gaps: 0
  Percent Similarity: 91.429      Percent Identity: 71.429

Alignment_block:
  US-09-289-346a-8 x SGU67926/rev

Align seg 1/1 to reverse of: SGU67926 from: 1 to: 554

1 ThleuValTrpGlyAlaAlaValaIaApolYAGseGalaAaglyG 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
290 ACATCATCGTGGGGGTATTCGACGCGCCAGCCGATCTCGTACAGGAG 241
17 YCGSLThrSerAsnAPAlaAlaAclAlaLeuAsnAlaSerSerL 34
240 TCAGCAACGCTACGACGCGCGCGAGCCATTCGATTCGGACA 191
34 YGSLGAlaAlaLeuGlnTlleAaglyuylslePProGlyuylsleu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
190 AAGAGAGATGCTCATATCATGAGAGAGAGATTCACAGAGATATTC 141
51 PhcGlnPhcHisAsnLeuAsnSerAsnLeuAspATGlllePhaSplyth 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
140 TTTCAGTATCCACACCTATCCAGTAAATATCATGAGATTCGATTAAGCC 91
67 PProGlyuylsle 70
|||||
90 TCAGCAACCC 81

seq_name: gb_v1:YEI132548

seq_documentation_block:
  LOCUS      YEI132548      2763 bp      DNA      circular VRL      01-FEB-1999
  DEFINITION  Ipomoea yellow vein virus YZ, VI, C3 and C2 genes.
  ACCESSION  A1132548
  VERSION    A1132548.1 GI:4210720
  KEYWORDS   C2 gene; C2 protein; C3 gene; C3 protein; coat protein; VI gene; VZ
  gene; V2 protein.
  SOURCE      Ipomoea yellow vein virus.
  ORGANISM    Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
  REFERENCE   1 (bases 1 to 2763)
  AUTHORS     Banks,G.K., Bedford,I.D., Bellis,J.P.,J., Cerezo,E.R. and Markham,P.G.
  TITLE       Direct Submission
  JOURNAL     Submitted (26-JAN-1999) Banks G.K., Virus Research, John Innes
  Centre, Norwich Research Park, Colney Lane, Norwich, NR4 6JL, UK
  JOURNAL     2 (bases 1 to 2763)
  JOURNAL     A novel geminivirus of Ipomoea indica (Convolvulaceae) from southern
  Spain
  JOURNAL     unpublished
  JOURNAL     Location/Qualifiers
  FEATURES    1..2763
  /organism="Ipomoea yellow vein virus"
  /strain="Ipomoea indica"
  /specific_host="Ipomoea indica"
  /db_xref="taxon:87832"

```



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34 ysglucualaleuglnlleielauglulysllepfcgulytyleu 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
194 AGAGAGGCGCTCATACGTACGAGACAGAGTTCGGAAGAGTTCTC 145
51 PhagInpHeIsaenIeuaSenSerntleuaSpaGlllePhaSpIySth 67
||||| ||||||| ||||||| ||||||| ||||||| |||||||
144 TTTCAATTCACACCTATCCAGTACGTACGATTCATTCATGACGA 95
67 rpfroglupro 70
||||| |||||||
94 TTCGGAACCA 85
seq_name: gb_v1:AF098940
seq_documentation_block:
LOCUS AF098940 1405 bp DNA VRL 04-MAR-1999
DEFINITION Macropitillum golden mosaic geminivirus strain 1
repliation associated protein (rep) and coat protein (cp) genes.
ACCESSION AF098940
VERSION AF098940
KEYWORDS AF098940.1 GI:4336584
SOURCE Macropitillum golden mosaic geminivirus.
ORGANISM Macropitillum golden mosaic geminivirus.
VIRUSES: ssDNA viruses; Geminiviridae; Begomovirus.
AUTHORS (bases 1 to 1405)
Roye,M.E., McLaughlin,M.A. and Maxwell,D.P.
TITLE Genetic diversity and phylogeny of whitefly-transmitted geminiviruses from Jamaica
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1405)
AUTHORS Roye,M.E., McLaughlin,M.A. and Maxwell,D.P.
Molecular characterization of two distinct geminiviruses infecting Macropitillum golden mosaic geminivirus from Jamaica
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1405)
AUTHORS Roye,M.E., McLaughlin,M.A. and Maxwell,D.P.
TITLE Direct Submissions
JOURNAL Submitted (14-OCT-1998) Biotechnology Centre, University of the West Indies, Mona, Kingston 7, Jamaica
FEATURES
location/Qualifiers
1..1405
/organism="Macropitillum golden mosaic geminivirus"
/species="Jamaica strain 1"
/strain="Jamaica strain 1"
/db_xref="taxon:51676"
/country="Jamaica"
/contig="pGEM4Z_PMSJ3"
/complement(<1..701)
/gene="rep"
/complement(<1..701)
/gene="cp"
/codon_start=1
/product="replication associated protein"
/protein_id="AA017849.1"
/translation="MTKPKSFKAKKATPLTQCSLKKEALSQLNTLNPNYKKEI KICRPHEDGPHLIVTFOGKQKTNLLEDYSPRSNAHRIHNIQKASSSYVS YVKEQDITLWGVPIQIGRSACGQTSNDAAALANSGIKFAARIVREKLEPFFL OYHNMSSMDRIEKNDEWMAFPFLSTFNVDEDMADYDTGKSNAAAPRMST IVEQSRCKTHMAC"
misc_feature
702..1030
/location="gemogenic region"
gene
1031..>1405
/genes="cp"
/genes="cp"
1031..>1405
/gene="cp"
/codon_start=1
/product="coat protein"
/protein_id="AA017849.1"
/db_xref="GI:4336583"
/translation="MKRDSGKHTTTPVKAKSRRLNYSFNGTIGPSKNAQDWKRMK

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YKPRATYRLTSHDVPKCEGPKCKVOSTEQRHDISSHVKYWCISDPTRGVITRHVK
RCVYKVEVITLKIWMEDNINSC*
BASE COUNT 328 a 333 c 357 g 386 t 1 others
ORIGIN
alignment_scores:
Quality: 267.00 Length: 70
Ratio: 4.306 Gaps: 0
Percent Similarity: 88.571 Percent Identity: 70.000
alignment_block:
US-09-289-346a-8 x AF098940/rev
Align seg 1/1 to reverse of: AF098940 from: 1 to: 1405
1 Thrlaewa1rfgylgylalalalaspdlvaygservlaaag1ygl 17
||||| ||||||| ||||||| ||||||| ||||||| |||||||
374 ACCATCATGCGCGCTCATACGTACGAGACAGAGTTCGGAAGAGTTCTC 325
17 ycsqtlpfrsopraspaalalalalagllalaleuaSpaGlllePhaSpIySth 34
||||| ||||||| ||||||| ||||||| ||||||| |||||||
324 TCAGCAACATTCATTCACACCTATCCAGTACGATTCATTCATGACGA 275
34 ysglucualaleuglnlleielauglulysllepfcgulytyleu 50
||||| ||||||| ||||||| ||||||| ||||||| |||||||
274 AGAGAGGCGCTCATACGTACGAGACAGAGTTCGGAAGAGTTCTC 225
51 PhagInpHeIsaenIeuaSenSerntleuaSpaGlllePhaSpIySth 67
||||| ||||||| ||||||| ||||||| ||||||| |||||||
224 TTTCAATTCACACCTATCCAGTACGTACGATTCATTCATGACGA 175
67 rpfroglupro 70
||||| |||||||
174 TTCGGAACCA 165
seq_name: gb_v1:AF026553
seq_documentation_block:
LOCUS AF026553 1165 bp DNA VRL 03-NOV-1997
DEFINITION Potceto yellow mosaic virus Tomato strain AV1 and AC1 genes, partial
cDS:26553
ACCESSION AF026553.1 GI:2683073
VERSION AF026553.1
KEYWORDS Geminiviridae.
SOURCE Geminiviridae.
ORGANISM Viruses; ssDNA viruses.
REFERENCE 1 (bases 1 to 1165)
AUTHORS Guzman,P., Arredondo,C.R., Emmitly,D., Portillo,R.J. and Gilchrist,S.P.
TITLE Partial Characterization of Two Whitefly-Transmitted Geminiviruses Infecting Tomatoes in Venezuela
JOURNAL Plant Dis. 81, 312-312 (1997)
JOURNAL 2 (bases 1 to 1165)
AUTHORS Guzman,P., Arredondo,C.R., Emmitly,D., Portillo,R.J. and Gilchrist,S.P.
TITLE Direct Submissions
JOURNAL Submitted (24-SEP-1997) Plant Pathology, University of California-Davis, Department of Plant Pathology, Davis, CA 95616, USA
FEATURES
location/Qualifiers
1..1165
/organism="Geminiviridae"
/species="Geminiviridae"
/strain="AV1"
/db_xref="taxon:10811"
/notes="Bipartite genome: whitefly-transmitted; DNA-A fragment obtained by PCR from tomato sample from State of Monagas (Venezuela)"
/complement(<1..153)
/notes="Capsid protein"
/product="AV1"

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CDS

/protein_id="AB282606.1"
/db_xref="GI:2583075"
/translation="MRRSDAHWSMAGTSKWSRNANVSPSGICPRLINKAEVNRPM
464 C>1165
/note="replication-associated protein"
/codon_start=1
/product="AC1"
/db_xref="GI:2583074"
/translation="MRGSGSTSKAKNTLTTCGSLSEKDAISQIQNTLTPNKKI
YKNSKDTLMDGTOIDSRNAGSGGOTDAADAAALNSGTEEMAKTIKELPERIF
VYNNLSNLDLRITPKAPVNMAPPPLSFSTIVPHEDQENSHCYCRSAANAGETISII
IEDSRCTKTMACRC"

BASE COUNT 350 a 264 c 256 g 295 t

ORIGIN

alignment_scores:
Quality: 261.00 Length: 70
Ratio: 4.078 Gaps: 0
Percent Similarity: 91.479 Percent Identity: 68.571

alignment_block:
US-09-289-346a-8 x AF026553 ..

Align seg 1/1 to: AF026553 from: 1 to: 1165

1 ThrleuValTrpGlyAlaIalaValaAspGlyArgSerAlaArgGly 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
791 ACCATCGATGAGGATGTCGACGATGTCGACGAGAGAGTGCAGAGTGG 840
17 yCysGlnTrpSerAsnAspAlaIalaIaGlyAlaLeuAsnAlaSerSerL 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
841 GCAGACAGACGAGACGAGACGAGACGAGACGAGACGAGACGAGACGAG 890
34 ySgLIuAlaLeuGlnIleIleArgGlyLysIleProGlyLysTyrLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
891 AGGAGAGACCATGAAATCATTAAGAAAGAGAGTCCCGAAGATTCTT 940
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgTllePheAspLysT 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
941 TTTCAGATGATCAACGATTCGACGATGACGATGACGATTCCTCATGAC 990
67 ProGluPro 70
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
991 TCCCAATCCG 1000

seq_name: gb.v1:AB001315

seq documentation block:
LOCUS AB001315 570 bp DNA 13-Feb-1999
DEFINITION Tobacco leaf curl virus CI and C4 genes, clone YOKOHMA3-1, partial
and complete cds.
ACCESSION AB001315
VERSION AB001315.1 GI:3798714
KEYWORDS
SOURCE tobacco leaf curl virus (isolate: YOKOHMA3,
tobacco leaf curl virus (tobacco leaf curl virus)
ORGANISM tobacco leaf curl virus
REFERENCE 1 (bases 1 to 570)
AUTHORS Ooi,K.
TITLE Direct Submission
JOURNAL Submitted (19-Feb-1997) to the DDBJ/EMBL/GenBank databases.
Kazuyuki Ooi, Kyushu University, Department of Biology, 6-10-1
Kasuga 816, Kasuga, Fukuoka 816, Japan.
(E-mail:kooi@bio.kyushu-u.ac.jp, Tel:+81-92-642-2624,
Fax:+81-92-642-2645)
REFERENCE 2 (bases 1 to 570)
AUTHORS Ooi,K., Ohshita,S., Ishii,I. and Yahara,T.
TITLE Molecular Phylogeny of Geminiiviruses Infecting wild plants in Japan

JOURNAL J. Plant Res. 110, 247-257 (1997)
FEATURES
source Location/Qualifiers
1..570
/isolate="YOKOHMA3"
/isolate="YOKOHMA3"
/specific_host="Nupatorium makinoi"
/db_xref="taxon:67762"
/clone="YOKOHMA3-1"
complement(1..570)
/gene="C1"
complement(4..>570)
/codon_start=1
/protein_id="BA34033.1"
/db_xref="GI:4426541"
/translation="EVALISQIQNTLTPNKLYIKRICRELHDSGPHLYLLOPEGKYK
ONARRFDIVSPFSRAPHNPITGAKSSDVSYIKDQPTLMDGTFOIDRARGCG
ONANDCAGALANASKAEKALATIRERLPKIDPTQVYNNLSNLDLRITAPPLEVCPPT
ASSFDVPERELDSMASHNSVSSAARNRPM"
gene
complement(231..488)
/gene="C4"
/codon_start=1
/protein_id="BA34034.1"
/db_xref="GI:3798715"
/translation="HEALISKCTGSSKANTNAKIDTSSITWPPQDQHSITPRELNP
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BASE COUNT 141 a 121 c 126 g 182 t

ORIGIN

alignment_scores:
Quality: 258.00 Length: 65
Ratio: 4.161 Gaps: 1
Percent Similarity: 72.941 Percent Identity: 60.000

alignment_block:
US-09-289-346a-8 x AB001315/rev ..

Align seg 1/1 to reverse of: AB001315 from: 1 to: 570

1 ThrleuValTrpGlyAlaIalaValaAspGlyArgSerAlaArgGly 17
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 ACCTCGATGAGGAGACTTCGACGATGACGAGAGAGTGCAGAGTGG 269
17 yCysGlnTrpSerAsnAspAlaIalaIaGlyAlaLeuAsnAlaSerSerL 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
268 CTGCGAGATGCTACGACGACGATGCGAGTGAATGATGATGCTGCTCC 219
34 ySgLIuAlaLeuGlnIleIleArgGlyLysIleProGlyLysTyrLeu 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
218 AGCGACAGACGATGACGATGACGAGACGAGACGAGACGAGACGAGAC 169
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgTllePheAspLysT 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
168 TTTCAGATGATCAATTAATGATTAATTAATGATTAATGATTAATGATTC 119
64

118 GTTCGAGGTTTTCCTTTCGCTTCACGATGACGATGATTCATGATGTC 69
68 ProGlu 69
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
68 CAGAA 64


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2216 AGCTAATGATGCTGCGCAGAGGCGCTTAATGCGTTTCAGCTGAGCAG 2167
37 1aLeuGlnIleIleArgGlnIleProGluIuYsTYrLeuPheGlnPhe 53
2166 CTTTACGATATATAGGAGAAAGCCCTGAAAGATTTTATTTTCATAT 2117
54 HisAsnLeuAsnSerAsnLeuAspArgIlePheAspIysThrPro 68
2116 CATATATTTAAATATATATAGATGATTTT.....ACCGCT 2078
seq_name: /cgnl_8/gcgdata/geneseq/NA1995.DAT:AA084371
seq_documentation_block:
ID AA084371 standard: DNA: 434 BP.
AC AA084371;
XX
XX 19-AUG-1995 (first entry)
XX
XX Gemini virus-specific poly(ribozyme)-E target sequence.
XX
XX Ribozyme target sequence: poly(ribozyme)-E:
KW Tomato leaf curl virus; RNA cleavage; tomato transgenic plant;
KV virus disease-resistance; ss.
XX
XX Tomato leaf curl virus.
XX
XX misc_feature 13..43
XX /tag= a
XX /note= "Ribozyme R1 target sequence"
XX
XX misc_feature 26..28
XX /tag= b
XX /note= "Ribozyme R1 cleavage site"
XX
XX misc_feature 32..42
XX /tag= c
XX /note= "Ribozyme R2 target sequence"
XX
XX misc_feature 325..327
XX /tag= d
XX /note= "Ribozyme R2 cleavage site"
XX
XX misc_feature 384..414
XX /tag= e
XX /note= "Ribozyme R3 target sequence"
XX
XX misc_feature 397..399
XX /tag= c
XX /note= "Ribozyme R3 cleavage site"
XX
XX W05030404-A.
XX
XX 02-FEB-1995.
XX
XX 22-JUL-1993: 93MO-EP01946.
XX
XX 22-JUL-1993: 93AU-0047014.
XX
XX 22-JUL-1993: 93MO-EP01946.
XX
XX (BIOC-) BIOCEN SA.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX Baudino S, Comau D, Dry JB, Gribner V, Lence P,
XX Mason J, Rezaiian MA, Rigden JE, Rezaiian MA:
XX WPI: 1995-075232/10.
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX and/or assembly of viruses by cleaving target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX
XX Example 10: Fig 11b, 90pp; English.
XX
XX The sequence is a tomato leaf curl virus target sequence for
XX poly(ribozyme)-E, which hybridizes to and cleaves the sequence and
XX thereby reduces replication, infection and/or assembly of the virus
CC

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CC substantially. The ribozyme may be expressed in a transgenic plant,
CC e.g. tomato, to confer virus disease-resistance.
XX
XX Sequence 434 BP: 126 A: 86 C: 91 G: 131 T: 0 other:
XX
XX alignment_scores:
XX      Quality: 230.00      Length: 85
XX      Ratio: 3.770      Gaps: 1
XX      Percent Similarity: 71.765      Percent Identity: 54.118
XX
XX alignment_block:
XX US-09-289-346a-8 x AA084371
XX
XX Align seq 1/1 to: AA084371 From: 1 to 434
XX
XX      1 ThrLeuValTrpGlyIuAlaIaValAspIYrGserAlaArgIyl 17
XX      |||||
XX      99 ACCCTGATATGAGGAGACATTTCAGATGAGCAGCTGCAAGAGGG 144
XX      17 CysGlnTrpSerAsnAspAlaAlaAlaGlnIleuAsnAlaSerSgt 34
XX      |||||
XX      145 AACACATGCCACATGACGCTTACGCCACGCGCTTACATCGAAGTA 194
XX
XX      34 yscIuGlnIaLeuGlnIleIleArgGlnIuYsIleProGluIuYrLeu 50
XX      |||||
XX      195 AGTCAGAGGCTCTTACGCTCTTACGCGAATTCAGCCCTTAAGATATGTT 244
XX      51 PheGlnPheIleAsnLeuAsnSerAsnLeuAspArgIle..... 63
XX      245 TTACATTTCTATATATTTAATNGTATTTAGATPGAGATTTTACACCTCC 294
XX      64 .....
XX      295 GTTGAGAGCTTATGCTTCCCTTTTATCTCTCTTTGATGAGATTC 344
XX      68 rooIu 69
XX      |||||
XX      345 CACGA 349
XX
XX seq_name: /cgnl_8/gcgdata/geneseq/NA1995.DAT:AA084372
XX
XX seq_documentation_block:
XX ID AA084372 standard: DNA: 479 BP.
XX
XX AC AA084372;
XX
XX 19-AUG-1995 (first entry)
XX
XX Gemini virus-specific poly(ribozyme)-F target sequence.
XX
XX Ribozyme target sequence: poly(ribozyme)-F:
KW Tomato leaf curl virus; RNA cleavage; tomato transgenic plant;
KV virus disease-resistance; ss.
XX
XX Tomato leaf curl virus.
XX
XX Key Location/Qualifiers
XX misc_feature 48..96
XX /tag= a
XX /note= "Ribozyme R4-R5 target sequence"
XX
XX misc_feature 58..60
XX /tag= b
XX /note= "Ribozyme R4 cleavage site"
XX
XX misc_feature 81..83
XX /tag= c
XX /note= "Ribozyme R5 cleavage site"
XX
XX misc_feature 389..386
XX /tag= d
XX /note= "Ribozyme R2 target sequence"
XX
XX misc_feature 370..372
XX /tag= c
XX /note= "Ribozyme R2 cleavage site"
XX
XX

```



```

1  ThrleuValTrpGlyGluAlaAlaValAspGlyValSerAlaArgGlyL 17
   |||||
328  KCAATGCAATGGGACAAATCCAAATCGACGCGCAATCTCAAGACAGG 377
   |||||
17  YCYSGLInThSerAsnAspAlaAlaValAsnAspAlaSerSerL 34
   |||||
378  TCAGCACTGCTCCACACATCCATATCCAAAGCATTTAAACGCGATTC 427
   |||||
34  YSGluGluAlaLeuGlnIleIleArgGlyIleProGlyuTyTrpLeu 50
   |||||
428  TTGACATCTGCTCCACAAATATGAGGAAGAAACAGATTCACGTC 477
   |||||
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspValIlePheAspLysTh 67
   |||||
478  CTTCACATCCACACATCCGCTCTATATCTCAACAGCATCTTCGCAAGT 527
   |||||
67  PProGluPro 70
   |||||
528  GCCGCAACCA 537

seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AA193292
seq_documentation_block:
ID   AA193292 standard. DNA: 1062 BP.
XX
XX
XX
AA193292:
XX
XX
27-APR-1998 (first entry)
XX
DE   Bean golden mosaic geminivirus CI mutant ORF BGAC228.
XX
XX   Geminivirus; BGWV; CI gene; transdominant mutation;
XX   transgenic plant; disease resistance; ss; cyclic; circular.
XX
XX   Bean golden mosaic virus type II isolate Guatemala.
XX
MO0739110-AI.
XX
XX
23-OCT-1997.
XX
XX
15-APR-1997: 97MO-US06300.
XX
XX
16-APR-1996: 96US-0015517.
XX
PA   (SPM-) SEMINIS VEGETABLE SEEDS INC.
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX
Abiquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX
XX   WPI: 1997-526447/48.
XX
XX   P-PSDB: AAM34334.
XX
XX
Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX
XX   mutant genes - have increased resistance to geminivirus infection
XX
XX   e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX
XX   golden mosaic geminivirus
XX
XX
Claim 13: Page 111-112; 13pp; English.
XX
XX
This DNA sequence comprises construct BGAC228 that codes for a
XX
XX   transdominant lethal mutant (see AAM34334) of the CI protein (see
XX
XX   AAM34338) of bean golden mosaic virus (BGWV). It was obtained by
XX
XX   Kunkel mutagenesis of the wild-type CI gene (see AA19314). CI is
XX
XX   required for replication. The invention involves production of
XX
XX   transgenic plants containing DNA comprising geminivirus CI or AC1
XX
XX   wild-type or mutant sequences that negatively interfere in trans
XX
XX   replication of geminivirus. Transgenic plants containing such
XX
XX   plants are resistant to viral infection. The AC1/C1 gene of
XX
XX   curl virus (see BGWV, tomato mottle virus or tomato yellow leaf
XX
XX   curl virus (see AA193282-93) and encode polypeptides (see AAM34324-35)
XX
XX   that have mutations in the highly conserved DNA-nicking and/or the
XX
XX   NTP-binding domains.

```

```

XX
XX   Sequence 1062 BP: 338 A; 247 C; 218 G; 259 T; 0 other;
XX
XX   Alignment scores:
XX       Quality: 216.00      Length: 70
XX       Ratio: 3.661        Gaps: 0
XX   Percent similarity: 84.286   Percent identity: 58.571

alignment_block:
US-09-289-346a-8 x AA193292
Align seg 1/1 to: AA193292 from: 1 to: 1062
1  ThrleuValTrpGlyGluAlaAlaValAspGlyValSerAlaArgGlyL 17
   |||||
328  KCAATGCAATGGGACAAATCCAAATCGACGCGCAATCTCAAGACAGG 377
   |||||
17  YCYSGLInThSerAsnAspAlaAlaValAsnAspAlaSerSerL 34
   |||||
378  TCAGCACTGCTCCACACATCCATATCCAAAGCATTTAAACGCGATTC 427
   |||||
34  YSGluGluAlaLeuGlnIleIleArgGlyIleProGlyuTyTrpLeu 50
   |||||
428  TTGACATCTGCTCCACAAATATGAGGAAGAAACAGATTCACGTC 477
   |||||
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspValIlePheAspLysTh 67
   |||||
478  CTTCACATCCACACATCCGCTCTATATCTCAACAGCATCTTCGCAAGT 527
   |||||
67  PProGluPro 70
   |||||
528  GCCGCAACCA 537

seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AA193293
seq_documentation_block:
ID   AA193293 standard. DNA: 1062 BP.
XX
XX
XX
AA193293:
XX
XX
27-APR-1998 (first entry)
XX
XX
DE   Bean golden mosaic geminivirus CI mutant ORF BGAC262.
XX
XX   Geminivirus; BGWV; CI gene; transdominant mutation;
XX   transgenic plant; disease resistance; ss; cyclic; circular.
XX
XX   Bean golden mosaic virus type II isolate Guatemala.
XX
MO0739110-AI.
XX
XX
23-OCT-1997.
XX
XX
15-APR-1997: 97MO-US06300.
XX
XX
16-APR-1996: 96US-0015517.
XX
PA   (SPM-) SEMINIS VEGETABLE SEEDS INC.
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX
Abiquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX
XX   WPI: 1997-526447/48.
XX
XX   P-PSDB: AAM34335.
XX
XX
Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX
XX   mutant genes - have increased resistance to geminivirus infection
XX
XX   e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX
XX   golden mosaic geminivirus
XX
XX
Claim 13: Page 115-116; 13pp; English.

```

13

XX
CH

, C O C T I W W

DT 07-NOV-1996 (first entry)

Alignment_scores: Quality: 216.00 Length: 69
 Ratio: 3.789 Gaps: 0
 Percent Similarity: 82.609 Percent Identity: 56.522

Alignment_block:

us-09-289-346a-8 x AAT12906

Align seg 1/1 to: AAT12906 From: 1 to: 1080

```

2  LeuValTrpGlyAlaAlaValAspGlyArgSerAlaArgGlyIcy 18
331  CTTCAGATGGGACTCTCCAGATCGACGACATCTCTGAGGAGACCA 380
18  sGlnThrSerAsnAspAlaAlaAlaGlyAlaLeuAsnAlaSerIysG 35
381  ACAGACACCCAGCCGCTTACCGCAAGCCAAATTCACCGAGATGAC 430
35  InGluAlaLeuGlnIleIleAlaArgGlyLeuIleProGlyLysTyrLeu 51
431  CGCAGCGCTCTGATGATTAATTAAGATTAATTCAGCTTTCCAGTTC 480
52  GlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThr 68
481  CATTTCATTAATTAATTAATTAATTAATTCAGTTCCTTCCAGTTC 530
68  ocLysPro 70
531  CGCAGCCT 537

```

seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA197.DAT: AAT93314

seq_documentation_block:

AAT93314 standard. DNA: 1183 BP.

AC AAT93314:

DT 27-APR-1998 (first entry)

XX Bean golden mosaic geminivirus CI open reading frame.

XX Geminivirus: RCMY, CI gene; transdominant mutation;

XX transgenic plant; disease resistance; ss; cyclic; circular.

OS Bean golden mosaic virus type II isolate Guatemala.

XX Key Location/Qualifiers

PH CDS 1..1062

XX MO9739110-A1. /'tag- a

XX 23-OCT-1997.

PD 15-APR-1997. 97MO-US06300.

XX 16-APR-1996. 96US-0015517.

XX (SEMI-) SPINISIN VEGETABLE SEEDS INC.

PA (MISC) SPINISIN ALUMINI RES FOUND.

XX Ahlquist PG, Hanson SF, Lau HT, Maxwell DP, Stout JF.

XX WPI: 1997-526447/48.

XX P-PSDB: AAM34336.

XX Transgenic plants expressing geminivirus AC1 and CI wild-type and

XX mutant genes - have increased resistance to geminivirus infection

XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean

XX golden mosaic geminivirus

XX Example 5: Page 100-102: 132pp: English.

CC This genomic DNA sequence includes the open reading frame (ORF) of
 CC the wild-type CI gene of bean golden mosaic virus (BGWV), a
 CC geminivirus that has a monopartite genome. The CI protein (see
 CC AAM34336) is required for replication. The wild-type CI ORF was
 CC subcloned into a pUC19-based expression vector and expressed in
 CC E. coli. Production of transgenic plants containing DNA comprising
 CC CI or AC1 wild-type or mutant sequences that negatively interfere
 CC in trans with geminiviral replication during infection. Such
 CC transgenic plants are resistant to viral infection. The AC1/CI
 CC genes are especially from BMV, tomato mottle virus or tomato
 CC yellow leaf curl virus (see AAT93282-93) and encode polypeptides
 CC (see AAT9324-35) that have mutations in the highly conserved
 CC DNA-binding domain and/or the ATP-binding domains.

SO Sequence 1183 BP: 372 A: 276 C: 248 G: 287 T: 0 other:

Alignment_scores: Quality: 216.00 Length: 70
 Ratio: 3.641 Gaps: 0
 Percent Similarity: 84.286 Percent Identity: 58.571

Alignment_block:

us-09-289-346a-8 x AAT93314

Align seg 1/1 to: AAT93314 From: 1 to: 1183

```

1  ThrLeuValTrpGlyAlaAlaValAspGlyArgSerAlaArgGlyIcy 17
328  ACAATCGAATGGGAGCAATTCGACAGTCCAGACGATCTCCAGACGAG 377
17  yCysGlnThrSerAsnAspAlaAlaAlaGlyAlaLeuAsnAlaSerSer 34
378  TCGACAGCTCGCAACGACTATATGCAACGCAATTAAAGCAATTCGA 427
34  yGlnGluAlaLeuGlnIleIleAlaArgGlyLysIleProGlyLysTyrLeu 50
428  TTGATCTGCTTGACATATTATTAAGGAGAACACGAAAGATTCATC 477
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThr 67
478  CTTCACATCGACACATCCGCTGATTAATTCGACAGATCTCTGCAAGCT 527
67  PTCGICupro 70
528  GCGGAGCA 537

```

seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA197.DAT: AAT93290

seq_documentation_block:

AAT93290 standard. DNA: 1183 BP.

AC AAT93290:

DT 27-APR-1998 (first entry)

XX Bean golden mosaic geminivirus CI mutant gene.

XX Geminivirus: RCMY, CI gene; transdominant mutation;

XX transgenic plant; disease resistance; ss; cyclic; circular.

OS Bean golden mosaic virus type II isolate Guatemala.

XX Key Location/Qualifiers

PH CDS 1..1062

XX MO9739110-A1. /'tag- a

XX 23-OCT-1997.

PD 15-APR-1997. 97MO-US06300.

XX

```

PR 16-APR-1996: 96US-0015517.
XX
XX (SEMI-) WISCONSIN VEGETABLE SEEDS INC.
FA (WISC-) WISCONSIN ALUMNI RES FOUNO.
XX
XX Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT.
XX WPI: 1997-526447/48.
XX P-PSDB: AAM34332.
XX
XX Transgenic plants expressing geminivirus AC1 and CI wild-type and
PT mutant genes - have increased resistance to geminivirus infection
PT e.g. tomato mottle virus, tomato yellow leaf virus or bean
XX golden mosaic geminiviruses
XX
XX Claim 13, Page 103-105; 132pp: English.
XX
XX This DNA sequence comprises construct BGAC190 that codes for a
CC control mutant (see AAM34332) of the CI protein (see AAM34338) of bean
CC golden mosaic virus (BGWV). It was obtained by Kunkel mutagenesis
CC of the wild-type CI gene (see AAT93290). CI is required for
CC replication of the virus genome in the host cell.
CC Plants containing DNA comprising geminivirus CI or AC1 wild-type or
CC mutant sequences that negatively interfere in trans with
CC geminiviral replication during infection. Such transgenic plants
CC are resistant to viral infection. The AC1/CI genes are especially
CC from BGWV, tomato mottle virus or tomato yellow leaf curl virus (see
CC AAT93282-93) and encode polypeptides (see AAM34324-35) that have
CC mutations in the highly conserved DNA-nicking and/or the NTP-binding
CC domain.
XX
XX Sequence 1183 BP: 371 A: 277 G: 249 G: 286 T: 0 other:
XX
XX Alignment_scores:
XX Quality: 216.00 Length: 70
XX Ratio: 3.661 Gaps: 0
XX Percent Similarity: 84.286 Percent Identity: 58.571
XX
XX alignment_block:
XX US-09-289-346a-8 x AAT93290 ..
XX
XX Align seq 1/1 to: AAT93290 from: 1 to: 1183
XX
XX 1 Thleuvalitfpclygualalawalaaspcgiayarscrlaargtgcyl 17
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 328 ACAATCGATGCGACCAATTCGACATCGACGCCGACATCTCGACAGACG 377
XX
XX 17 ycygclnthserasnsapalalalagualaleuansalaseSertL 34
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 378 TCGACAGTGCACGACCTCATATCGAACAAGCATTAACGACATTCGCA 427
XX
XX 34 ysglucualaleuglcnllleltagtcluyylleprogluySryleu 50
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 428 TTGAATCTGCTTCACAAATATTGAAGGAGAACACGGAACATTTCGTC 477
XX
XX 51 Phcglntpheihsaenleuansersaslnleuasparglllephaaspyrth 67
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 478 CTTCAATCATCGACAAATCTGCTTCATCTGACACGATCTTCGTGTCAAAGT 527
XX
XX 67 progluypro 70
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 528 GCGGGAACCA 537
XX
XX seq_name: /cgnl_8/gcdata/geneseq/geneseq/NA2000.DAT:AAA94700
XX
XX seq_documentation_block:
XX seq AAA94700 Standard: DNA: 1651 BP.
XX
XX AAA94700:
XX
XX 15-JAN-2001 (first entry)
XX

```

```

DE PMIG 2288 35S-rep gene cassette.
XX
XX Geminivirus; DNA-A: geminivirus replication inhibition; ac3 gene;
XX transgenic plant; antiviral; gene therapy; bean golden mosaic virus;
XX BGWV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CMV; ds.
XX
XX Bean golden mosaic virus.
XX
XX Cauliflower mosaic virus.
XX
XX Alfalfa mosaic virus.
XX
XX Synthetic.
XX
XX USG118048-A.
XX
XX 12-SEP-2000.
XX
XX 24-APR-1998: 98US-0065999.
XX
XX PR 25-APR-1997: 97US-0044925.
XX
XX (WISC-) WISCONSIN ALUMNI RES FOUNO.
XX
XX WPI: 2000-610861/58.
XX
XX PT Genetic construct comprising a mutant geminiviral rep gene, useful for
XX producing a plant resistant to geminiviral infection.
XX
XX Example: Column 15-16; 14pp: English.
XX
XX The present sequence is a 35S-rep gene cassette comprising the rep gene
XX of the bean golden mosaic virus (BGWV) genome. The rep gene is the
XX 35S promoter and an alfalfa mosaic virus (AMV) leader sequence. The
XX sequence was integrated into pBSII-KS+ to produce a rep gene expression
XX vector. DNA-nicking domain mutations may be incorporated into rep gene
XX to produce a genetic construct that acts as a trans-dominant inhibitor
XX of geminiviral replication. When expressed in a plant cell, this
XX inhibitor is able to dramatically reduce replication of geminivirus.
XX The genetic construct may be used to produce transgenic plants that
XX are resistant to geminivirus infection. In addition, the construct may be
XX used to produce transgenic plants that produce sequences inhibiting
XX efficiency and broadened specificity of inhibition of geminiviral
XX replication. Geminiviruses are one of the greatest constraints on
XX production of important crops, including cassava, beans, cowpeas,
XX peppers, tomatoes and cotton. The effects of the virus can be overcome
XX by using the genetic construct.
XX
XX Sequence 1651 BP: 517 A: 393 C: 342 G: 399 T: 0 other:
XX
XX Alignment_scores:
XX Quality: 216.00 Length: 70
XX Ratio: 3.661 Gaps: 0
XX Percent Similarity: 84.286 Percent Identity: 58.571
XX
XX alignment_block:
XX US-09-289-346a-8 x AAA94700 ..
XX
XX Align seq 1/1 to: AAA94700 from: 1 to: 1651
XX
XX 1 Thleuvalitfpclygualalawalaaspcgiayarscrlaargtgcyl 17
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 796 ACAATCGATGCGACCAATTCGACATCGACGCCGACATCTCGACAGACG 845
XX
XX 17 ycygclnthserasnsapalalalagualaleuansalaseSertL 34
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 846 TCGACAGTGCACGACCTCATATCGAACAAGCATTAACGACATTCGCA 895
XX
XX 34 ysglucualaleuglcnllleltagtcluyylleprogluySryleu 50
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 896 TTGAATCTGCTTCACAAATATTGAAGGAGAACACGGAACATTTCGTC 945
XX
XX 51 Phcglntpheihsaenleuansersaslnleuasparglllephaaspyrth 67
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 946 CTTCAATCATCGACAAATCTGCTTCATCTGACACGATCTTCGTGTCAAAGT 995
XX

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26 agtataatcaaaattacccggcgaacttttcgaaaccgaatgcagmac 699
   |||
47 ..gtlutyrtleuphbglnphehtasnlenuasenservn 59
   |||.....|||.....|||
700 ctctcgacgccctctccaaaagtctctcacacattctcatctccgat 741
   |||

seq_name: gb_est2.BF342302

seq document location: block: 646 bp mRNA EST 22-NOV-2000
LOCUS BF342302
DEFINITION 602015083pl NCICGAP_Brn64 Homo sapiens cDNA clone IMAGE:4148757
5', mRNA sequence.
ACCESSION BF342302.1 GI:11289259
VERSION BF342302.1
KEYWORDS EST
SOURCE Homo sapiens
ORGANISM Homo sapiens
EXTRACTOR Metrzon; Chorrida; Catarrhi; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
REFERENCE 1 (bases 1 to 646)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
          Department of Biology,
          Tissue Research Laboratory, Room 1409,
          University of Maryland School of Medicine,
          P.O. Box 7070, Baltimore, MD 21205
          DNA library preparation: Life Technologies, Inc.
          cDNA library prepared by: The I.M.A.G.E. Consortium (LLNI)
          DNA sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNI at:
          http://image.llni.gov
          Place: LLN49409 row: 1 column: 22
          High quality sequence stop: 613.
FEATURES
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            /db_xref="taxon:9606"
            /clone="IMAGE:4148757"
            /clone_lib="NCI-CGP_Brn64"
            /tissue_type="glioblastoma with EGFR amplification"
            /lab_note="DblO8 (711 phase-resistant)"
            /Vec_Org="Human brain; Vector: pCMV-Sport6; Site:1; MolCl:
            Average insert size:1.57 kb Constructed by: Billie
            Technology: Note: this is a NCI-CGP Library."
ORIGIN
      150 a 158 c 197 g 141 t
      +-----+
alignment_scores:
      Overall: 71.00 Length: 42
      Ratio: 2.448 Percent Identity: 42.857
Percent Similarity: 69.048
alignment_block:
US-09-289-346A-x BF342302 ..
Align seq 1/1 to: BF342302 from: 1 to 646
3 valuetgly...guuaalaualeuanslnserisvsglunlaaleuglnletfvaagc 43
|||||.....|||.....|||
202 gtcttgaggctgacgacacacctctctgcacagcagcagcagcagcagcagc 251
|||||.....|||.....|||
18 sglnthrseasnspnslalaalaglualeuanslnserisvsg 35
|||||.....|||.....|||

```

```

252 TGAATCGAGGACGGGACGCCAACGAGGCCTCAGCGGGCCCAAAACCTTG 301
35 JtGUlAalEuGIInIleItLeITgTtU 43
11 |-----|
302 AA.....ATCGGTAA 312

seq_name: gb_gss:A0906722

seq_documentation_block:
LOCUS      A0906722          412 bp    DNA             GSS              09-JAN-2001
DEFINITION GSSFC03166 Trypanosoma cruzi random genomic library Trypanosoma
cruzi genomic clone G40C19, DNA sequence.
ACCESSION  A0906722.3
VERSION     GI:10136203
KEYWORDS   GSS.
SOURCE      Trypanosoma cruzi.
ORGANISM   Trypanosoma cruzi.
            Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma cruzi.

REFERENCE   1 (bases 1 to 412)
            Agudon, M., Leano, R., Frasch, A.C.G. and Sanchez, P.O.
            A genome map approach for the analysis of the trypanosoma
            cruzi genome: general structure, large gene and repetitive DNA
            families, and gene discovery
            Genome Res. 10 (12), 1996-2005 (2000)
            2058489
            On Sep 14, 2000 this sequence version replaced gi:9377231.

COMMENT     Contact: Sanchez P.O.
            Institute de Investigaciones Biotecnologicas (Univ. Nac. de Gral
            San Martin)
            Av. Gral Paz entre Albarellos y Constituyentes, INTI edificio 24
            CP(1650). San Martin, Prov. de BS AS. Argentina
            Tel.: 54-11-4590-7255 ext 309
            Fax: 54-11-4752-9639
            Email: dsanchez@ib.usnsm.edu.ar
            Sequences were basecalled with phred and vector was masked with
            Trnascan! (see http://genome.washington.edu). Sequences were then
            trimmed from both ends to remove low quality bases and masked
            vector.
            Seq primer: 77
            Class: shotgun.

FEATURES             Location/Qualifiers
     source           I..412
                     /organism="Trypanosoma cruzi"
                     /strain="L-Brener"
                     /clone="G40C19"
                     /clone_1b="Trypanosoma cruzi random genomic library"
                     /cell_type="separateligote"
                     /note="Vector: pBS(-) (Stratagene); T. cruzi DNA was
randomly sheared using a nebulizer and the 1 to 2 kb range
was gel purified and cloned into the dephosphorylated
HincII site of the vector."
ORIGIN              113 a
                    110 c 59 g 30 t

alignment_scores:
Quality: 70.00 Length: 50
Ratio: 2.121 Gaps: 1
Percent Similarity: 66.000 Percent Identity: 38.000

Alignment Block:
US-09-289-346A-8 x A0906722 ..

Align seg 1/1 to: A0906722 from: 1 to: 412

10 AcgcAlgaSrArLaAgclYcylrCySnlrTrSerAnaSpAlaAlaNI 26
11 |-----|
22A GAtGcTAcCGACAAGACAGCCGCTACTGTAATTACGACCAGCCGAC 273
26 acGUlAalEuSIaSaSrLyglSlUlaEluIdnI...JleItEay 42
27 |-----|

```


[illegible]

```

ACCESSION      AQ950848
VERSION        AQ950848.1
KEYWORDS       GSS.
SOURCE         Trypanosoma brucei.
ORGANISM       Eukaryota; Eukaryozoa; Kinetoplastida; Trypanosomatidae;
REFERENCE      1 (bases 1 to 572)
AUTHORS        El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujilli, C.,
                Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J.C.,
                Ferrar, C. and Adams, M.
TITLE          Determination of clone end sequences from Trypanosoma brucei cDNA
COMMENT        10.1 Sheared DNA library
                10.1 Sheared DNA library
                Other GSS: Sheared DNA-51M3-TR
                The Institute for Genomic Research
                9712 Medical Center Dr., Rockville, MD 20850, USA
                Tel.: 301 838 0200
                Fax: 301 838 0208
                Email: gss@igrr.org
                Clones are derived from the Trypanosoma brucei cDNA 10.1 sheared
                DNA library constructed at IGRR. Clones will be available for
                distribution through ATCC. Sheared DNA end sequences search page:
                http://www.tlgr.org/cdb/mdb/tbdb/.
                Seq primer: M13-Forward
                Class: Shotgun.
                Location/Qualifiers
                source
                /organism="Trypanosoma brucei"
                /strain="TRE927/4 cDNA 10.1"
                /db_xref="taxon:5691"
                /clone_lib="Sheared DNA"
                /note="Vector: pUC18; Site_1: Small; Constructed at the
                Institute for Genomic Research (IGRR), Rockville, MD.
                Trypanosoma brucei (TRE927/4 cDNA 10.1) was mechanically
                sheared to give a light size distribution (approx 2 kb).
                The +1 method used for the library construction is
                described in detail in Smith, H.O. and Venter, J.C.
                (Moking small insert libraries for whole genome shotgun
                sequencing projects. In Genome Sequencing: A Practical
                Approach, eds. M. Vaudin and B. Bartell, Oxford University
                Press, 1993) 180 g 159 t
BASE COUNT     115 a 118 c 180 g 159 t
ORIGIN
alignment_scores:
Quality: 68.00 Length: 31
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Percent similarity: 87.097 Percent identity: 38.710
alignment_block:
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291 GCGTCCTTCGCGCATGCGCGATTCGCAACACGACAGAGGCGATTCGTA 340
27 uAlAlaLaLaLaLaLaSeSeSeLySGGtGtGtAlAlAlAlAlAlfLe 41
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341 AGGtGtGtTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 383
seq_name: qb_gss-AQ947513
seq_documentation_block:
LOCUS      AQ947513          587 bp            DNA                GSS
DEFINITION Sheared DNA-4M1-1917 bp Sheared DNA Trypanosoma brucei genomic clone

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VERSION      BG593614.1  GI:13611754
KEYWORDS
SOURCE
ORGANISM     Solanum tuberosum
              potato.
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
Asterales: Solanales: Solanaceae: Solanum.
REFERENCE    1 (bases 1 to 603)
AUTHORS      van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A.,
              Bougri, O., Buell, C. R., Romling, C., Tanksley, S. and Baker, B.
              Generations of ESTs from sprouting potato eyes
              Unpublished (2000)
JOURNAL
COMMENT       Contractually Romling
              Department of Genetic Research
              Pot clone info: Please contact Research Genetics, Libraries
              Division tel 1-800-711-6195, email cda@resgen.com
              Seq primer: M13P-R.
FEATURES
  source      Location/Qualifiers
              1..603
               /organism="Solanum tuberosum"
               /db_xref="taxon:4133"
               /db_xref="taxon:4133"
               /clone="csts44"
               /clone_1lb="csts"
               /tissue_type="sprouting eyes from tubers"
               /dev_stage="12-14 weeks post harvest"
               /lab_host="SOLR"
               /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
               /note="KOD. TUBERS: sizes of sprouting eyes (tuber 1mg) were
               /note="dark from tubers. Phases were labeled 1-603 in the
               /note="frozen in liquid nitrogen immediately upon removal from
               /note="tubers."
BASE COUNT   160 a 131 c 135 g 177 t
ORIGIN
alignment_scores:
  Quality: 67.50      Length: 54
  Ratio: 1.929      Gaps: 3
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alignment_block:
  US-09-289-346A-8 x BG593614/rev
Align seg 1/1 to reverse of: BG593614 from: 1 to: 603
11 GYArgserAlaArgIyGySGInThrSerAsnASP.....AlaAl 25
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393 GGAAGGTCGGCTGCTTCAGATGCTAGAGCGAATGCAATGAGACTG 344
25 bAlaGluAlaLeuAsnAlaSerSerIySGluGluAlaLeuGluIleIleA 42
343 TATTAGAGCCGAAATAGCAGAGCTTTTACATCTTATCCAGATT..... 298
42 rGluIySileProGluIySTyLeuPheGlnPheHisAsn...LeuAsn 57
297 ..AGCAATATAAGATTCTTCACCTTTCAGATTCACCAATAGAGCTCAAC 250
58 SerAsnLeuAsp 61
249 AACATATATCAAC 238

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2216 AGCTAATGATGCTCCGACAGAGCCCTTAATGACGTTCCAGCTGAAGACG 2167
37 lalenglnlllellatrglulalyallleproglulystylleahneglnphe 53
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2166 CTTTCACACATATGCGACATTCGACACGACGCTGACACACATTTATTTTCACAT 2117
54 hlsanleuanserlasenleuasparglllephaaplysthp 68
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seq_name: /cgnl_7/plodata/1/lna/6E_COMB.seq:us-08-838-151A-48
seq documentation block:
: Sequence 48: Application US/08838151A
: Patent No. 6591743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Lou, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Hanson, Steve
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milunow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838,151A
: FILING DATE:
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SVS3801PQ260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5460
: INFORMATION FOR SEQ ID NO: 48:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1062 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: circular
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGIN: SOURCE:
: ORGANISM: Bean Golden Mosaic Gemlinivirus
: STRAIN: Type II
: INDIVIDUAL ISOLATE: Guatemala
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1059
: US-08-838-151A-48

alignment_scores:
: Quality: 216.00 Length: 70
: Ratio: 3.661 Gaps: 0
: Percent similarity: 84.286 Percent identity: 59.571

alignment_block:
US-09-289-346a-8 x US-08-838-151A-48

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17 yCyslnthSerlasenleuasparglllephaaplysthp 34
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
378 TCAGCAGCTCCGACGACGCTCATATGACGACGATTAAGCGCAATTCGAA 427
34 ystlglulalaleuglnlllellatrglulalyallleproglulystylleu 50
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428 TGCATTCGCTCCTTCACATATTCGACACGACGCTGACACACATTCGCTC 477
51 Phagllphehlsanleuanserlasenleuasparglllephaaplysthp 67
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
478 CTTTCACACATACACATTCGCTTCATATTCGACACGACGATTCGCAACGT 527
67 tproglupro 70
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528 GCGGACAC 537

seq_name: /cgnl_7/plodata/1/lna/6E_COMB.seq:us-08-838-151A-51
seq documentation block:
: Sequence 51: Application US/08838151A
: Patent No. 6591743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Lou, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Hanson, Steve
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Gemlinivirus
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milunow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838,151A
: FILING DATE:
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SVS3801PQ260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5460
: INFORMATION FOR SEQ ID NO: 51:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1062 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: circular
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGIN: SOURCE:
: ORGANISM: Bean Golden Mosaic Gemlinivirus
: STRAIN: Type II
: INDIVIDUAL ISOLATE: Guatemala

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STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22002
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103b
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
FILING DATE: NONE
PCT NO: P/94,11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/FR95,01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCII, And+ew J.
REGISTRATION NUMBER: 32,925
COUNTRY: US
TELECOMMUNICATIONS INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMOB
APPLICATION FOR SEQ ID NO: 1:

City: **WYLLING** ;
 Country: **USA**

; sequence 3, application US/08809103B


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seq_documentation_block:
1 Sequence 5, Application US/08809103B
2 Patent No. 6133505
GENERAL INFORMATION:
1 ORGANISM: BRUNO
2 TITLE OF INVENTION: PHYTOGENIC DNA VIRUS RESISTANT
3 TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHOD
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/VMS-POS
SOFTWARE: PATLICH Release #1.0, Version #1.30
CHUNK LENGTH: 1000
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO 94/007/F/95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELEPHONE: (703) 521-2297
FAX: (703) 521-8073
TELEX: 248425 EMBRO
SEQUENCE CHARACTERISTICS:
LENGTH: 1150 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
ORGANISM: linear
MOLECULAR TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1077
US-08-809-103B-5

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Percent Similarity: 82.609 Percent Identity: 56.522

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331 CTTCAGATGCAGCGCTTCCTTCACGTGACGACGATCTCTCAAGGGAGAGACA 380
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APPLICATION NUMBER: US/08/838.151A
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SYS3801.P0250
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 70
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHEetical: NO
 ANTI-SENSE: NO
 ORIGIN: SOURCE:
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 STRAIN: Type II
 INDIVIDUAL ISOLATE: Guatemala
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 NAME/KEY: CDS
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 US-08-838-151A-45

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seq_documentation_block:
 : Sequence 5, Application US/09065999
 : Patent No. 6118048
 : GENERAL INFORMATION:
 : APPLICANT: Hanson, Stephen F.
 : ATTORNEY: Hanson, Stephen F.
 : TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
 : REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
 : NUMBER OF SEQUENCES: 8
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Charles & Brady
 : STREET: One South Pinckney Street

CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/065.999
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27,386
 REFERENCE/DOCKET NUMBER: 960296.94754
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-251-5000
 TELEFAX: 608-251-9186
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1651 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-065-999-5

alignment_scores:
 Quality: 216.00 Length: 70
 Ratio: 3.661 Gaps: 0
 Percent Similarity: 84.286 Percent Identity: 58.571

alignment_block:
 US-09-289-346a-8 x US-09-065-999-5

Align seq 1/1 to: US-09-065-999-5 from: 1 to: 1651

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896 TTGAATCTGCTTCACATATTCAGAGAGAGAGAGAGAGATTCAGTC 945
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seq_name: /cgnl_7/ptodeta/1/lna/6A.COMB.seq:us-09-065-999-6

seq_documentation_block:
 : Sequence 6, Application US/09065999
 : Patent No. 6118048
 : GENERAL INFORMATION:
 : APPLICANT: Hanson, Stephen F.
 : ATTORNEY: Hanson, Stephen F.
 : TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
 : REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
 : NUMBER OF SEQUENCES: 8
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Charles & Brady

ADDRESS: Quailis & Brady
STREET: One South pinkney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-1113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/09/065_999
FILING DATE:
PUBLICATION DATE:
AUTHOR/AGENT INFORMATION:
NAME: Sassy, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960206_94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
SOURCE: 1894
TYPE: nucleic acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

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alignment_scores:
  Quality: 216.00    length: 70
  Ratio: 3.661      Gaps: 0
Percent Similarity: 84.286    Percent Identity: 56.571

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10

[illegible]

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seq_name: /cgn1-7/plcoda1/L1/lna/6a.COHb.seq;US-09-065-999-7
seq_documentation_block:
: Sequence 7: Application US/09065999
: Patent No. 6118048
: GENERAL INFORMATION:
: APPLICANT: Hanson, Stephen F.
: APPLICANT INVENTOR: Douglas
: APPLICANT INVENTOR:
: TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
: NUMBER OF SEQUENCES: 8

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APPLICANT: AUTO

371 McMAIC

371 ACAATCGAATGGGAGATTTCCAGATCGACGGCAGATCTGCCAGAGGAGG 420

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373  GSGUGUALALALEGALINLELEAGGCUUGYSLEDFGUSYSTLEU 50
474  TTCCACATGCTGCTTACGACGCTTAAAGGACAAACACACAGTTTGTGA 520
51  PhociniphehissertanSPALALALALGUALALEMNSALSERSE 67
521  TTTCACAAATTAATACATCCGCTCACTACAGCAATATTGCAAGGC 570
67  rProGluPro 70
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571  TCCCGAACGC 580

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OM of: US-09-289-346A-9 to: GenEmbl:* out_format: pif
Date: Jan 3, 2002 8:17 PM

About: Results were produced by the GenCore software, version 4.5
Copyright (c) 1993-2000 Compugen Ltd.

Command Line parameters:

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MODEL=lrmm; E2m_model = BEVx16;
DAYS=10; VSP=0; SPOOL=0; SPOOLSIZE=67; ZUNIT=0; 01/30/2002; 153304.16362; dep_query; fasteq_1.11665;
GADGET=4; 0.000; MINMATCH=0; 0.166; LOGEXP=0; 0.000; LOGEXPT=0; 0.000;
OGAPOP=4; 500; OGAEXPT=0; 0.000; XAPOP=10; 0.000; XAEXPT=0; 0.500;
FGAPOP=6; 0.000; FGAEXPT=7; 0.000; YAGOP=10; 0.000; YAEPT=0; 0.500;
DELTOP=6; 0.000; BELTEPT=7; 0.000; STAYOP=1; 0.000; NARRIA=1; osuime2;
NARRIA=0; 0.000; ELIST=4; 5;
NARRIA=0; 0.000; ELIST=4; 5;
NARRIA=0; 0.000; ELIST=4; 5;
NORMEXT = MINEXT=0; MAXLEN=200;0000000000;
NORMEXT = MINEXT=0; MAXLEN=200;0000000000;
USER=US09289316; @C@N_1.10412; -NCPB=6; -ICUD=3; -LONGLOG;
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Query length: 70
Database: GenBank1:*
Database sequences: 1472140
Database length: -341344837
Search time (sec): 7316.720000
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score_list:

[illegible]

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gb.vi.:BCHVCOMP      -   247.00    553.99    1.6e-22    2923    | x97203 Beet curly top virus
gb.vi.:AC023111     -   247.00    553.01    1.6e-22    2927    | AC023111 Beet curly top virus
gb.vi.:AB001304     -   246.00    565.51    3.2e-23    570    | AB001304 Beet curly top virus
gb.vi.:AF155064     -   246.00    551.16    2.0e-22    2764    | AF155064 Okra leaf curl v
gb.vi.:CL2870867    -   245.00    558.79    7.6e-23    922    | AJ270867 cotton leaf curl V
seq_name: gb.vi:MGA

seq_documentation_block:
LOCUS       MGA                      2588 bp ss-DNA             circular   VRL           02-AUG-1993
DEFINITION  Tomato golden mosaic virus, complete A of complete genome.
ACCESSION   K02025
VERSION     K02025.1
KEYWORDS    GI:332213
SOURCE      GenBank
ORGANISM    tomato golden mosaic virus
REFERENCE   1 (bases 1 to 2588)
            Hamilton,W.D., O'Neil, S.J., Coutts,R.H.A. and Buck,K.W.
            Complete nucleotide sequence of the infectious cloned DNA
            component of tomato golden mosaic virus: Potential coding regions
            identified by computer analysis. J. Virol. 57:1987-1994 (1987).
            EMBO j. 3, 2197-2205 (1984).
COMMENT     Geminiviruses are characterized by twin isometric virions, major
            capsid polypeptides of about 28 kD, and ss-DNA genomes. The genomes
            consist of two circular components, while that of maize streak
            virus (MSV), consists of a single circular open reading frames on the
            complementary strand that would code for proteins with >10 kd:
            AL1 -- 13-1543 (passing through origin)
            AL2 -- 1461-1212
            AL3 -- 1465-1657
            The sequence at 1-2335 is highly homologous to an equivalent region
            on component B; it does not appear to code for protein and has the
            same GC content as the rest of the genome. It may form a stable hairpin [1]. An analogous region is
            found in CSV.
FEATURES             Location/Qualifiers
     source          1..2588
                     /organism="tomato golden mosaic virus"
     CDS             1..2588
                     /db_xref="taxon:10831"
                     /note="coat protein (ARI)"
                     /codon_start=1
                     /protein_id="AA46582.1"
                     /db_xref="GI:332214"
                     /translation="MPPRDAWMLMAQTSWSKANSYSPGSIPEPRDAWRNDRPKP
                     RTVSILGRPVGVPCRGKPYDVSEEDHDIISLVKIMGSLSDVTRGNCTTHVCKRECY
                     KSVYLITGLIMDENIKLRKHNSVWELTQVETLQVETLQVETLQVETLQVETLQVETLQVETLQ
                     LTMNQNTSGVATLTKLYSDSN"
BASE COUNT         672 a      605 g      798 t
ORIGIN            140 bp upstream of HpaII site; beginning of A-B homology region.
...
alignment_scores:
Quality: 356.00 Length: 70
Mismatch: 13.50 Deletion: 0
Percent Similarity: 98.571 Percent Identity: 98.571

Alignment block:
US-09-2893-346A-9 x MGA/cv ..

Align seg 1/1 to reverse of: MGA from: 1 to: 2588
1 TTTTCAGATTTCCTGTGCTGGTCAAGTCCAGCGTCCAGTGCTCAGTCAAGACGAC 17
|||||
2271 ACTCTGTATGGGAAATTCACGATCCAGCGTCCAGTGCTCAGTCAAGACGAC 2222
|||||
17 TCTGCATTTCTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 34
|||||
2221 TTTCAGATTTCCTGTGCTGGTCAAGTCCAGCGTCCAGTGCTCAGTCAAGACGAC 2172

```


[illegible][illegible]


```

gene      995...1390
CDS       995...1390
          /gene="V2"
          /codon_start=1
          /product="p22"
          /protein_id="CA10695.1"
          /db_xref="GI:4210721"
          /translation="MTLLYKQSDGRAMCFSTAEKMDPLQNPDLPTLYGRFCLISVY
          LQGLLKPERGLFGLSELIIRIFRYROYRANRSPFAEISLSWGSGTKESELRDSY
          RALHMDCCPCPCPLGCFGRKRRDEKC"
          1215...1979
          /gene="V19"
          /codon_start=1
          /product="coat protein"
          /protein_id="CA10696.1"
          /db_xref="GI:4210722"
          /translation="MGRTRVSRFRPFGGQGRQSLMETALPYPTGNAPVIAASY
          KRVQIKSKSIDKVMNDVANDVANDRHRNTITVYTHIDRPNDDIATWROJFYVNDP
          TTKIKMDLDEPMOVLKFEFVYSGSGFSEHQAALIKRFKCLINHYVYNNKEADKE
          NOLENAALVYSSASHSNPVPYVCEAFYDSHRN"
          complement(1976...2413)
          /gene="C3"
          /complement(1976...2413)
          /gene="C3"
          /codon_start=1
          /product="C3 protein"
          /protein_id="CA10697.1"
          /db_xref="GI:4210723"
          /translation="MOSRTSGSLSHAQITRAAEFPNPNKSVGQTAFPHILRYVHTNN
          LDKSTIMKVLQVQVHNNRRRRTGOKIFLOPRLIFPRLIGATFNWTCISNRLKRWICNS
          LASIIGFSEFNLYVIRHLRPOGLWEVVDLCKDQIKVLY"
          complement(2127...2576)
          /gene="C2"
          /complement(2127...2576)
          /codon_start=1
          /product="C2 protein"
          /protein_id="CA10698.1"
          /db_xref="GI:4210724"
          /translation="MSTVYRCNAPQPIHNAKRGRTREPPRIYKCGCCS
          AFTINDKRGPHFGRYKSCDYSSALLOSNGSCYCTISTNYCKYQRIK
          DDHSSASQPPRQEGNMTPEPDLPIPDHRTNANSCVSLDMYQSP"
          BASE COUNT      734 a      570 c      671 g      788 t
          ORIGIN

alignment_scores:
  Quality: 280.00      Length: 68
  Ratio: 4.590      Gaps: 0
  Percent Similarity: 89.706      Percent Identity: 79.412

alignment_block:
US-09-289-346a-9 x IYEL32548/rev ..
Align seg 1/1 to reverse of: IYEL32548 from: 1 to: 2763
1  ThleuValITPGLYGLupheGlnValAlaGlyArgSerAlaArgLYGI 17
  |||||||
469 ACCCTCATGTGGGTGATTCCAGATCCAGCAAGCAATCTGCTGAGAGAG 420
17 yCysGlnThrSerAsnAspAlaAlaGlnValaLeuAsnAlaSerSerL 34
  |||||||
419 TCAGAGATCTCTACGACGAGCCGACAGAGCGATACACCGATGCTTA 370
34 yGluGluValaLeuGlnIleIleArgLysuylLeuPheGlnLysArgL 50
  |||||
369 AAGAGAGCTGCTTGCAATATATATACGAGCAACGATCCCTGAAAAATATTTTA 320
51 PhcGlnPheHisAsnLeuAsnSerAsnLeuAsnAspArgTllePheAspLysTh 67

```

```

|||||
319 TTTCATATATCATTAATTAGTATGATTAATTAAGAGATTTTTCCTCC 270
67 pPro 68
269 TCCT 266
seq_name: gb_v1:MGU75278

seq_documentation_block:
LOCUS      MGU75278      447 bp      DNA
DEFINITION Macrotellium golden mosaic geminivirus replication-associated
ACCESSION protein (MCI) gene, partial cds.
VERSION    U75278.1 GI:1688188
KEYWORDS
SOURCE     Macrotellium golden mosaic geminivirus.
ORGANISM   Macrotellium golden mosaic geminivirus.
REFERENCE  1 (bases 1 to 447)
            Dye, M.E., and J. D. B. 1996.
            Title   Dye, M.E., and J. D. B. 1996.
            JOURNAL Phesias (1996)
            REFERENCE 2 (bases 1 to 447)
            AUTHORS   Roye, M.E., McLaughlin, W.A. and Maxwell, D.P.
            TITLE     Three distinct geminiviruses infecting M. lachryoides from Jamaica
            JOURNAL   but not BCMV (1996)
            REFERENCE 3 (bases 1 to 447)
            AUTHORS   Roye, M.E., McLaughlin, W.A. and Maxwell, D.P.
            TITLE     Direct Submission
            JOURNAL   Submitted (17-OCT-1996) Biochemistry, University of the West
            INDICES   Indies, Mona, Kingston 7, Jamaica
            FEATURES   location/qualifiers
                     1..447     name="Macrotellium golden mosaic geminivirus"
                     /strain="Jamaican"
                     /isolate="2"
                     /db_xref="taxon:51676"
                     /clone="pMGJA2"
                     complement(1..447)
                     /gene="MCI1"
                     complement(<1..>447)
                     /codon_start=1
                     /product="replication-associated protein"
                     /protein_id="AMB56919.1"
                     /translation="HTVIGFGFNCTNNRLPDLVPSRSARFHPRIQKASSDVS
                     YKEDIDDTKMSVPRQIDGSGKGGQTSNDAAABALNSGKRAKRIYKELPEFLE
                     QTHMSISLDRITPKDDEWMAWPTPLASPSNPVDMQKMTIRGSK"
                     BASE COUNT      97 a      112 c      110 g      128 t
                     ORIGIN

alignment_scores:
  Quality: 273.00      Length: 70
  Ratio: 4.333      Gaps: 0
  Percent Similarity: 90.000      Percent Identity: 71.429

alignment_block:
US-09-289-346a-9 x MGU75278/rev ..
Align seg 1/1 to reverse of: MGU75278 from: 1 to: 447
1  ThleuValITPGLYGLupheGlnValAlaGlnValArgSerAlaArgLYGI 17
  |||||||
294 ACCATCGAATGGGAGAGCTGTTCCAGAGAGAGAGAGAGAGAGAGAGAG 245
17 yCysGlnThrSerAsnAspAlaAlaGlnValaLeuAsnAlaSerSerL 34
  |||||||
244 TCAGCAAAACATCTAACGATCAGACCGCGCAAGCAATTAAATCTCGACAA 195

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/ protein_id="AAB82606.1"
/db_xref="GI:2593075"
/translation="MFRKDAFMRSMQATSKVSNKNTSPRSGIGPINKAAEWNRPM
148 PCS 1 165
/ note="replication-associated protein"
/codon_start=1
/product="AC1"
/ protein_id="AAB82605.1"
/db_xref="GI:2593074"
/translation="MFRGSPSTRKANKFLYTPQCSLKEDLSQIQTTPVKKFI
YKRLKRNKDEPHATLIDKSNFCKNNRLPLVPSYSTRHPKVIKSSDYVS
VYKSLKSLKSLKSLKSLKSLKSLKSLKSLKSLKSLKSLKSLKSLKSLKSL
OYNSLSLDRIIPKAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP
160 DSRKGTMMACRC"
BASE COUNT      350 a      264 c      256 g      295 t
ORIGIN

alignment_scores:
  Quality: 267.00      Length: 70
  Ratio: 4.108      Gaps: 0
  Percent Similarity: 92.857      Percent Identity: 70.000

alignment_block:
US-09-289-346a-9 x AF026553 ..
Align seg 1/1 to: AF026553 from: 1 to: 1165

1   ThrLeuValTrpGlyGluPheGlnValAlaGlyArgSerAlaArgGlyG 17
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
791  ACCCTCGAATGGGAGTGTCTTCGATGATGACGAGAGAGTGTCTGAGGTGG 840

17  YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSetL 34
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
841  CCAGACACGACGACACGACGACGACGACGACGACGACGACGACGACGAC 890

34  YsGluGluAlaLeuGlnIleIleArgGluGlyIleProGluLysTrpLeu 50
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
891  AGGAGACACCATCAAAATCATCAAAAGAGAGATGCGGAGAAAGTTTCCT 940

51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTr 67
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
941  TTTCGATATCATACATTCGATGATGATGATGATGATGATGATGATGATG 990

67  rProGluPro 70
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
991  TCCCAATTCG 1000

seq_name: qb.v1:AB001315
seq_documentation_block:
LOCUS      AB001315      570 bp      DNA      13-FEB-1999
DEFINITION  Tobacco leaf curl virus C1 and C4 genes, clone YOKOHMA3-1, partial
and complete cds.
ACCESSION   AB001315
VERSION     AB001315.1 GI:3798714
KEYWORDS
SOURCE
ORGANISM    tobacco leaf curl virus (Isolate:YOKOHMA3,
            tobacco leaf curl virus (strain maki1nol) DNA, clone:YOKOHMA3-1,
            Tobacco leaf curl virus
            Viruses: ssDNA viruses; Geminiviridae; Begomovirus.
            1 (bases 1 to 570)
Ool.K.
Direct Submission
Submitted (19-FEB-1997) to the DDBJ/EMBL/GenBank databases.
Author(s) H. Kato, T. Kato, T. Kato, T. Kato, T. Kato, T. Kato,
Hakozaki H, Hasegawa K, Fukuchi K, Kato T, Kato T, Kato T,
(E-mail: kotoj@chembox.nc.kyushu-u.ac.jp, Tel.:81-92-642-2624,
Fax:81-92-642-2645)
2 (bases 1 to 570)
Ool.K., Ohshita,S., Ishii,I. and Yahara,T.
Molecular Phylogeny of geminivirus infecting wild plants in Japan

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JOURNAL      J. Plant Res. 110, 247-257 (1997)
FEATURES
  SOURCE
  1..570
    Location/Qualifiers
      /organism="tobacco leaf curl virus"
      /host="YOKOHMA3-1"
      /specific_host="Bidnatorium maki1nol"
      /db_xref="taxon:67762"
      /clone="YOKOHMA3-1"
      complement(1..570)
      /gene="C1"
      complement(41..570)
      /gene="C4"
      complement(1..570)
      /gene="C1"
      complement(41..570)
      /protein_id="AAB84033.1"
      /db_xref="GI:4426541"
      /translation="EVALSLQIINVTPTKLYLKICRELHEDGSPHLVLLQFRRK
      CONNRFEDLVPTSRANFPIIQGAKSSDYKSYIDKDGDTLENGTFQIGRSARGCC
      ONANDCAEALMASSRAEALAIIRKLPDFTFOYHINLSNLDRIFAAPLEPVCPPT
      ASSPDVPEELELEWASEWSSAANFRRP"
      complement(231..488)
      /gene="C4"
      complement(231..488)
      /protein_id="BA34034.1"
      /db_xref="GI:3798715"
      /translation="MRAILSMKFCSSKANTNAKIDDSWTYFQPDQHSIRFRRELNP
      APTSPSTSTETLSNKGHSSTSEVLEBANMLUTHVQNR"
BASE COUNT      141 a      121 c      126 g      182 t
ORIGIN

alignment_scores:
  Quality: 264.00      Length: 85
  Ratio: 4.190      Gaps: 1
  Percent Similarity: 74.118      Percent Identity: 61.176

alignment_block:
US-09-289-346a-9 x AB001315/rev ..
Align seg 1/1 to reverse of: AB001315 from: 1 to: 570

1   ThrLeuValTrpGlyGluPheGlnValAlaGlyArgSerAlaArgGlyG 17
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
318  ACCCTCGAATGGGAGTGTCTTCGATGATGACGAGAGAGTGTCTGAGGTGG 265

17  YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSetL 34
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
268  CTCCAGATGCTTACGACGATGTCAGAGGGGTGTAATGCAAGTGTCTA 219

34  YsGluGluAlaLeuGlnIleIleArgGluGlyIleProGluLysTrpLeu 50
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
218  AGGAGACACCATCAAAATCATCAAAAGAGAGATGCGGAGAAAGTTTCCT 163

51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
168  TTTCGATATCATACATTTAAATAGTAATTTAGATAGGATTTTGTCTCTCC 119

64  .....
118  GTTGGAGGTTTTGTTGTTGCTCTTTCACAGGCTGATACCTTTTCACAGTTC 69

68  rGlu 69
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
68  CAGAA 64

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2216 AGCTAATGATGCTGCCCCAGAGCCCTTAAATGACGCTCAGTGAAGCA 2167
37 JaleuGlnllelearglulphedlproglulstYrleupheslaph 53
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2166 CTTTACGCAATATTAAGGCAAGACCTCCGACAAACATTTTATTTTCATAT 2117
54 HisanleuAsnSerAsnleuAspAqgilephasplpYrPro 68
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2116 CATATTTAAATGATATTAGATAGAGATTTT.....ACACCT 2078

seqname: /cgn1_8/gcdata/geneseq/geneseq/MA1995.DAT:MA084371
seq_documentation_block:
ID MA084371 standard; DNA: 434 BP.
XX
AC MA084371;
XX
DT 19-AUG-1995 (first entry)
XX
XX Gemini1 virus-specific poly(ribozyme)-E target sequence.
XX
XX ribozyme target sequence: poly(ribozyme)-E:
XX tomato leaf curl virus; RNA cleavage; tomato transgenic plant;
XX virus disease-resistance; ss.
XX
XX Tomato leaf curl virus.
XX
XX Key location/Qualifiers
XX misc_feature 13..43
XX /tag= a
XX /note= "ribozyme R1 target sequence"
XX
XX misc_feature 26..28
XX /tag= b
XX /note= "ribozyme R1 cleavage site"
XX
XX misc_feature 32..42
XX /tag= c
XX /note= "ribozyme R2 target sequence"
XX
XX misc_feature 325..327
XX /tag= d
XX /note= "ribozyme R2 cleavage site"
XX
XX misc_feature 384..414
XX /tag= e
XX /note= "ribozyme R3 target sequence"
XX
XX misc_feature 397..399
XX /tag= c
XX /note= "ribozyme R3 cleavage site"
XX
XX W09030404-A.
XX
XX 02-FEB-1995.
XX
XX 22-JUL-1993: 93MO-EP01946.
XX
XX 22-JUL-1993: 93AO-0047034.
XX
XX 22-JUL-1993: 93MO-EP01946.
XX
XX (BIOC-) BIOCEN SA.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Baulino S, Comeau D, Dry IB, Gruber V, Lange P;
XX Mason J, Rezaiian MA, Rigden JE, Rezaiian MA:
XX WPI: 1995-075232/10.
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX and/or assembly of viruses by cleaving target virus sequence.
XX
XX useful for preparing resistant plants, esp tomatoes.
XX
XX Example 10: Fig 11b: 90pp: English.
XX
XX The sequence is a tomato leaf curl virus target sequence for
XX poly(ribozyme)-E, which hybridizes to and cleaves the sequence and
XX thereby reduces replication, infection and/or assembly of the virus

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CC substantially. The ribozyme may be expressed in a transgenic plant,
XX e.g. tomato, to confer virus disease-resistance.
XX
XX Sequence 434 BP; 126 A; 86 C; 91 G; 131 T; 0 other:
XX
XX alignment_scores:
XX      Quality: 236.00      Length: 85
XX      Ratio: 3.806      Gaps: 1
XX      Percent Similarity: 72.941      Percent Identity: 55.294
XX
XX alignment_block:
XX US-09-289-346a-9 x MA084371 ..
XX
XX Align seg 1/1 to: MA084371 from: 1 to: 434
XX
1 ThrleuValTPRGIyglulphedlnlearglulstYrleupheslaph 17
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
95 ACCGTCGATAGGAGACGCTTACAGATGACGACATCGCAAGAGAGAG 144
17 yCGslGTPRtSerAspAspAqgilephasplpYrPro 34
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
145 ACAACATTCACGCAAGACCTCCGACCAAGCCGCTTAAACATCGCAAT 194
34 yslGluAlaleuGlnllelearglulstYrleupheslaph 50
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
195 AGTCAGACGCTTACACGCTCTTACGAGATTAACCGCAAGCATATAT 244
51 PhaglnPheHIsanleuAsnSerAsnleuAspAqgile..... 63
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
245 TTCAATTTCAATTAATTAAATGATATTAGATAGAGATTTTACACCTCC 294
64 .....PheAspLYsrP 68
295 GTTGGAGCTTATGTTTCTCTTTTATCTCTTCTTTTACAGATG 344
68 rodLu 69
XX |||||
XX 345 CACAA 349
XX
seqname: /cgn1_8/gcdata/geneseq/geneseq/MA1995.DAT:MA084372
seq_documentation_block:
ID MA084372 standard; DNA: 479 BP.
XX
AC MA084372;
XX
DT 19-AUG-1995 (first entry)
XX
XX Gemini1 virus-specific poly(ribozyme)-F target sequence.
XX
XX ribozyme target sequence: poly(ribozyme)-F:
XX tomato leaf curl virus; RNA cleavage; tomato transgenic plant;
XX virus disease-resistance; ss.
XX
XX Tomato leaf curl virus.
XX
XX Key location/Qualifiers
XX misc_feature 43..95
XX /tag= a
XX /note= "ribozyme R4-R5 target sequence"
XX
XX misc_feature 58..60
XX /tag= b
XX /note= "ribozyme R4 cleavage site"
XX
XX misc_feature 81..83
XX /tag= c
XX /note= "ribozyme R5 cleavage site"
XX
XX misc_feature 356..386
XX /tag= d
XX /note= "ribozyme R2 target sequence"
XX
XX misc_feature 370..372
XX /tag= c
XX /note= "ribozyme R2 cleavage site"
XX

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401 TCCGTTGAGGTTTAAAGTTCCTTTTATCTCTCTTTGATCGAG 450
67 h-rpoclu 69
|||||
451 TTCAGAA 458

seq_name: /cgnl_8/gcdata/geneseq/geneseq/NA198.DAT:AAV29761

seq_documentation_block:
ID AAV29761 standard. DNA: 2766 BP.
AC
XX
XX AAV29761:
XX
XX 11-AUG-1998 (first entry)
XX
XX Tobacco leaf curling virus gene.
DE
XX Tobacco leaf curling virus gene: TILCV; promoter: ds.
XX
XX Tobacco leaf curling virus.
OS
XX JPI0070982-A.
XX
XX 17-MAR-1998.
PD
XX 30-AUG-1996: 96JP-0230394.
XX
XX 30-AUG-1996: 96JP-0230394.
XX
XX (NORO ) MORINSUISANSIRO KYUSHU NOGOO SHIKENJO.
XX
XX MPI: 1998-233630/21.
DR
XX Tobacco leaf curling virus gene - useful for inserting into vectors
XX for expression in, e.g. tomato plants
XX
XX Claim 1: Figs 1-3: 9pp: Japanese.
XX
XX This sequence represents the tobacco leaf curling virus (TILCV) gene of
CC the invention. TILCV gene or its promoter can be inserted into a vector
CC for expression in plants, e.g. tobacco and tomato. This sequence is
CC believed to encode the TILCV proteins shown in AAW56493-AW56496.
XX
XX Sequence 2766 BP: 722 A: 576 C: 609 G: 859 T: 0 other:

Alignment_scores:
Quality: 226.00 Length: 84
Percent Similarity: 73.810 Caps: 1
Percent Identity: 54.762

alignment_block:
US-09-289-346A-9 x AAV29761/rev ..
Align seg 1/1 to reverse of: AAV29761 from: 1 to: 2766

2 Levalatrrpctlygubhecinvalalagivrgserlalatgiclycy 18
2436 CTTCATTTCGACTTTCGCAATTCAGTGAAGTCACTACGAGAGATG 2367

18 sginhrSerAnspAlaAlaAlaGluAlaLeuAsnAlaSerSerly 35
|||||
2386 CCACCTGTCACCAAGCAGATATGCGGAGGCAACCAATCGATCAAAAT 2337
35 lucilAlaLeuGlnIleIleIleATGgtlulylefrcglulyltyrleuphe 51
|||||
2336 CATCGGCTCAATATATATATAGCGAAGAACTCCCAAAATTTGTTTA 2287
52 GlAphehIsnLeuAsnSerAsnLeuAspArgIle..... 63
|||||
2286 CAATTTCATATTTAAATTCAAATTTAGATGATTTTGTCTCCTCAAT 2237

seq_name: /cgnl_8/gcdata/geneseq/geneseq/NA1997.DAT:AAV93291

seq_documentation_block:
ID AAV93291 standard. DNA: 1062 BP.
AC
XX
XX AAV93291:
XX
XX 27-APR-1998 (first entry)
XX
XX Bean golden mosaic geminivirus C1 mutant ORF BGAC221.
XX
XX Geminivirus: RCMV; C1 gene: transposant mutation;
XX transgenic plant; disease resistance: ss; cyclic; circular.
XX
XX Bean golden mosaic virus type II isolate Guatemala.
OS
XX WO9739110-A1.
XX
XX 23-OCT-1997.
PD
XX 15-APR-1997: 97WO-US06300.
XX
XX 16-APR-1996: 96US-0015517.
XX
XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX (WISC ) WISCONSIN ALOMNT RES FOUND.
XX
XX Ahiquiet PG, Hanson SF, Liu HT, Maxwell DP, Stout JT;
XX
XX MPI: 1997-526447/48.
DR
XX P-PSDB: AAW34333.
XX
XX Transgenic plants expressing geminivirus AC1 and C1 wild-type and
XX mutant genes - have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or Bean
XX golden mosaic geminivirus
XX
XX Claim 13: Page 107-109: 132pp: English.
XX
XX This DNA sequence comprises construct BGAC221 that codes for a
CC transposant lethal mutant (see AAW34333) of the C1 protein (see
CC AAW34338) of bean golden mosaic virus (BGMV). It was obtained by
CC transposon insertion. The insertion involves production of a
CC transgenic plant containing DNA comprising geminivirus C1 or AC1
CC wild-type or mutant sequences that negatively interfere in trans
CC with geminiviral replication during infection. Such transgenic
CC plants are resistant to viral infection. The AC1/C1 genes are
CC especially from BGWY, tomato mottle virus or tomato yellow leaf
CC curl virus (see AAV93282-93) and encoded polyprotein (see AAW34324-35)
CC encodes mutations in the highly conserved DNA-nicking end/or the
CC NTP-binding domains.
XX
XX Sequence 1062 BP: 339 A: 245 C: 219 G: 259 T: 0 other:

Alignment_scores:
Quality: 222.00 Length: 70
Percent Similarity: 85.714 Caps: 0
Percent Identity: 60.000

alignment_block:
US-09-289-346A-9 x AAV93291 ..
Align seg 1/1 to: AAV93291 from: 1 to: 1062

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:1 ThrLeuValTrpGlyGluPheGlnValAlaGlyArgSerAlaArgGlyCyl 17
||||| ||||||| ||||||| ||||||| |||||||
328 ACAATCGAATGGGAGCAATTCGACAGTCGACGAGCAATTCGCAAGAGG 377
17 YCysGlnTrpSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerL 34
TCAGCAATCTGCACAGCACTCATATTCGCAAGAGCATTCGCAAGATCA 427
34 YsgLGlAlaLeuGlnIleAlaArgIleLysLSPProGlyLysTyrLeu 50
||||| ||||||| ||||||| ||||||| |||||||
428 TTGCAATCGCTGCACATATTCGCAAGAGCAAGCAATTCACATTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAsnGlyIlePheAspLysTh 67
||||| ||||||| ||||||| ||||||| |||||||
478 CTTCACACATGCACATCCGCTCTATCTTCACACGATCTTCGCAAG 527
67 rProGluPro 70
||||| |||||||
528 GCCGCAACCA 537

seq_name: /cgnl_8/gcdata/geneseq/geneseq/NA1997.DAT:AA793292
seq_documentation_block:
ID AA793292 standard; DNA; 1062 BP.
XX
AC AA793292:
XX
AD 27-APR-1998 (first entry)
XX
DE Bean golden mosaic geminivirus CI mutant ORF BGAC228.
XX
KM Geminivirus; BGWV; CI gene; transdominant mutation;
KM transgenic plant; disease resistance; ss: cyclic; circular.
XX
OS Bean golden mosaic virus type II isolate Guatemala.
XX
PN M09739110-A1.
XX
PD 23-OCT-1997.
XX
PE 15-APR-1997; 97MO-US06300.
XX
PF 16-APR-1996; 96DS-0015517.
XX
PA (SEMT-) SEMINIS VEGETABLE SEEDS INC.
PA (WISC) WISCONSIN ALDUMNI RES FOUND.
XX
P1 Ahlquist PG, Hanson SF, Lou HT, Maxwell DP, Stout JT;
P1 WPI: 1997-526447/48.
P1 P-PSDB: AAM34335.
XX
PT Transgenic plants expressing geminivirus AC1 and CI wild-type and
PT mutant genes - have increased resistance to geminivirus infection
PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
PT golden mosaic geminivirus
XX
PS Claim 13: Page 111-112; 132pp; English.
XX
CC This DNA sequence comprises construct BGAC228 that codes for a
CC transdominant lethal mutant (see AAM34334) of the CI protein (see
CC AAM34338) of bean golden mosaic virus (BGWV). It was obtained by
CC Kunik mutagenesis of the wild-type CI gene (see AA793314). CI is
CC required for replication. The invention involves production of a
CC transgenic plant containing DNA complementing geminivirus CI or AC1
CC wild-type or mutant sequences that negatively interfere in trans
CC geminivirus replication during infection. Such transgenic
CC plants are resistant to AC1 and CI geminivirus infection. AC1
CC curl virus (see AA793282-93) and encode polypeptides (see AAM34324-35)
CC especially from BGWV, tomato mottle virus or tomato yellow leaf
CC curl virus.
CC That have mutations in the highly conserved DNA-nicking and/or the
CC NTP-binding domains.

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XX
SQ Sequence 1062 BP; 338 A; 247 C; 218 G; 259 T; 0 other;
alignment_scores:
Quality: 223.00 Length: 70
Score: 3700
Percent Similarity: 85.724 Percent Identity: 60.000
alignment_block:
US-09-289-346a-9 x AA793292
Align seg 1/1 to: AA793292 from: 1 to: 1062
1 ThrLeuValTrpGlyGluPheGlnValAlaGlyArgSerAlaArgGlyCyl 17
||||| ||||||| ||||||| ||||||| |||||||
328 ACAATCGAATGGGAGCAATTCGACAGTCGACGAGCAATTCGCAAGAGG 377
17 YCysGlnTrpSerAsnAspAlaAlaAlaGluAlaLeuAsnAlaSerSerL 34
TCAGCAATCTGCACAGCACTCATATTCGCAAGAGCATTCGCAAGATCA 427
34 YsgLGlAlaLeuGlnIleAlaArgIleLysLSPProGlyLysTyrLeu 50
||||| ||||||| ||||||| ||||||| |||||||
428 TTGCAATCGCTGCACATATTCGCAAGAGCAAGCAATTCACATTC 477
51 PheGlnPheHisAsnLeuAsnSerAsnLeuAsnGlyIlePheAspLysTh 67
||||| ||||||| ||||||| ||||||| |||||||
478 CTTCACACATGCACATCCGCTCTATCTTCACACGATCTTCGCAAG 527
67 rProGluPro 70
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528 GCCGCAACCA 537

seq_name: /cgnl_8/gcdata/geneseq/geneseq/NA1997.DAT:AA793293
seq_documentation_block:
ID AA793293 standard; DNA; 1062 BP.
XX
AC AA793293:
XX
AD 27-APR-1998 (first entry)
XX
DE Bean golden mosaic geminivirus CI mutant ORF BGAC262.
XX
KM Geminivirus; BGWV; CI gene; transdominant mutation;
KM transgenic plant; disease resistance; ss: cyclic; circular.
XX
OS Bean golden mosaic virus type II isolate Guatemala.
XX
PN M09739110-A1.
XX
PD 23-OCT-1997.
XX
PE 15-APR-1997; 97MO-US06300.
XX
PF 16-APR-1996; 96DS-0015517.
XX
PA (SEMT-) SEMINIS VEGETABLE SEEDS INC.
PA (WISC) WISCONSIN ALDUMNI RES FOUND.
XX
P1 Ahlquist PG, Hanson SF, Lou HT, Maxwell DP, Stout JT;
P1 WPI: 1997-526447/48.
P1 P-PSDB: AAM34335.
XX
PT Transgenic plants expressing geminivirus AC1 and CI wild-type and
PT mutant genes - have increased resistance to geminivirus infection
PT e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
PT golden mosaic geminivirus
XX
PS Claim 13: Page 115-116; 132pp; English.

```

CC This DNA sequence comprises construct BGAC262 that codes for a
 CC transdominant lethal mutant (see AAM4335) of the CI protein (see
 CC AAM4338) of bean golden mosaic virus (BGMV). It was obtained by
 CC random mutagenesis of the wild-type CI gene (see AAT9314). CI is
 CC required for replication. The invention involves production of CI
 CC mutants that are resistant to viral infection. Such transgenic
 CC wild-type or mutant sequences that negatively interfere in trans
 CC with geminiviral replication during infection. CC transgenic
 CC plants are resistant to viral infection. The ACI/CI genes are
 CC especially from BGMV, tomato mottle virus or tomato yellow leaf
 CC curl virus (see AAT9348-93) and encode polypeptides (see AAM43324-35)
 CC that have mutations in the highly conserved DNA-nicking and/or the
 CC NTP-binding domains.

CC Sequence 1062 BP; 340 A; 245 C; 219 G; 258 T; 0 other;

alignment_scores:

Quality: 222.00 Length: 70
 Ratio: 3.700 Gaps: 0
 Percent Similarity: 85.714 Percent Identity: 60.000

alignment_block:

US-09-289-346a-9 x AAT93293 ..

Align seg 1/1 to: AAT93293 from: 1 to: 1062

1 ThrLeuValTrpGlyGluPheGlnValAlaGlyArgSerAlaGlnGly 17
 328 ACATTCGATGGGACATTCGACATTCGACGCGACATTCGACAGAG 377
 17 yCysGlnHisSerAspAlaAlaGlnAlaLeuAsnAlaSerSerL 34
 378 TCAGCAGCTCTCCACAGCATTGACGACATTAAGCGACATTCGA 427
 34 yGluGlnAlaLeuGlnAlaGlnGluValSerProGluLysTrpLeu 50
 428 TTCGATCTGCCTTCGACATTAAGAGGACGACGAGAAATTCCTC 477
 51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspValGlu1PheAspLysTrp 67
 478 CTTTCACATCTCCACATTCGCTTCATCTTCACGACGATCTTCGCAAGT 527
 67 ProGluPro 70
 528 GCCGCAACCA 537

seq_name: /cgnl_8/gcdata/geneseq/geneseq/NA1996.DAT: AAT12904

seq_documentation_block:

1 AAT12904 standard: DNA: 1080 BP.

AC AAT12904:

DT 07-NOV-1996 (first entry)

XX Sardinian tomato yellow leaf curl virus mutated CI gene (K227A).
 XX Nucleotide triphosphate binding site: DNA helicase: RNA helicase:
 XX modification: mutation: viral replication: deficient: inhibition:
 XX viral resistance: geminivirus: tomato yellow leaf curl virus:
 XX Sardinian isolate: SYLVV: transgenic plant: P-loop: CI gene:
 XX All gene: dominant negative phenotype: ss.

XX Sardinian tomato yellow leaf curl virus.

Key Location/Qualifiers
 CDS 1..1080

FT /tag- a
 FT /product- Rep-(K227A)
 FT /note- Encodes Rep protein in which wild-type Lys
 FT at position 227, i.e. within the NTP-
 FT binding site, is replaced by Ala

XX M09608573-A1.

XX 21-MAR-1996.

XX 15-SEP-1995. -95MO-F00192.

XX 15-SEP-1994. 94PR-001040.

XX (CNRS) CENT NAT RECH SCI.

XX Groningen B.

XX WPI: 1996-1179947/18.

XX P-PSDB: AAR88670.

XX Prodn. of virus-resistant transgenic plants - using mutated genomic
 XX sequence from phytopathogenic DNA virus

XX Disclosure: Fig 13; 93pp; French.

CC Mutation of consensus amino acids in the NTP-binding site of
 CC geminivirus Rep protein is used to produce replication deficient
 CC viruses. The mutated viral nucleic acid is used for producing
 CC transgenic plants that are resistant to, or tolerant of, the native
 CC virus. The present sequence encodes a mutant form of the Rep (or CI)
 CC protein from the Sardinian isolate of tomato yellow leaf curl virus
 CC (SYLVV) in which the wild-type lysine residue at position 227 is
 CC replaced by alanine. The mutant virus is generated by
 CC transformation with the mutated virus was found to be resistant to
 CC SYLVV. I.e the mutation results in a dominant negative phenotype.

CC Sequence 1080 BP; 355 A; 248 C; 210 G; 267 T; 0 other;

alignment_scores:

Quality: 222.00 Length: 69
 Ratio: 3.828 Gaps: 0
 Percent Similarity: 84.058 Percent Identity: 57.971

alignment_block:

US-09-289-346a-9 x AAT12904 ..

Align seg 1/1 to: AAT12904 from: 1 to: 1080

2 LeuValTrpGlyGluPheGlnValAlaGlyArgSerAlaGlnGly 18
 331 CTTGATGCGGCTTCGACATTCGACGACGACATTCGACGACGAC 380
 18 sGlnHisSerAspAlaAlaGlnAlaLeuAsnAlaSerSerLys 35
 381 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 430
 35 LuGlnAlaLeuGlnAlaGlnGluValSerProGluLysTrpLeu 51
 431 CGCAGCCTCTTGATGATTAAAGATTAGCGCTAGATTAAGCTTGA 480
 52 GluPheHisSerAsnLeuAsnSerAsnLeuAspValGlu1PheAspLysTrp 68
 481 CATTTCATATATATATATATATATATATATATATATATATATAT 530
 68 OgluPro 70
 531 GCCACCT 537

seq_name: /cgnl_8/gcdata/geneseq/geneseq/NA1996.DAT: AAT12905

seq_documentation_block:

ID AAT12905 standard: DNA: 1080 BP.

AC AAT12905:

DT 07-NOV-1996 (first entry)

[illegible]

```

seq.name: /cgnl_8/gsgdata/cgenseq/geneseqn/NM1996.DAT.AAT12906
seq.documentation_block:
AC AAT12906 standard; DNA; 1080 BP.
XX
XX
AC AAT12906;
XX
XX
DE 07-NOV-1996 (first entry)
XX
XX
NM Sardinian tomato yellow leaf curl virus mutated C1 gene (#Z273).
XX
XX
XX Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
KM modification; mutation; viral replication; deficient; inhibition;
KM viral resistance; geminivirus; tomato yellow leaf curl virus;
KM Sardinian isolate; STYLGV; transgenic plant; P-loop; C1 gene;
All gene; ss.
XX
XX Sardinian tomato yellow leaf curl virus.
XX
XX Key Location/Qualifiers
FT CDS 1..1080
FT     /*tag= a
FT     /product= Rep.(#Z273)
FT     /note= "encodes Rep protein in which wild-type lys
FT         at position 227, i.e. within the MTP-
FT         binding site, is replaced by Arg"
XX
XX MO9608573.AL.
XX
PD 21-MAR-1996.
XX
PF 15-SBP-1995;   G5MO-FR01192.
XX
PA 15-SBP-1994;   9dFR-0011040.
XX
XX (CNRS ) CENT NAT RECH SCI.
XX
XX Gronenborn B;
P1 WP1; 1996-178547/18.
P2 WP2; 1996-178547/18.
P3 F-P50B; AAH08872.
PT Prodn. of virus-resistant transgenic plants - using mutated genomic
PJ sequence from Phytopathogenic DNA virus
XX
PS Disclosure: Fig 13; 93pp; French.
XX
XX Mutation of consensus amino acids in the ATP-binding site of
XX the replicase of tobacco etch virus results in non-viable or deficient
XX viruses. The mutated viral nucleic acid is used for producing
XX transgenic plants that are resistant to, or tolerant of, the native
XX virus. The present sequence encodes a mutant form of the Rep (or C1)
XX protein from the Sardinian isolate of tomato yellow leaf curl virus
XX (STYLGV) in which the wild-type Lys227 residue has been changed to an
XX Arg residue; Transgenic Nicotiana benthamiana plants generated by an
XX Agrobacterium-mediated transformation protocol containing the STYLGV
XX construct, in contrast, plants transformed with a virus in which Lys227 had been
XX replaced by Ala were found to be resistant.
XX
SQ Sequence 1080 BP; 356 A; 247 C; 210 G; 267 T; 0 other;

```

Alignment_scores:

Quality: 222.00 Length: 69
 Ratio: 3.828 Gaps: 0
 Percent Similarity: 84.058 Percent Identity: 57.971

Alignment_block:

US-09-289-346a-9 x AMT92906 ..

Align seg 1/1 to: AMT92906 From: 1 to: 1080

```

2 LeuValITrpolgIuPhcIGInValAlaIGIATYSerAlaATGATGlyCY 18
|||||
331 CTGGAATGCGGGTACCTTCCAGATCGACGCGACATCTCTGAGSAGAGCA 380
18 sGlnThrSerAsnAspAlaAlaIGIAlaLeuAsnAlaSerSerLysG 35
|||||
381 ACAGACAGCCACACGAGCTTACGCAAGGCAATTTACGACGAGAGTAAGT 430
35 IuGluAlaLeuGlnIleIleATGAGIuLysIleProGluLysSTYLeuPhe 51
|||||
431 CGAGAGCTCTGATGATTAATTAAGCAATTTAGCGCTCAAGATTTACGTC 480
52 GIophenIAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrP 68
|||||
481 CATTTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 530
68 OGluPro 70
531 GCGACCT 537

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seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AMT93314

seq_documentation_block:

AMT93314 standard; DNA; 1183 BP.

AMT93314:

DT 27-APR-1998 (first entry)

DE Bean golden mosaic geminivirus CI open reading frame.

GM Geminivirus; BCMV; CI gene; transdominant mutation;

transgenic plant; disease resistance; ss; cyclic; circular.

OS Bean golden mosaic virus type II isolate Guatemala.

Key Location/Qualifiers

FT CDS 1..1062

W09729110-A1.

23-OCT-1997.

15-APR-1997; 97MO-US06300.

16-APR-1996; 95US-0015517.

PA (SEM-) SEMINIS VEGETABLE SEEDS INC.

WISCONSIN ALUMNI RES FOUND.

PI Ahlquist PG, Hanson SF, Lau HT, Maxwell DP, Stout JT;

WPI; 1997-526447/48.

P-PSDB: AAM3438.

Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant genes - have increased resistance to geminivirus infection e.g. tomato mottle virus, tomato yellow leaf curl virus or bean golden mosaic geminivirus

Example 5; Page 100-102; 132pp; English.

CC This genomic DNA sequence includes the open reading frame (ORF) of
 CC the wild-type CI gene of bean golden mosaic virus (BGMV), a
 CC geminivirus that has a monopartite genome. The CI protein (see
 CC AAM3438) is required for replication. The wild-type CI ORF was
 CC subjected to Konkel mutagenesis (see A93290-93). The invention
 CC provides a library of CI genes of BGMV, including the wild-type
 CC CI or AC1 wild-type or mutant sequences that negatively interfere
 CC in trans with geminiviral replication during infection. Such
 CC genes are especially from BCMV, tomato mottle virus or tomato
 CC yellow leaf curl virus (see A93282-93) and encode polypeptides
 CC (see AAM3434-35) that have mutations in the highly conserved
 CC DNA-nicking domain and/or the ATP-binding domains.

Sequence 1183 BP; 372 A; 276 C; 248 G; 287 T; 0 other;

Alignment_scores:

Quality: 222.00 Length: 70
 Ratio: 3.700 Gaps: 0
 Percent Similarity: 85.714 Percent Identity: 60.000

Alignment_block:

US-09-289-346a-9 x AMT93314 ..

Align seg 1/1 to: AMT93314 From: 1 to: 1183

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1 ThrLeuValITrpolgIuPhcIGInValAlaIGIATYSerAlaATGATGlyC 17
|||||
328 ACATTCGATGAGGACATTCACAGCTGACGCGAGATCTGCAAGAGAG 377
17 yGsgIuThrSerAsnAspAlaAlaIGIAlaLeuAsnAlaSerSerL 34
|||||
378 TCAGCAGCTGTCGCAAGCTCATATGCAAGGCAATTAAGCGAGATTC 427
34 yGsgIuGlnAlaLeuGlnIleIleATGAGIuLysIleProGluLysSTY 50
|||||
428 TTCATCTGCTTGACATATTAATTAATTAATTAATTAATTAATTAATTA 477
51 PheGlnPheIAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThr 67
|||||
478 CTTCACATCTGACATCTTCATTAATTAATTAATTAATTAATTAATTA 527
67 ProGluPro 70
528 CCGCGACCA 537

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seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT:AMT92920

seq_documentation_block:

AMT92920 standard; DNA; 1183 BP.

AMT92920:

DT 27-APR-1998 (first entry)

DE Bean golden mosaic geminivirus CI mutant gene.

GM Geminivirus; BCMV; CI gene; transdominant mutation;

transgenic plant; disease resistance; ss; cyclic; circular.

OS Bean golden mosaic virus type II isolate Guatemala.

Key Location/Qualifiers

FT CDS 1..1062

W09729110-A1.

23-OCT-1997.

15-APR-1997; 97MO-US06300.


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seq_name: /cgnl_8/gcgdata/geneseq/geneseqn/MA2000.DAT::AAA94701
ID ID seq_documentation_block:
XX AAA94701 standard: DNN: 1651 BP.
AC AAA94701;
DT 15-JAN-2001 (first entry)
XX piRepn nucleotide sequence.
DM
KM Geminivirus: DNA-A: geminivirus replication inhibition; ac3 gene:
KM transgenic plant: antiviral; gene therapy; bean golden mosaic virus;
KM BGMV; alfalfa mosaic virus; AMV; calliflower mosaic virus; CMV; ds.
XX Bean golden mosaic virus.
OS Bean golden mosaic virus.
OS Alfalfa mosaic virus.
OS Synthetic.
PN US6118048-A.
PR
PD 12-SEP-2000.
XX
XX 24-APR-1998; 96US-0065999.
XX
XX 25-APR-1997; 97US-0044925.
PA (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX MPI: 2000-610861/58.
DR
XX Genetic construct comprising a mutant geminiviral rep gene, useful for
PT producing a plant resistant to geminiviral infection.
XX
PS Example: Column 17-18; 14ppr: English.
CC The present sequence is piRepn, a vector containing a CaMV-35S
CC promoter-driven rep gene derived from bean golden mosaic virus (BGMV)-GA
CC Site-directed mutagenesis was used to engineer an NcoI site in the start
CC codon of the rep gene to facilitate cloning of DNA-nicking domain
CC mutants. The resulting genetic constructs act as trans-dominant
CC inhibitors. These constructs are able to dramatically reduce replication of
CC geminivirus. Genetic constructs that include sequences containing a
CC portion of the ac3 gene in addition to the trans-dominant inhibitor
CC exhibit increased efficiency and broadened specificity of inhibition of
CC geminiviral replication. Geminiviruses are one of the greatest
CC constraints on production of important crops, including cassava, beans,
CC cowpeas, peppers, tomatoes and cotton. The effects of the virus can be
CC overcome by using the genetic construct.
SQ Sequence 1651 BP; 517 A; 392 C; 343 G; 399 T; 0 other:

alignment_scores:
Quality: 222.00 Length: 70
Ratio: 3.700 Gaps: 0
Percent Similarity: 85.714 Percent Identity: 60.000

alignment_block:
US-09-289-346A-x AAA94701 ..

Align seg 1/1 to: AAA94701 from: 1 to: 1651

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1 ThrLeuValTrpGlyGluPheGlnValAlaGlyArgSerAlaArgGlyGly 17
 |||::: |||||:::||||||| |||||:::||||||| |||||:::|||||||
 796 ACAATCGAATGGGGACAAATTCACAAGTCGACGGCAGATCTGCCAAGAGGAGG 845

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us-09-289-346a-9.p2n.rng

Page 11

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KEYWORDS EST.
SOURCE Fruit fly.
ORGANISM *Drosophila melanogaster*
REFERENCE Bkaryota: Metazoa; Arthropoda: Tracheata; Hexapoda: Insecta; Pharyngota: Meopoda; Endopterygota: Diptera: Heteroptera: 1 (bases 1 to 765)
AUTHORS M. Stapleton, M. Brokstein, P.-J. Hong, L. Agbayani, A. Baxter, E. Berman, B. Carlson, J. Champ, M. Chavez, C. Chew, M. Dorsett, V. Farfan, D. Frisoe, E. George, R. Gonzalez, M. Guarlin, H. Harris, N. Li, P. Liao, C. Miranda, A. Mista, S. Munagi, C. J. Nuno, J. Paclet, J. Pargay, V. Park, S. Pounanavong, S. Yan, K. Yu, C. Lewis, S. E. Goto, J. S. and Rubin, S. B. *Drosophila* EST Project
TITLE Unpublished (2000)
JOURNAL On Dec 6, 2000 this sequence version replaced gi:11589485.
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd. Berkeley, CA 94720, USA
Fax: 1-916-863-0796
E-mail: fruitfly@fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic: A603442; arm: X (1761665,790735)
estimated: cyto: 702-7011; 04/07/2001
Plate: AT 85 row: H column: 4
High quality sequence stop: 616.
Location/Qualifiers
1..765
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_1lb="AT Drosophila melanogaster adult testes POTB7"
/sex="male"
/dev_stage="0-3 day old Ore-R males"
/lab_notes="Plates AT-10-AT-120: DHS-alpha. Plates AT-102-AT-115: alpha-embryo. Vector: POTB7. Site 1: Front; Site 2: XhoI; the mRNA for the testis library was made from testes and seminal vesicles hand dissected from 0-3 day old Ore-R males. RNA kindly provided by the lab of Margaret Fuller. Sized fractionated cDNAs were directly ligated into POTB7. Plasmid cDNA library."
BASE COUNT 199 a 205 c 225 g 136 t
ORIGIN
alignment_scores:
Quality: 70.50 Length: 63
Ratio: 2.136 Gaps: 2
Percent Similarity: 52.381 Percent Identity: 34.921
alignment_block:
US-09-289-346a-9 x BF506184 ..
Align seg 1/1 to: BF506184 from: 1 to: 765
11 G1YArGerA1aTg1yG1yG1nThs0rAsnspAla1a1a1a1 27
111

seq_documentation_block:
LOCUS BE954992 1512 bp mRNA EST 14-DEC-2000
DEFINITION 601658759R1 N1R-MGC_59 Homo sapiens cDNA 1KAGE:3886169 3', 5' UTR sequence.
ACCESSION BE954992
VERSION BE954992.2 GI:11768902
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Bkaryota: Metazoa; Chordata: Craniata; Vertebrata: Euteleostomi; Mammalia: Eutheria; Primates: Catarrhini; Homnidae: Homo.
REFERENCE M. Stapleton, M. Brokstein, P.-J. Hong, L. Agbayani, A. Baxter, E. Berman, B. Carlson, J. Champ, M. Chavez, C. Chew, M. Dorsett, V. Farfan, D. Frisoe, E. George, R. Gonzalez, M. Guarlin, H. Harris, N. Li, P. Liao, C. Miranda, A. Mista, S. Munagi, C. J. Nuno, J. Paclet, J. Pargay, V. Park, S. Pounanavong, S. Yan, K. Yu, C. Lewis, S. E. Goto, J. S. and Rubin, S. B. *Drosophila* EST Project
TITLE Unpublished (1999)
JOURNAL On Oct 3, 2000 this sequence version replaced gi:10575697.
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@p5-remail.nih.gov
Tissue Procurement: DCTD/dp/632daz
cDNA Library Preparation: The technology, Inc.
DNA Sequencing by: Inyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILN1 at: http://image.llnl.gov
Plate: ILN1649 row: 1 column: 18
High quality sequence stop: 291.
Location/Qualifiers
1..1512
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="MGC:3886169"
/tissue_type="large cell carcinoma, undifferentiated"
/tissue="Ovarian (phagocytic) SPO9P6, Site 1: Not; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 kb. Library constructed by Life Technologies."
BASE COUNT 481 a 308 c 357 g 363 t 3 others
ORIGIN
alignment_scores:
Quality: 70.50 Length: 77
Ratio: 1.533 Gaps: 3
Percent Similarity: 59.740 Percent Identity: 31.169
alignment_block:
US-09-289-346a-9 x BE954992 ..
Align seg 1/1 to: BE954992 from: 1 to: 1512
4 TRG1yG1yPheG1nVal1a1a1AAGSeR1a1a1yG1yG1yG1nTh 20
111

were sequenced additional times to assess quality

control."
 BASE COUNT 141 a 130 c 161 g 128 t
 ORIGIN

alignment_scores:
 Quality: 69.00 Length: 61
 Ratio: 1.917 Gaps: 2
 Percent Similarity: 59.016 Percent Identity: 31.148

alignment_block:
 US-09-289-346a-9 x A1959235 ..

Align seg 1/1 to: A1959235 from: 1 to: 560

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1  ThrLeuValTTPGyluPhedlnValAlaGlyATGserAlaArgLysI 17
   ||||| |||||
22 ACATTGCTGTGGCG.....CGGCTGTGGCGCG 50
17 YCSClntSerAmApAlaAlaAlaAlaAlaLeuAnaIserSerI 34
   ||||| |||||
51 GTGTACCCCTCTCTCTCCAGCTCCGCCACGCCACGCCACGATC 100
34 YSClGluAlaLeuGlnIleIleArgLysIlePcdLysTyrIleu 50
   ||||| |||||
101 AGATGCTCTCTCT.....GTACCTCCAGAGAGAGATTTCAG 135
51 PhedlnPhelAsnLeuAsnSerAsnLeuArg 61
   ||||| |||||
136 CACATCTCTCTCTCTCCACGCCACGCCACGCCACGATC 168

```

seq_name: gp_gss:A0950848

seq_documentation_block:

LOCUS A0950848 572 bp DNA GSS 27-JAN-2000
 DEFINITION Sheared DNA Trypanosoma brucei genomic clone
 ACCESSION A0950848
 VERSION A0950848.1 GI:6774113
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei.
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE
 1. Trypanosoma brucei, 10.1 sheared DNA (1999)
 AUTHORS El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Sub, E., Malek, J., Fujii, C.,
 Gerard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donaldson, J.,
 Frazer, C. and Adams, M.
 Determination of clone end sequences from Trypanosoma brucei cDNA
 10.1 sheared DNA library
 Unpublished (1999)
 JOURNAL COMMENT
 Contact: Naji M. El-Sayed
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel.: 301 838 0200
 Fax: 301 838 0208
 Email: nelsayed@tifg.org
 Comments: This is a clone from the Trypanosoma brucei cDNA 10.1 sheared
 DNA library constructed at TIGR. Clones will be available for
 distribution through ATCC. Sheared DNA end sequences search page:
 http://www.tifg.org/tldb/mdb/tldb/.
 Seq primer: M13-Forward
 Class: shotgun.

FEATURES
 source
 location/Qualifiers
 1..572
 /strain="TREM927/4 cDNA 10.1"
 /db_xref="taxon:5691"
 /clone_lib="Sheared DNA-51M3"
 /clone_lib="Sheared DNA"

/note="Vector: pUC18; site_1: SmaI; Constructed at The
 Institute for Genomic Research (TIGR), Rockville, MD.
 Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREM927/4 cDNA 10.1) was mechanically
 sheared to give a tight size distribution (approx 2 kb).
 The DNA was then ligated into the SmaI site of the
 pUC18 vector. The resulting library was then sequenced
 (making small insert libraries for whole genome shotgun
 sequencing projects). In Genome Sequencing: A Practical
 Approach, eds. M. Vaundin and B. Barrell, Oxford University
 Press, 1999)."
 BASE COUNT 115 a 118 c 180 g 159 t
 ORIGIN

alignment_scores:
 Quality: 69.00 Length: 32
 Ratio: 2.464 Gaps: 0
 Percent Similarity: 87.500 Percent Identity: 37.500

alignment_block:
 US-09-289-346a-9 x A0950848 ..

Align seg 1/1 to: A0950848 from: 1 to: 572

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10 AlaGlyATGserAlaArgLysIYCYSGlnPhSerAmApAlaAlaI 26
   ||||| |||||
289 AGTGTCTCTCTCCAGCTCCGCCACGCCACGCCACGATC 337
26 AcGluAlaLeuAnaIserSerIYSClGluAlaLeuGlnIleIle 41
   ||||| |||||
338 TGAAGCTGTCTCTCTCCAGCTCCGCCACGCCACGCCACGATC 383

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seq_name: gp_gss:A0947513

seq_documentation_block:

LOCUS A0947513 587 bp DNA GSS 27-JAN-2000
 DEFINITION Sheared DNA Trypanosoma brucei genomic clone
 ACCESSION A0947513
 VERSION A0947513.1 GI:6770778
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei.
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE
 1. Trypanosoma brucei, 10.1 sheared DNA (1999)
 AUTHORS El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Sub, E., Malek, J., Fujii, C.,
 Gerard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donaldson, J.,
 Frazer, C. and Adams, M.
 Determination of clone end sequences from Trypanosoma brucei cDNA
 10.1 sheared DNA library
 Unpublished (1999)
 JOURNAL COMMENT
 Contact: Naji M. El-Sayed
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel.: 301 838 0200
 Fax: 301 838 0208
 Email: nelsayed@tifg.org
 Comments: This is a clone from the Trypanosoma brucei cDNA 10.1 sheared
 DNA library constructed at TIGR. Clones will be available for
 distribution through ATCC. Sheared DNA end sequences search page:
 http://www.tifg.org/tldb/mdb/tldb/.
 Seq primer: M13-Forward
 Class: shotgun.

FEATURES
 source
 location/Qualifiers
 1..587
 /strain="TREM927/4 cDNA 10.1"
 /db_xref="taxon:5691"
 /clone_lib="Sheared DNA-49M17"
 /clone_lib="Sheared DNA-49M17"

/lssue_type="Cell cultures derived from root tissues"
 /dev_stage="Cell suspensions were subcultured every 14
 days". Cells were induced six days after subculture"
 /note="Sector: Lambda zap. Cells were induced with yeast
 final concentration. Samples were taken at 0, 12, 24
 24 hours after induction. Equal amounts of RNA from each
 time point were pooled and used for mRNA isolation."

BASE COUNT 207 a 117 c 143 g 186 t 1 others

ORIGIN

alignment_scores:
 Quality: 69.00 Length: 64
 Ratio: 1.683 Gaps: 2
 Percent Similarity: 64.062 Percent Identity: 32.812

alignment_block:
 US-09-289-346A-9 x BF649762 ..

Align seg 1/1 to: BF649762 from: 1 to: 654

4 TrrpLgALpdpdlaVlaLagIyAysrAlaIayrAgLyLcYcsyGlnh 20
 |||||
 195 TGCGCGCTCTTTCAAGTTCACCAACCTAGCGCCCTTGAGTATACCA 244
 20 rSerAsnApAlaIaLagLualaLalaLnaLlSrSerLyvAgLuclua 37
 245 AAGCTTCCTTAAGATCTCCCAATCTCTTCTTCCTCCAGATTCGCGA 294
 37 lalaGlnlAlleIayrGlyLysIte...PrGluLysrTYLeuPhgGln 52
 :|||:|||||
 295 AAAGCAAGGTTGGCGAGGATGATGATCAACCAATTCGTTATGTAA 344
 53 pHeHlAsnLnaLna...SerAsnLeuAspArgIlePhaSp 65
 345 GAGCGACGACAGAGATCTGACAGACCTGACAGATCTGTTGANT 386

seq_name: gb_gss:AZ208697

seq_documentation_block:
 LOCUS AZ208697 910 bp DNA GSS
 DEFINITION SP_0150.A2.C02.SP6E Strongylocentrotus purpuratus, purple sea 31-AUG-2000
 urchin, sperm genomic BAC library Strongylocentrotus purpuratus
 A2208697, clone Placer-150 COL-4 Row-E, DNA sequence.
 ACCESSION KEYWORDS
 A2208697.1 GI:8421872
 GSS:
 SOURCE
 ORGANISM
 Strongylocentrotus purpuratus.
 Strongylocentrotus purpuratus.
 Eukaryote; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 Strongylocentrotidae; Strongylocentrotidae.
 REFERENCE
 AUTHORS
 1. (bases 1 to 910)
 Cameron, R.A., Mohlins, G., Rast, J. P., Martinez, P., Blondin, T. R.,
 Swartzell, S., Wallage, J. C., Postka, A. J., Livingston, B. T., Wray
 , G. A., Ettensohn, C. A., Lehnach, H., Bitten, R. J., Davidson, E. H. and
 Hood, L.
 Human urchin genome project: Sequence scan, virtual map, and
 physical map. *Proc. Natl. Acad. Sci. U. S. A.* 97 (17), 9514-9518 (2000)
 20402366
 CONTACT: Cameron, R.A., Davidson, EH, Hood, L
 DIVISION of Biology 156-29
 Pasadena California 91125, USA
 TEL: (626) 793-8047
 FAX: (626) 793-8047
 Email: acameron@caltech.edu
 Plate: 150 row: E. Column: 4
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 1010.

```

FEATURES
source
Location/Qualifiers
1. 910
/organism="Strongyloides purpuratus"
/Db_xref="taxon:7688"
/clone="114-115130 C04 B06-g"
/submitter="Strongyloides purpuratus, purple sea urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BAC3.6; BAC clones in E-coli DH10b"
BASE COUNT
248 a 255 c 170 g 237 t
alignment_scores:
Quality: 68.50 Length: 56
Ratio: 1.957 Gaps: 3
Percent similarity: 62.500 Percent identity: 35.714
alignment_block:
US-09-289-346A x AZ208697 ..
Align seq 1/1 to: AZ208697 from: 1 to: 910
18 CysGlnPhSeSerAspArgAlaAlaGlu...AlaGluAsnAlaSerse 33
|||||:|||||:|||||:|||||:|||||:|||||
604 TGCACCTGTCTTACGGCGCAATACCGGAAAAGCTTTTAAACAATGTAT 653
33 rlysgGluGluAlaGluGlnIlele.....ArgGluYliLeProGluL 48
654 CTTTATGTGCACAGACACACACTCTACAGAAATATGCAAACTACGCGAA 703
48 ySTyTleuPhaGlnPhaHisAsnSerPheAsnLeuAspArgIlePhe 64
|||||:|||||:|||||:|||||:|||||:|||||
704 AATGC.....CACACTTTTGCGAAAAAATTTACCCGACGAATTCG 741
65 AspIysThrProGluPro 70
|||||:|||||:|||||:|||||:|||||:|||||
742 GGTAAACCCCTTGCCTCG 759
seq_name: gb_est2:W89594
seq_documentation_block:
LOCUS
W89594 978 bp mRNA EST 12-SEP-1996
DEFINITION
M73509.r1 Soares mouse embryo NM613.5 14.5 Mus musculus cDNA
ACCESSION
W89594.1 J0605:419321.5, mRNA sequence.
VERSION
W89594.1 GI:1404927
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus.
REFERENCE
Bukhariola: Megascora: Chordata: Craniata: Vertebrata; Euteleostomi;
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae; Murinae; Mus.
Garral: 1973.
Merrill.M., Allen.M., Bowles.M., Dietrich.N., Dubuque.T.,
Geisel.S., Kuwaba.T., Lacey.M., Le.M., Martin.J., Morris.M.,
Schelienberg.K., Steptoe.M., Tan.F., Underwood.K., Moore.B.,
Thelning.B., Wylie.T., Lemmon.C., Soares.B., Wilson.R. and
Waterston.R.
The WashU-HMI Mouse EST Project
GenBank accession: U03900
COMMENT
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel.: 314 286 1810
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
The WashU-HMI Mouse EST Project is a resource through LNL; contact the
LNL Manager, Dr. David L. Page (dpage@lml.wustl.edu) for further information.
NCI:254473
Seq primer: -28M13 rev2 from Amerham
High quality sequence stop: 474.
Location/Qualifiers

```

```

source
1 . -978 /organism=Mus musculus"
/Sstrain=C57BL/6J
/OLNucleotide=AA029007"
/CodonTable=NC_0119921"
/clone_lib=Scares mouse embryo NHEK13.5 14.5"
/gsex="unknown"
/tissue_type="embryo"
/dew_stage="13.5-14.5dpv total fetus"
/lab_host="DHIOB"
/note=Vector: pT73D-Pac (pharmacia) with a modified EcoRI site. The 15 nt strand cDNA was primed with a Not I oligo(dG). TCGTCACATCCAGCAATGGACGCCGCAGATAATTCTTTTTTTTTTTTTT
T 3' ), on equal amounts of mRNA from 2.13 dpv and 2
14.5dpv embryos [total RNA prepared by Micro Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated to Eco RI adaptors (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified "pT73D-Pac" vector. * Sequences were determined after normalization.
M.Patino Bonaldo.
BASE COUNT      226 a   171 c   263 g   313 t       6 others
ORIGIN

Alignment_scores:
Quality:    68.00          Length:        61
Ratio:     1.659           Gaps:         3
Percent Similarity: 67.213 Percent Identity: 34.426

alignment_block:
05-09-289-1346A-g x MB9594 ..
Align seg 1/1 to: MB9594 from: 1 to: 978
      8 GTGAAGAAGTAGCAGCATATGAGTGATGYCYSGITnTherSAnaspa1 24
|||||..... :|||:|||..... :|||..... :|||.....
370 CAAATGTGGCGCACATCCCCAACAGCAGATGATCCACCACAACGAGATGC 419
      24 AAlAAtAgUA..L...LeuAnaIalSerBetLygUluAlaDeag 39
|||||..... :|||:|||..... :|||..... :|||.....
420 TAGAGCTACATCACTTACACTACAGCAGTCCAGCAA....GGCAAGCTTA 466
39 InlletleArgGUylySliePcdollurYtyrLeaphagInPhelisaan 55
|||||..... :|||:|||..... :|||..... :|||.....
467 CATGGGTAAATATFACAGATGCCTGTGACCTAC....CAT 501
56 LeuaNSerSaenLeudspaRgtylePhaspplis 66
|||||..... :|||:|||..... :|||..... :|||.....
502 TTGGGGTCTAGAGATCAATCAAGCAATTCtTCAGC 534
seq_name: gb_est1.AA29185
req_documentation_block:
LOCUS      AA239185      361 bp      mRNA
DEFINITION my39hd9.r1 Bacteriophage pooled organs MRLR4 Mus musculus EST
ACCESSION NC_0119921
VERSION     1.0
KEYWORDS   AB029185.1 GI:1863272
SOURCE      house mouse,
ORGANISM   Mus musculus.
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 361)
Gelsel S., Kuaba T., Lach M., Allen M., Boyles M., Dietrich N., Dubnque T.,
Schellenberg R., Stepien M., Tan F., Underwood K., Moore B.,
Theising R., Wyllie T., Lemon C., Soares B., Wilson R. and
Walerston R.
TITLE      The Mash1-HmH Mouse EST Project
JOURNAL    Unpublished (1996)
```

```

COMMENT
Contact: Marra M/Mouse EST Project
WashU-HM1 Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LINDT; contact the
IMAC Consortium (info@imac.llnl.gov) for further information.
MI:43133
Seq primer: -20m13 rev2 ET from Amersham
High quality sequence stop: 312.
FEATURES
source
1
locus 361
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAC:598273"
/clone_id="Barestead mouse pooled organs MPR84"
/sex="male"
/development="pooled organs"
/day_stage="7 day"
/lab_host="MH 08"
/molecule="mRNA"
/note="Organ: pooled; Vector: p773D-Pac (Pharmacia) with
a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer 15
bp upstream of the polylinker. The cDNA was ligated to Eco
adaptor and ligated to EcoRI sites. The cDNA was ligated
to the Not I and Eco RI sites of the modified p773 vector.
Library constructed by Bob Barestead."
BASE COUNT
95 a 105 c 90 g 91 t
ORIGIN
alignment_scores:
Quality: 67.50 Length: 72
Ratio: 1.406 Caps: 5
Percent Similarity: 66.667 Percent Identity: 38.889
alignment_block:
US-09-209-346A-9 x AA239185
Align seg 1/1 to: AA239185 from: 1 to: 381
1 ThrLeuValTTPd1G1uPheClnVAla1Gc1AysGSeAa1aRg1yG1 17
|||||
37 AAcCGGTGGGGCT..TTTACGCTTCCTGGCGCAAAAGCAGCCGCA 83
|||||
17 TcyScIn..ThrSerAspAla1a1a1aG1u1a1aLeuAsnAla1SerSe 33
|||||
84 GTGTCAAAATTGACCAACAG..GGAATGAGAGCTTACAGACCAACAGC 130
|||||
33 TlySc1uG1u1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a 49
|||||
131 CTTCACACACCTCCGCTGCGACGCAAAAGCAAGCGCCCAAAAGTCGTA 180
|||||
50 LeuPheClnPheH1s..AsnLeuAsnSerAsnLeuAsnPat1a1PheAs 65
|||||
181 GTGTTTAACTGATCATCTCCCTGCACACAGCTGAGATCTCGCTGCTCC 230
|||||
65 plyStrPhePro1u 69
|||||
231 AAGAGATGCCCA 243
seq_name: gb_gss:AZ26150
locus:
locus 466 bp DNA GSS 01-APR-2001
DEFINITION 476.d1d1h11.s1.saccharomyces castellii NRRL Y-12650 saccharomyces
castellii genomic clone 476.d1d1h11.s1. DNA sequence.
ACCESSION
AZ26150.1 GI:13497051
VERSION

```

```

KEYWORDS      CCS.
SOURCE         Saccharomyces castellii.
ORGANISM       Saccharomyces castellii
REFERENCE      Sakayota: Fungi: Ascomycota: Saccharomycotina: Saccharomycetes:
AUTHORS        1) Sakayota, T.
                2) Sakayota, T.
                3) Cliften, F. H.
                4) M. R. Materston, R. H. and Johnston, M.
TITLE          Surveying Saccharomyces genomes to identify functional elements by
                comparative DNA sequence analysis
JOURNAL        Unpublished (2001)
COMMENT        Contact: Johnston M
                Department of Genetics
                Washington University Medical School
                Box 8232 4566 Scott Ave., St. Louis, MO 63110, USA
                Tel: 314 362 2735
                Fax: 314 362 7855
                Email: mjgenetics.wustl.edu
FEATURES       Class: random plasmid subclone.
                Location/Qualifiers
                source          1..468
                /db_xref="taxon:27288"
                /strain="NRRL Y-12630 (CBS 4309)"
                /clone="476.dio4h1.s1"
                /clone_1lb="Saccharomyces castellii NRRL Y-12630"
                /note="Random genomic sequence"
BASE COUNT    131 a          94 c          76 g          167 t
ORIGIN
alignment_scores:
  Quality: 67.50          Length: 55
  Ratio: 1.875           Gaps: 2
  Percent Similarity: 65.455 Percent Identity: 30.909
alignment_block:
  US 09-289-346a-9 x AZ926150/rev ..
  Align seg 1/1 to reverse of: AZ926150 from: 1 to: 468
      8 GioValAlaGlyArgSerAlaArgIylGyGInThrSerAsnAspAl 24
         |||:::|||||:::|||||
      201 CAAATTAACCGAGCTTCGAGCTGGGTTCCTGAGAAACATTAAGATTA 152
         |||:::|||||:::|||||
      24 aAlaAlaGluAlaLeuAspAlaSerSerIylGluAlaLeuGlnIleT 41
         :::::|||||:::|||||
      151 TGTCAACGCTGCTCGAGATTACCATAGAAAGACCTACTTGAAGATAC 102
         |||:::|||||:::|||||
      41 leArgIluIysIle:::ProGluIylStyLeuPheGlnPhe 53
         ::|:::|||||:::|||||
      101 TTGAGAGTAAAGGTACAGAAAGAAATTCAGATGATATAT:::..TAC 61
         |||:::|||||
      54 HisAsnLeuAsnSer 58
         |||:::|||||
      60 CATGCATCATTCATCA 46

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```

2216 ACCTAATGATGCTCCGACAGAGCCCTTAAATGACAGTTCCAGCTGAAGCA 2167
37 lalenglnllleatgclulysllleproglulyslyrleuphaglnp 53
2166 CTTTACGATNATNAGGAGAAAGCCGACGACATTTATTTTTCAMANT 2117
54 HlIsanleuanserIsanleuasparylllephasaplysrhPro 68
2116 CATMATTTTAAATGTATTTAGATGAGATTTT.....ACACT 2078
seq_name: /cgnl_7/ptodata/1/lna/6b.COMB.seq:us-08-838-151A-48
seq_documentation_block:
: Sequence 48: Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Luu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milanow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: SOFTWARE: PC-DOS/MS-DOS
: CURRENT APPLICATION DATA: Patent Release #1.0, Version #1.30
: APPLICATION NUMBER: US/08/838.151A
: FILING DATE:
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SVS3801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5460
: INFORMATION FOR SEQ ID NO: 48:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1062 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: circular
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Bean Golden Mosaic Gemminivirus
: STRAIN: Type II
: INDIVIDUAL ISOLATE: Guatemala
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1059
: US-08-838-151A-48
alignment_scores:
: Quality: 222.00 Length: 70
: Ratio: 3.700 Gaps: 0
: Percent Similarity: 85.714 Percent Identity: 60.000
alignment_block:
US-09-289-346a-9 x US-08-838-151A-48

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17 yGsglThtserIsanleuanserIsanleuasparylllephasaplysrh 34
378 TCAGCAGCTGCGACAGCAGCTATGCGAAGCAGTAAACCGCATTTAA 427
34 yslglnlalenglnllleatgclulysllleproglulyslyrleu 50
428 TTGAATCTCTTCAATATTTTCAGAGACAGCAGCATTTACATC 477
51 PhagInPhelIsanleuanserIsanleuasparylllephasaplysrh 67
478 CTTCAACATTCACACATCTCTTAATCTCGACACGATCTCTGTCNAAGT 527
67 EPFOGLUPRO 70
528 GCCGACACCA 537
seq_name: /cgnl_7/ptodata/1/lna/6b.COMB.seq:us-08-838-151A-51
seq_documentation_block:
: Sequence 51: Application US/08838151A
: Patent No. 6291743
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Luu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milanow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: REGISTRATION NUMBER: 38,978
: FILING DATE: 05/08/838.151A
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SVS3801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5460
: INFORMATION FOR SEQ ID NO: 51:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1062 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: circular
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Bean Golden Mosaic Gemminivirus
: STRAIN: Type II
: INDIVIDUAL ISOLATE: Guatemala

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?       FEATURE:
?       NAME/KEY:   CDS
?       LOCATION:   1..1059
?       US-08-838-151A-51
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? Alignment_scores:
?     Quality: 222.00      Length: 70
?     Ratio: 3.700        Gaps: 0
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? Alignment_block:
?   US-09-289-346a-9 x US-08-838-151A-51
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? 17  YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSetL 34
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? 378 TCAGCACTGCTCGACAGACGACTCATCTGCAAGAGCGATTAACCGACAGATCA 427
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? 428 TGAATCTGCTGCAACATTCGACAGAGACCAAGCAAGATTAACGTC 477
? 51  PhcGlnPheHisAsnIleuAsnSerAsnLeuAspArgIlePheAspIuyl 67
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? 478 CTCACACATCAACACATCCGTCCTTAATCTCGACAGCGATCTTCGCAAGT 527
? 67  rProGluPro 70
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? seq_name: /cgnl_7/prodata1/1/na/9A.COMB.seq:US-08-838-151A-54
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? seq_documentation_block:
?   Sequence 54, Application US/08838151A
?   Patent No. 6291743
?   GENERAL INFORMATION:
?     APPLICANT:  SCOTL, John T
?     APPLICANT:  Lau, Heng T
?     APPLICANT:  Muesel, Douglas
?     APPLICANT:  Hanson, Steve
?     TITLE OF INVENTION:  Transgenic Plants Expressing Geminitovirus
?     TITLE OF INVENTION:  Transgenic Plants Expressing Geminitovirus
?     NUMBER OF SEQUENCES:  63
?     CORRESPONDENCE ADDRESS:
?       ADDRESSEE:  Dressler, Rodney, Milnamow & Ketz
?       STREET:  Two Presidential Plaza, Suite 4700
?       CITY:  Chicago
?       STATE:  Illinois
?       COUNTRY:  U.S.A.
?       ZIP:  60601
?     COMPUTER READABLE FORM:
?       MEDIUM TYPE:  Floppy disk
?       OPERATING SYSTEM:  PC-DOS/MS-DOS
?       SOFTWARE:  PatentIn Release #1.0, Version #1.30
?     CURRENT APPLICATION DATA:
?       APPLICATION NUMBER:  US/08/938,151A
?       FILING DATE:
?     CLASSIFICATION:  800
?     ATTORNEY/PATENT INFORMATION:
?       NAME:  PatentIn
?       REGISTRATION NUMBER:  38,978
?       REFERENCE/DOCKET NUMBER:  SYS3801P0260
?     TELECOMMUNICATION INFORMATION:
?       TELEPHONE:  312-616-5400
?       TELEFAX:  312-616-5460

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?       INFORMATION FOR SEQ ID NO: 54:
?       SEQUENCE CHARACTERISTICS:
?         LENGTH: 1062 base pairs
?         TYPE: nucleic acid
?         STRAND: single
?         ORIGIN:
?         MOLECULE TYPE: DNA (genomic)
?         RECOMBINATION: NO
?         HYPOTHETICAL: NO
?         ANTI-SENSE: NO
?         ORIGINAL SOURCE:
?           ORGANISM:  Bean Golden Mosaic Geminitovirus
?           STRAIN:  Type 11
?           TISSUE:  Leaf
?           FRAGMENT:  ISOLATE:  Guatemala
?       NAME/KEY:  CDS
?       LOCATION:  1..1059
?       US-08-838-151A-54
?
? Alignment_scores:
?     Quality: 222.00      Length: 70
?     Ratio: 3.700        Gaps: 0
?     Percent Similarity: 85.714      Percent Identity: 60.000
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? Alignment_block:
?   US-09-289-346a-9 x US-08-838-151A-54
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? Align seg 1/1 to: US-08-838-151A-54 from: 1 to: 1062
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? 17  YCysGlnThrSerAsnAspAlaAlaGluAlaLeuAsnAlaSerSetL 34
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? 378 TCAGCACTGCTCGACAGACGACTCATCTGCAAGAGCGATTAACCGACAGATCA 427
? 34  yslGluAlaLeuGlnIleIleArgGlyIuylsLeprGluIuylsTyrlu 50
?   |||.....|.....|.....|.....|.....|.....|.....|.....|
? 428 TGAATCTGCTGCAACATTCGACAGAGACCAAGCAAGATTAACGTC 477
? 51  PhcGlnPheHisAsnIleuAsnSerAsnLeuAspArgIlePheAspIuyl 67
?   |||.....|.....|.....|.....|.....|.....|.....|.....|
? 478 CTCACACATCAACACATCCGTCCTTAATCTCGACAGCGATCTTCGCAAGT 527
? 67  rProGluPro 70
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? seq_name: /cgnl_7/prodata1/1/na/9A.COMB.seq:US-08-809-103B-7
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? seq_documentation_block:
?   Sequence 57, Application US/08809103B
?   Patent No. 6133503
?   GENERAL INFORMATION:
?     APPLICANT:  GROENBERG, Bruno
?     TITLE OF INVENTION:  PHYTOPATHOGENIC DNA VIRUS RESISTANT
?     TITLE OF INVENTION:  PHYTOPATHOGENIC DNA VIRUS RESISTANT
?     NUMBER OF SEQUENCES:  17
?     CORRESPONDENCE ADDRESS:
?       ADDRESSEE:  Thompson
?       STREET:  745 South 23rd Street
?       CITY:  Arlington
?       STATE:  Virginia
?       COUNTRY:  U.S.A.
?       ZIP:  22202
?     COMPUTER READABLE FORM:
?       MEDIUM TYPE:  Floppy disk
?       OPERATING SYSTEM:  IBM PC compatible
?       SOFTWARE:  PatentIn Release #1.0, Version #1.30
?     CURRENT APPLICATION DATA:
?       APPLICATION NUMBER:  US/08/809,103B

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? FILING DATE: 17-MAR-1997
? CLASSIFICATION: 800
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: FR 94.11040
? FILING DATE: 15-SEP-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: NO PCT/FR95/01192
? FILING DATE: 15-SEP-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: PATCH, Andrew J.
? REGISTRATION NUMBER: 32,925
? REFERENCE/DOCKET NUMBER: US94AL CNR TOM
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 521-2297
? TELEFAX: (703) 685-0573
? TELEX: 248425 EMBON
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1145 base pairs
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1077
? US-08-809-103B-7

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alignment_scores:
? Quality: 222.00      length: 69
? Ratio: 3.828      gaps: 0
? Percent Similarity: 84.058      Percent Identity: 57.971

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alignment_block:
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18 sGlnTrpSerAsnAspAlaValAlaGluAlaLeuAsnAlaSerSerIysG 35
|||||
381 ACAGACGCCACCGACCTTACCGACGCAATTAACGCGAGGAATAGT 430
35 IucAlaIalaLeuGlnIleIleArgGluIysIleProGluIysTyrLeuPhe 51
|||||
431 CGCAGGCTCTTGATGATTAATTAAGCATTAACGCGCTTCAAGATTCCTA 480
52 GluPheIlaSerAsnLeuAsnSerAsnLeuAspArgIlePheAspIysThrP 68
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68 OGluPro 70
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seq_name: /cgnl_7/pdata/1/lna/FA_COMB.seq:US-08-809-103B-1
seq_documentation_block:
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? Patent No. 6133505
? GENERAL INFORMATION:
? AGENCY: GENECON, BRUS
? TITLE: PHYTOPATHOGENIC DNA VIRUS RESISTANT
? NUMBER OF SEQUENCES: 17
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: YOUNG & THOMPSON
? STREET: 745 South 23rd Street
? City: Arlington

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? STATE: Virginia
? COUNTRY: U.S.A.
? ZIP: 22202
? COMPUTER READABLE FORM:
? COMPUTER TYPE: PC-DOS/MS-DOS
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/809-103B
? FILING DATE: 17-MAR-1997
? CLASSIFICATION: 800
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: FR 94.11040
? FILING DATE: 15-SEP-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: NO PCT/FR95/01192
? FILING DATE: 15-SEP-1995
? ATTORNEY/AGENT INFORMATION:
? NAME/KEY: PATCH, Andrew J.
? REGISTRATION NUMBER: 32,925
? REFERENCE/DOCKET NUMBER: US94AL CNR TOM
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 521-2297
? TELEFAX: (703) 685-0573
? TELEX: 248425 EMBON
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1148 base pairs
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1077
? US-08-809-103B-1

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alignment_scores:
? Quality: 222.00      length: 69
? Ratio: 3.828      gaps: 0
? Percent Similarity: 84.058      Percent Identity: 57.971

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Align seq 1/1 to: US-08-809-103B-1 from: 1 to: 1148

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18 sGlnTrpSerAsnAspAlaValAlaGluAlaLeuAsnAlaSerSerIysG 35
|||||
381 ACAGACGCCACCGACCTTACCGACGCAATTAACGCGAGGAATAGT 430
35 IucAlaIalaLeuGlnIleIleArgGluIysIleProGluIysTyrLeuPhe 51
|||||
431 CGCAGGCTCTTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 480
52 GluPheIlaSerAsnLeuAsnSerAsnLeuAspArgIlePheAspIysThrP 68
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481 CATTTCATATATAATTAATTAATTAATTAATTAATTAATTAATTAATTA 530
68 OGluPro 70
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? Sequence 3, Application US/08809103B

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? Patent No. 6133505
? GENERAL INFORMATION:
? APPLICANT: GROENBORN, Bruno
? TITLE OF INVENTION: PHYTOPTHOGENIC DNA VIRUS RESISTANT
? INVENTOR: GROENBORN, Bruno
? NUMBER OF SEQUENCES: 17
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: YOUNG & THOMPSON
? STREET: 745 South 23rd Street
? CITY: Arlington
? STATE: Virginia
? COUNTRY: U.S.A.
? PUBLICATION NO.: 22202
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US-09/809-1038
? FILING DATE: 17-SEP-1995
? CLASSIFICATION: 800
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: FR 94.11040
? FILING DATE: 15-SEP-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: WO PCT/FR95/01192
? FILING DATE: 15-SEP-1995
? APPLICANT: INFORMATION:
? NAME/ PATCH
? REGISTRATION NUMBER: 32,925
? REFERENCE/DOCKET NUMBER: US94AL CNR TOM
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 521-2297
? TELEFAX: (703) 685-0573
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1150 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE: CDS
? LOCATION: 1..1077
US-08-809-1038-3

Alignment scores:
Quality: 222.00 Length: 69
Ratio: 3.828 Gaps: 0
Percent Similarity: 84.058 Percent Identity: 57.971

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381 ACAGACAGCCACAGCGCTTACCGACAGCAATTTACGCGAGAGTAGCT 430.
35 luGuaAlaLeuGlnIleIaTargUlyIlePrgGlyUlyrTyrlaPhe 51
|||||
431 CGCAGCGCTCTGATGTAATTAAGAGATTAGCGGCTPAGACATTACCTCT 480
52 GlapPheIAsnIleuAsnSerIAsnLeuAspAlaIlePheAspLystrHP 68
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? Sequence 5, Application US/088091038
? Patent No. 6133505
? GENERAL INFORMATION:
? APPLICANT: GROENBORN, Bruno
? TITLE OF INVENTION: PHYTOPTHOGENIC DNA VIRUS RESISTANT
? INVENTOR: GROENBORN, Bruno
? NUMBER OF SEQUENCES: 17
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: YOUNG & THOMPSON
? STREET: 745 South 23rd Street
? CITY: Arlington
? STATE: Virginia
? COUNTRY: U.S.A.
? PUBLICATION NO.: 22202
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US-08/809-1038
? FILING DATE: 17-MAR-1997
? CLASSIFICATION: 800
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: FR 94.11040
? FILING DATE: 15-SEP-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: WO PCT/FR95/01192
? FILING DATE: 15-SEP-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: PATCH, Andrew J.
? REGISTRATION NUMBER: 32,925
? REFERENCE/DOCKET NUMBER: US94AL CNR TOM
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 521-2297
? TELEFAX: 248425 EMBOW
? INFORMATION FOR SEQ ID NO: 5:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1150 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE: CDS
? LOCATION: 1..1077
US-08-809-1038-5

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Quality: 222.00 Length: 69
Ratio: 3.828 Gaps: 0
Percent Similarity: 84.058 Percent Identity: 57.971

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39 |-----|-----|-----|-----|-----|-----|
431 InClAlaLenGlnttAlaArgBlgUslsPheColUsPtyLeuPhe 51
42 |-----|-----|-----|-----|-----|-----|
431 CGCAGCCCTGTGATGATATTATAAAGATTACCACCTGAGNATATTACCTTCCA 480
44 |-----|-----|-----|-----|-----|-----|
52 GlnPheHisAsnLeuIenAserAsnLeuAspAlaPheAspLysThrPr 68
481 CATTTCATCATTAATAATTAATGATATTATTAATTAACGCTTTTCACAGGTCCTCC 530
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531 GCACACT 537

seq.name.: /cgn_7/prodataca/1/lna/6B.COMB.seq.us-08-838-151A-43
seq.documentation_block:
seq.id.: 43
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seq.genbank.accession.no.: F030000000
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Lou, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
APPLICANT: Hanson, Steven
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milwaukee & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
ZIP: 60601
S.A.: S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 05/08/83B,151A
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0Z60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-4500
TELEFAX: 312-616-1640
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1183 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: circular
MOLWT TYPE: kbp (genomic)
HYPERIDENTICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean golden Mosaic Geminivirus
STRAIN: Type II Isolates
INDIVIDUAL ISOLATE: Guatemala
FEATURE KEY: CMS
LOCATION: IL 1059
INFORMATION:
AUTHORS: Paria, JC
AUTHORS: Gilbertson, RL
AUTHORS: Hanson, SP

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1 AUTHOES: Morales, F
2 AUTHOES: Ahlquist, PJ
3 AUTHOES: Lontieio, AO
4 AUTHOES: Maxwell, D
5 TITLE: Isen solidan Mesic Gemiliviruse Type II
6 TITLE: Isen solidan Mesic Gemiliviruse Type II
7 TITLE: Isen solidan Mesic Gemiliviruse Type II
8 TITLE: Pseudorecombinants, and Phylogenetic Relationships
9 JOURNAL: Phycopathology
10 VOLUME: 84
11 ISSUE: 3
12 PAGES: 321-329
13 DATE: 1994
14 US-08-838-151A-43
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16 alignment_scores:
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18     Ratio: 3.700        Gaps: 0
19     Percent Similarity: 85.714    Percent Identity: 60.000
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24 Align seq 1/1 to: US-08-838-151A-43 from: 1 to: 1183
25
26 1   ThruValvTrrGlyUphechInvalAdyATgSerAlaArgylcL 17
27     |||||.....|.....|.....|.....|.....|.....|
28 328 ACACATCAATCGAGGGGCACATTCACACGTCCACGCCACATC 377
29     |||||.....|.....|.....|.....|.....|.....|
30 17   ycySlnPTrGrSerAspRAlAlAlAcIAlAlaAmnAlasrScst 34
31     | .....|.....|.....|.....|.....|.....|
32 378 TCAGCATCTGTCGACAGCGATTCGTAACGACATTAACGCAATCA 427
33
34 yscJGluAlaHengInlleleArglyLusyleProGlyUysTryeu 50
35     |||||.....|.....|.....|.....|.....|.....|
36 428 TrGhInPhetGtGtGtCACATTCACACAGAACACACACACATAC 477
37
38 51   ProGInPhetGtGtGtCACATTCACACAGAACACACACATAC 67
39     |||||.....|.....|.....|.....|.....|.....|
40 478 CTTCACATCAATCGAGGGGCACATTCACACGTCCACGCCACAT 527
41
42 67 ProGluPro 70
43     |||||.....|.....|.....|.....|.....|.....|
44 528 GCGGACACCA 537
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46 seq_name : /cpnl_7/prodata/1/Lna/GB_COMB.seq;US-08-838-151A-45
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48 seq_documentation_block:
49     ? Sequence 45, Application US/08838151A
50     ? Patent No. 6291743
51     ? GENERAL INFORMATION: John T
52     ? APPLICANT: Luo, Hong T
53     ? APPLICANT: Maxwell, Douglas
54     ? APPLICANT: Ahlquist, Paul
55     ? APPLICANT: Hanson, Steve
56     ? TITLE OF INVENTION: Transgenic Plants Expressing GeminiViruses
57     ? INVENTOR ADDRESS: Genes
58     ? CORRESPONDENCE ADDRESS: 63
59     ? ADDRESS: Dressler, Rocky, Milinow & Katz
60     ? STREET: Two Prudential Plaza, Suite 4700
61     ? CITY: Chicago
62     ? STATE: Illinois
63     ? COUNTRY: U.S.A.
64
65 ZIP: 60601
66
67 COMPUTER READABLE FORM: disk
68 COMPUTER: IBM PC compatible
69 OPERATING SYSTEM: PC-DOS/MS-DOS
70 SOFTWARE: Plentlin Release 11.0, Version #1.30
71 CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/838,151A
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Mueller, Lisa V
 ADDRESS: 38, 978
 REFERENCE/DOCKET NUMBER: SVS801P0260
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1183 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHEetical: NO
 ANTI-SENSE: NO
 ORIGIN: bean Golden Mosaic GeminiVirus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1059
 US-08-838-151A-45

alignment_scores:

Quality: 222.00 Length: 70
 Ratio: 3.700 Gaps: 0
 Percent Similarity: 85.714 Percent Identity: 60.000

alignment_block:

US-09-289-346A-9 x US-08-838-151A-45

Align seg 1/1 to: US-08-838-151A-45 from: 1 to: 1183

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1  ThrLeuValTTPGlyGUphedIvalAlaGlyATGserAlaAatGlyGI 17
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17  YCysGlnThrSerAsnAspAlaAlaAGluAlaLeuAsnAlaSerSerI 34
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
378 TCAGCATCTGCACACGATCTGCATTCGCAAGCGATTTAAACCCATTC 427
34  YsGLGluAlaLeuGlnAlaIleArgGluGlyslLeProGluGlyTyrLeu 50
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
428 TTGAATCTCCCTTCACAAATTTGAGAGAAACACCGAAGATTAAGTC 477
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspGly 67
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
478 CTTCACATCAACAAATCGCTTCAATCTGAAAGGATTTCTCTCAAGT 527
67  rProGluPro 70
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528 GCCGCAACCA 537
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seq_name: /cgnl_7/prodata/1/lna/6A.COMB.seq:US-09-065-999-5
 seq_documentation_block:
 : Sequence 5, Application US/09065999
 : Patent No. 6118048
 : GENERAL INFORMATION:
 : APPLICANT: Hanson, Stephen F.
 : APPLICANT: Maxwell, Douglas P.
 : TITLE OF INVENTION: SEQUENCING AND CLONING INITIATION OF GEMINIVIRAL
 : NUMBER OF SEQUENCES: 8
 : CORRESPONDENCE ADDRESS: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
 : ADDRESSEE: Charles & Brady
 : STREET: One South Plackney Street

CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/065,999
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: SEAY, NICHOLAS J
 REGISTRATION NUMBER: 27,386
 REFERENCE/DOCKET NUMBER: 960296, 94754
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-251-5000
 TELEFAX: 608-251-9166
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1055 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-065-999-5

alignment_scores:

Quality: 222.00 Length: 70
 Ratio: 3.700 Gaps: 0
 Percent Similarity: 85.714 Percent Identity: 60.000

alignment_block:

US-09-289-346A-9 x US-09-065-999-5

Align seg 1/1 to: US-09-065-999-5 from: 1 to: 1651

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796 ACAATCATGATGGGACAAATTCACAGTCGCGAGCATCTGCAGAGAGG 845
17  YCysGlnThrSerAsnAspAlaAlaAGluAlaLeuAsnAlaSerSerI 34
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
846 TCAGCATCTGCACACGATCTGCATTCGCAAGCGATTTAAACCCATTC 895
34  YsGLGluAlaLeuGlnAlaIleArgGluGlyslLeProGluGlyTyrLeu 50
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
896 TTGAATCTCCCTTCACAAATTTGAGAGAAACACCGAAGATTAAGTC 945
51  PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspGly 67
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
946 CTTCACATCAACAAATCGCTTCAATCTGAAAGGATTTCTCTCAAGT 995
67  rProGluPro 70
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996 GCCGCAACCA 1005
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seq_name: /cgnl_7/prodata/1/lna/6A.COMB.seq:US-09-065-999-6
 seq_documentation_block:
 : Sequence 6, Application US/09065999
 : Patent No. 6118048
 : GENERAL INFORMATION:
 : APPLICANT: Hanson, Stephen F.
 : APPLICANT: Maxwell, Douglas P.
 : TITLE OF INVENTION: SEQUENCING AND CLONING INITIATION OF GEMINIVIRAL
 : NUMBER OF SEQUENCES: 8
 : CORRESPONDENCE ADDRESS: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
 : ADDRESSEE: Charles & Brady

STREET: One South Plinckney Street
 City: Madison
 STATE: WI
 ZIP: 53703-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patentln Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 05/09/065.999
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27,386
 REFERENCE/DOCKET NUMBER: 960296.94754
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-251-5000
 TELEFAX: 608-251-9166
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1651 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 ORIENTATION: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-065-999-6

alignment_scores:
 Quality: 222.00 Length: 70
 Ratio: 3.700 Gaps: 0
 Percent Similarity: 85.714 Percent Identity: 60.000

alignment_block:

US-09-289-346A-9 x US-09-065-999-6

Align seq 1/1 to: US-09-065-999-6 from: 1 to: 1651

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1 ThleuvalTTPGCljyGlphecllnvalAlaglyarSerAlaArGlyG1 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
796 ACATTCGAATGGGACATTCGACATTCGACGACGACATTCGACGAGG 845
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 yCysGlnThSerAsnAspAlaAlaIaIaIaIaIaIaIaIaIaIaIa 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
846 TCACGACTCTCCGACGACATTCATTCGAAGCGATTAACCGAGATTC 895
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 ySGLcIuAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
896 TTGATCTCTGCTTGAAGGAAAGAACACCGAAGCATTCGCTC 945
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 PheGlnPheIIsAsnIeuAsnSerAsnLeuAspArgIaIaIaIaIaIa 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
946 CTTCAACATCAACAACATCGCTCTTAATCTCGAACGCGATTCGCAAG 995
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67 ProGluPro 70
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996 GCCGGAACCA 1005
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seq_name: /cgnl_7/prodata/1/lna/6A.COMB.seq:US-09-065-999-8

seq_documentation_block:

Sequence 6, Application US/09065999
 Patent No. 6118048
 GENERAL INFORMATION:
 APPLICANT: Hanson, Stephen F.
 APPLICANT: Maxwell, Douglas P.
 TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
 TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:

ADDRESSER: Charles & Brady
 STREET: One South Plinckney Street
 City: Madison
 STATE: WI
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patentln Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 05/09/065.999
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27,386
 REFERENCE/DOCKET NUMBER: 960296.94754
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-251-5000
 TELEFAX: 608-251-9166
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1894 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 ORIENTATION: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-065-999-8

alignment_scores:
 Quality: 222.00 Length: 70
 Ratio: 3.700 Gaps: 0
 Percent Similarity: 85.714 Percent Identity: 60.000

alignment_block:

US-09-289-346A-9 x US-09-065-999-8

Align seq 1/1 to: US-09-065-999-8 from: 1 to: 1894

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1 ThleuvalTTPGCljyGlphecllnvalAlaglyarSerAlaArGlyG1 17
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796 ACATTCGAATGGGACATTCGACATTCGACGACGACATTCGACGAGG 845
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 yCysGlnThSerAsnAspAlaAlaIaIaIaIaIaIaIaIaIaIaIa 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
846 TCACGACTCTCCGACGACATTCATTCGAAGCGATTAACCGAGATTC 895
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 ySGLcIuAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
896 TTGATCTCTGCTTGAAGGAAAGAACACCGAAGCATTCGCTC 945
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 PheGlnPheIIsAsnIeuAsnSerAsnLeuAspArgIaIaIaIaIaIa 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
946 CTTCAACATCAACAACATCGCTCTTAATCTCGAACGCGATTCGCAAG 995
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 ProGluPro 70
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996 GCCGGAACCA 1005
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seq_name: /cgnl_7/prodata/1/lna/6A.COMB.seq:US-09-065-999-7

seq_documentation_block:

Sequence 7, Application US/09065999
 Patent No. 6118048
 GENERAL INFORMATION:
 APPLICANT: Hanson, Stephen F.
 APPLICANT: Maxwell, Douglas P.
 TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
 TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: One South Pluckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 05/09/065.999
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27,386
 REFERENCE/DOCKET NUMBER: 950296.94754
 TELEPHONE: 608-251-9150
 TELEFAX: 608-251-9166
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2072 base pairs
 TYPE: nucleic acid
 STRANDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-065-999-7

Alignment_scores:
 Quality: 222.00 Length: 70
 Ratio: 3.700 Gaps: 0
 Percent Similarity: 85.714 Percent Identity: 60.000

Alignment_block:
 US-09-289-346a-9 x US-09-065-999-7 ..

Align seq 1/1 to: US-09-065-999-7 from: 1 to: 2072
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 796 ACAATGATGGGGAATTCGACATTCGACGACATTCGACAGAGAG 845
 17 YCysGlnTrSerAspAlaAlaGluAlaLeuAlaSerSerI 34
 846 TCAGCATCTCGACACGATCATATCAAGCGATTAAACCGATTAA 895
 34 YSGLuGluAlaLeuGlnIleIleArgGluLysIleProGluLysTrpLeu 50
 896 TTGAATCTCCCTTCACATATTAAGAGAGACACAGAAAGATTAC 945
 51 PhcGlnPhcHisAsnLeuAsnSerAsnLeuAsnArgIlePheAspLysTrp 67
 946 CTTCACATCATCAACATCATCTTCATTCATTCGACGATCTTCGCAAGT 995
 67 PProGluPro 70
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seq_name: /cgnl_7/prodata1/lna/6A_Comb.seq:US-08-838-151A-1
 seq_documentation_block:
 : Sequence 1, Application US/08838151A
 : Patent No. 6291743
 : Applicant: INVERAX INC.
 : APPLICANT: Stout, John T
 : APPLICANT: Linn, Bang T
 : APPLICANT: Maxwell, Douglas
 : APPLICANT: Ahlquist, Paul

APPLICANT: Hanson, Steve
 TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
 TITLE OF INVENTION: Genes
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ruckey, Milamov & Katz
 STREET: 100 Prudential Plaza, Suite 4700
 CITY: Chicago
 STATE: Illinois
 COUNTRY: U.S.A.
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838.151A
 FILING DATE:
 CLASSIFICATION: B00
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, Steve
 REGISTRATION NUMBER: 38,978
 REFERENCE/DOCKET NUMBER: SVS3801P0260
 TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2072 base pairs
 TYPE: nucleic acid
 STRANDNESS: single
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 ORIGIN: SOURCE:
 ORGANISM: Mottie Gemini Virus
 INDIVIDUAL ISOLATE: Florida
 FEATURE:
 NAME/REV: CDS
 LOCATION: 44..1127
 PUBLICATION INFORMATION:
 AUTHORS: Gilbertson, RL
 AUTHORS: Hildyell, SH
 AUTHORS: Johnson, RJ
 AUTHORS: Rojals, MR
 AUTHORS: Hou, YM
 AUTHORS: Maxwell, DP
 TITLE: Pseudorecombination between the infectious
 TITLE: cloned DNA components of tomo mottle and bean
 TITLE: dwarf mosaic geminiviruses.
 JOURNAL: Jour. General Virol.
 VOLUME: 7
 PAGES: 21-31
 DATE: 1993
 US-08-838-151A-1

Alignment_scores:
 Quality: 220.00 Length: 70
 Ratio: 3.657 Gaps: 0
 Percent Similarity: 85.714 Percent Identity: 57.143

Alignment_block:
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 371 ACAATGATGGGGAATTCGACATTCGACGACATTCGACAGAGAG 420


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34 ysglunlualaleuglnlalleaarglulyslleproglulyslyrleu 50
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2171 AAGGAGAGAGCCCTCCAGATTAATTAAGAGGAAATCCCGAAGAAATTTTA 2122
|||||PhageInPheliasenleuanserfaleuansgafylephaeaplyrth 67
51 |||||||TTTCAGTTTCACATCTAAATGATTTTAAGATTTGATGAGAC 2072
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67 rProgluPro 70
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2071 TCCCGAGGCC 2062
seq_name: gb_v1:AY029750

seq_documentation_block:
LOCUS AY029750 2588 bp DNA circular VRL 08-MAY-2001
DEFINITION Tomato severe rugose virus DNA-A, complete sequence.
ACCESSION AY029750
VERSION AY029750.1 GI:14009278
KEYWORDS
SOURCE
ORGANISM
Tomato severe rugose virus.
Tomato severe rugose virus.
Viruses: ssDNA. Virusses: Gemnivalitidae: Begomovirus.
REFERENCE
1 (bases 1 to 2588)
Rezeinde,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
The full-length DNA-A nucleotide sequence of a novel
Tomato-infecting begomovirus, Tomato severe rugose virus, in Brazil
JOURNAL
1 (bases 1 to 2588)
Rezeinde,W.L., Goulart,L.R., Parreira,K.S. and Figueiredo,J.E.F.
Direct Submission
Submitted (03-APR-2001) Instituto de Genetica e Bioquimica,
Universidade Federal de Uberlandia, Av. Amazonas s/n, Bloco 2E,
Sala 24, Campus Umuarama, Uberlandia, Minas Gerais 38.400-000,
Brazil
FEATURES
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/db_xref="taxon:158463"
/country="Brazil"
/protein_coding=DNA-A"
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34 ysglunlualaleuglnlalleaarglulyslleproglulyslyrleu 50
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51 |||||||TTTCAGTTTCACATCTAAATGATTTTAAGATTTGATGAGAC 2072
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67 rProgluPro 70
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2071 TCCCGAGGCC 2062
seq_name: gb_v1:AY029750

seq_documentation_block:
LOCUS AY029750 2622 bp DNA circular VRL 25-SEP-2000
DEFINITION Tomato severe mosaic virus DNA-A, complete sequence.
ACCESSION AY029750
VERSION AY029750.1 GI:10201644

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JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1193)
 AUTHORS Parla, J.C. and Maxwell, D.P.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAR-1997) Plant Pathology, University of Wisconsin,
 1630 Linden Dr., Madison, WI 53706-1598, USA
 FEATURES
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 /db_xref="taxon:58177"
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 gene complement(1..678)
 CDS complement(1..678)
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 /product="rep protein"
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 /db_xref="GI:1183135"
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 SYVKGQDTVEGPEFQVDDRSRSGQOTVDAAEALPAAPKRTALQITIKKIKPEYL
 FQFHNLNSNLDRIFAKAPPPVPPPLSFTVWDENQEMADRYGHSARLRPPMS
 LIVEGSSR
 YCSMKPNS"

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 676..797
 1105
 /note="1105"
 gene /gene="cp"
 1039..21193
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 YCSMKPNS"
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alignment_scores:
 Quality: 281.00 Length: 70
 Ratio: 4.607 Gaps: 0
 Percent Similarity: 87.143 Percent Identity: 77.143

alignment_block:
 US-09-289-346a-10 x LM092532/rev ...

Align seg 1/1 to reverse of: LM092532 from: 1 to: 1193

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 348 ACAGTTGATGCGCTGATTCACAGTGCAGGAGAGATCTCTAGAGAGG 299
 |||:|||||
 17 TCGSGCTInThSerAsnAppLeuLeuGlnAlaLeuAsnAlaSerSerL 34
 |||:|||||
 298 CCAACGACAGTAAATGACGTCGACGTCAGGCTTAATGCTCCAGTA 249
 |||:|||||
 34 TSGGUGUAlaLeuGlnIle1e1eArgGluLysIleProGluLysTleu 50
 |||:|||||
 248 AACGAAACGCGCTCTCAAAATATTAAGACAAATATCCGCGAAGATATCTT 199
 |||:|||||
 51 PheGluPheIleAlaLeuAsnSerTrsIleuAsnArgGluIleAspLysTh 67
 |||:|||||
 198 TTTCATTTCAATTAATTAACTCAATTGATGGAATAAATTTTGCAAGGC 149
 |||:|||||
 67 PProGluPro 70
 |||:|||||
 148 YTCGAGAGCA 139
 |||:|||||
 seq_name: gb_v1:AF131071

seq_documentation_block:
 LOCUS AF131071 1345 bp DNA VR1 17-JUN-1999
 DEFINITION Tomato mild mottle geminivirus segment A replication-associated
 protein (rep) and coat protein (cp) genes, partial cds.
 ACCESSION AF131071.1
 VERSION AF131071.1 GI:4928223
 KEYWORDS
 SOURCE
 ORGANISM
 tomato mild mottle geminivirus.
 Viruses: ssDNA viruses; Geminiviridae: Unclassified Geminiviridae.
 1 (bases 1 to 1345)
 AUTHORS Parla, J.C., Maxwell, D.P., Remiez, P., Karkashian, J.P., Doyle, M.M. and
 Maxwell, D.P.
 TITLE
 Molecular characterization and DNA-based detection methods for
 vegetable-infecting geminiviruses in Central America
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1345)
 AUTHORS Nakha, M.K., Welland, G., Kamel, S. and Maxwell, D.P.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAR-1999) Plant Pathology, University of
 Wisconsin-Madison, 1630 Linden Dr., Madison, WI 53706-1598, USA
 FEATURES
 source 1..1345
 /organism="Tomato mild mottle geminivirus"
 /isolate="HN96-H5Kv"
 /specimen_voucher="HS"
 /db_xref="taxon:32443"
 /gene="cp"
 /clone="pRIN55Kv"
 /country="Honduras: Comayagua Valley"
 /note="Obtained from a tomato plant collected in Dec. 1996
 by M.K. Nakha and D.P. Maxwell"
 complement(1..678)
 gene /gene="rep"
 1001..21145
 /note="cp"
 /codon_start=1
 /product="rep protein"
 /protein_id="AA053371.1"
 /translation="MKRQPSMRPWQTSKISRTSNFSPGQIGPKPKNSENVKPK
 YCSMKPNS"

BASE COUNT 329 a 289 c 313 g 414 t
 ORIGIN

alignment_scores:
 Quality: 281.00 Length: 70
 Ratio: 4.391 Gaps: 0
 Percent Similarity: 91.429 Percent Identity: 72.857
 alignment_block:
 US-09-289-346a-10 x LM092532/rev ...


```

CDS      complement(815..1072)
         /gene="AC4"
         /note="AL4"
         /codon_start=1
         /product="AC4"
         /protein_id="AB01007.1"
         /translation="MGRITSMCKVCSKANSNOIADSSISHRDTRFFTPFSRELAP
         APMSPSTIRFCIPRQVNSPADLLEAFASRLTTPORGL"

BASE COUNT      359 a      296 c      327 g      401 t

ORIGIN

Alignment scores:
  Quality: 277.00      Length: 68
  Ratio: 4.617      Gaps: 0
  Percent Similarity: 88.235      Percent Identity: 79.412

alignment_block:
us-09-289-346a-10 x AF288227 rev ..

Align seq 1/1 to reverse of: AF288227 from: 1 to: 1383

1  ThleValtTgGtYglUpheGtNValAspAlaYgSerAlaAsgYlgi 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
902 ACCATCACCTGGGGGTATTCAGAGTCGACGACAGATCTGTCAGACAG 853
   17 YGSGlntHSeTasNasHapLeuLeuGluAlaLeuAsnAlaSerS 34
   852 CGAGAGAGTGTATGAGAGCCGACGAGAGGCTGTACAGAGGTGTA 803
   34 YSGlGluAlaLeuGlnIle1eAsgYlGtYstPrcGtYlGtYrLeu 50
   ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||
802 AAGAGAGCTGGCTTCGAATATACAGAGAGAACTCCCTGAAAAATATTA 753
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
752 TTTCATTTCATTAATTAGTAGTAATTTAGATAGATTTTCTCAGC 703
   51 PhcGlNpHhLlAsnIlePnAsnSerLlGlnLlGAspAgtlPheAspYstH 67
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 rPro 68
   |||
702 ACCT 699

seq_name: gb_vl:AF104036

seq_documentation_block:
LOCUS      AF104036      2828 bp      DNA      circular      VR1      05-AUG-1999
DEFINITION Sweet potato leaf curl virus DNA A, complete sequence.
ACCESSION      AF104036
VERSION      AF104036.1      GI:5702158
KEYWORDS
  SWEET POTATO LEAF CURL VIRUS
ORGNISM
  Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE
  1 (bases 1 to 2828)
  Lotrakul,P., Valverde,R.A., Clark,C.A., Sim,J. and De La Torre,R.
  Detection of a geminivirus infecting sweet potato in the United
  States. Dis. 82, 1253-1257 (1998)
REFERENCE
  2 (bases 1 to 2828)
  Lotrakul,P. and Valverde,R.A.
  Cloning of a DNA-A-like genomic component of sweet potato leaf curl
  virus : nucleotide sequence and phylogenetic relationships
  Molecular Plant Pathology On-line (1999)
  http://www.bspp.org.uk/mpvol/1999/0422lotrakul/
REMARK
  3 (bases 1 to 2828)
  Lotrakul,P. and Valverde,R.A.
  Detection of a geminivirus infecting sweet potato in the United
  States. Dis. 82, 1253-1257 (1998)
JOURNAL
  Submitted (02-NOV-1998) Plant Pathology and Crop Physiology,
  Louisiana State University, 302 Life Sciences Bldg., LSU, Baton
  Rouge, LA 70803, USA
FEATURES
  source
    1..2828
    Location/Qualifiers

```

```

gene
CDS      /organism="sweet potato leaf curl virus"
         /db_xref="taxon:100755"
         /chromosome="DNA A"
         /country="USA"
         /gene="AV2"
         132..476
         /gene="AV1"
         301..1065
         /gene="AV1"
         301..1065
         /gene="AV1"
         /note="AV1"
         /product="coat protein AV1"
         /protein_id="AB017170.1"
         /db_xref="GI:5702160"
         /translation="MTCGRARSPRRHYGGRPRRLNFEATIVPTGNAPVIAKSY
         VVSRGVNKRKRHRDRILPKCGVGPKVQVYEPKMDVPHDTQVCSDFPRTGTLNHL
         GRKRVKSNGLDKVWMDNNKARQHNITLWLLIDRRNRKDPFLNPLTPYDNEP
         NQNNKRLKSAKSNKQVLSKQVTSKSNKLLKFLKGLINHTYTNKLEAKTE
         complement(1081..1515)
         /gene="AC3"
         complement(1081..1515)
         /gene="AC3"
         complement(1081..1515)
         /note="AC3"
         /codon_start=1
         /product="coat protein AC3"
         /protein_id="AB017171.1"
         /db_xref="GI:5702161"
         /translation="MDSRTGSGTISHAQTTRAVEFDTPNPSVGTAPFLRLMYHST
         OGRTILKFOLRVNVERRRDLQFRTFLQRTLLTTLTCAIHSMTGLIERLKRNICEL
         ANLQFSLVNLVETVRYLIRVCSMIDELDQVDDVAVLY"
         complement(1232..1678)
         /gene="AC2"
         complement(1232..1678)
         /note="AC2"
         /codon_start=1
         /product="transactivator protein AC2"
         /protein_id="AB017172.1"
         /db_xref="GI:5702163"
         /translation="MAPPARKLOAKVETTPYPCSLSKEDCLAQLLNIGTPSNKKYI
         HVARELHDEDFPLVAVPGQFCVPCNSPFDLVSPNRSNHFHPNIGQASSSVYS
         QNHMLSLNLTGSPVSNVSSPSSSSWVPLSLMARNWASDARDELSL
         AKQMSKYSKPYKIGKIPGTLINPGEGSSPYMLDNKEGALKNMAYTNMLIC
         DQSPVQVEESRSGATNGEQQEES"
         complement(2267..2524)
         /gene="AC4"
         complement(2267..2524)

```


[illegible][illegible]

```

alignment_scores:      235.00      Length:      85
                        Quality:      3.852
Percent Similarity: 71.765      Percent Identity: 54.118

alignment_block:
us-09-289-346a-10 x AA084372 ..

Align seg 1/1 to: AA084371 from: 1 to: 434

1 ThrleuValTrpGlygluPheGluValAspIValArgSerAlaIaArgIYcI 17
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
95 ACCCTGATGCGGACAGCTTCACATGATGACATGACATGACATGACAGGG 144

17 yCysGlnThrSerAsnAspLeuIleuGluAlaIleuAsnAlaSerSert 34
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
145 AACACATACGCCAAGACGCTTACGCCACCGCTTACACCTGACATCA 194

34 ysgIuGlAlaIeuGlnIleIleArgIuYsIleProGluYrIeu 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
195 AGTCACAGGCTTACAGCTTCCTTAGGAAATACCCCTTAAGGATTTGTC 244

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
245 TTACATTTCATATTTAATTAATAGATATTAAGATAGATTTTACACCTCC 294

64 ..... PheAspIyS7HP 68
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
295 GTTGAGAGTTATGTTTCCTTTTATCTCTTTTATCTCTTTTATCTGACATTC 344

68 PGLu 69
|||||
345 CAGAA 346

seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT:AA084372
seq_documentation_block:
ID AA084372 standard: DNA: 479 BP.

AA084372:
19-AUG-1995 (first entry)

Gemini1 virus-specific polyribozyme-F target sequence.
DE
XX ribozyme target sequence: polyribozyme-F:
KM tomato leaf curl virus: RNA cleavage: tomato transgenic plant:
XX virus disease resistance: ss.
OS
XX Tomato leaf curl virus.

Key
PH Location/Qualifiers
PT misc_feature 46..96
  /tag= "a"
  /note= "ribozyme R4-R5 target sequence"
PT misc_feature 97..160
  /tag= "b"
  /note= "ribozyme R4 cleavage site"
PT misc_feature 81..83
  /tag= "c"
  /note= "ribozyme R5 cleavage site"
PT misc_feature 356..386
  /tag= "d"
  /note= "ribozyme R2 target sequence"
PT misc_feature 370..4372
  /tag= "c"
  /note= "ribozyme R2 cleavage site"
PT misc_feature 429..459
  /tag= "e"
  /note= "ribozyme R3 target sequence"
PT misc_feature 442..444

```

```

PT /tag= "d"
XX /note= "ribozyme R3 cleavage site"
XX W05503404-A.
XX
XX
PD 02-FEB-1995.
XX
XX 22-JUL-1993: 93WO-EP01946.
XX
XX 22-JUL-1993: 93AO-0047014.
XX
XX 22-JUL-1993: 93WO-EP01946.
XX
XX (BIOC-) BIOCEM SA.
XX (CSTR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Baudino S, Comeau D, Dry IB, Gruber V, Lemee P;
XX Mason J, Rezakan MA, Rytgen JE, Rezakan MA;
XX WPI: 1995-075232/10.
XX
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX and/or assembly of viruses by cleaving target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX
XX Example 10: Fig 11c: 90pp: English.
XX
XX The sequence is a tomato leaf curl virus target sequence for
XX polyribozyme, which hybridized to and cleaved the target
XX polyribozymes. The ribozyme may be expressed in a transgenic plant,
XX e.g. tomato, to confer virus disease resistance.
XX
XX Sequence 479 BP: 145 A: 95 C: 97 G: 142 T: 0 other:
50

alignment_scores:      235.00      Length:      85
                        Ratio:      3.852
Percent Similarity: 71.765      Percent Identity: 54.118

alignment_block:
us-09-289-346a-10 x AA084372 ..

Align seg 1/1 to: AA084372 from: 1 to: 479

1 ThrleuValTrpGlygluPheGluValAspIValArgSerAlaIaArgIYcI 17
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
140 ACCCTGATGCGGACAGCTTCACATGATGACATGACATGACATGACAGGG 189

17 yCysGlnThrSerAsnAspLeuIleuGluAlaIleuAsnAlaSerSert 34
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
190 AACACATACGCCAAGACGCTTACGCCACCGCTTACACCTGACATCA 239

34 ysgIuGlAlaIeuGlnIleIleArgIuYsIleProGluYrIeu 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
240 AGTCACAGGCTTACAGCTTCCTTAGGAAATACCCCTTAAGGATTTGTC 289

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIle..... 63
| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
290 TTACATTTCATATTTAATTAATAGATATTAAGATATTTTACACCTCC 339

64 ..... PheAspIyS7HP 68
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
340 GTTGAGAGTTATGTTTCCTTTTATCTCTTTTATCTCTTTTATCTGACATTC 389

68 PGLu 69
|||||
390 CAGAA 394

seq_name: /cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT:AA084375
seq_documentation_block:
ID AA084375 standard: DNA: 550 BP.

```



```

XX AC AA084375;
XX 19-AUG-1995 (first entry)
XX Tomato leaf curl virus Australian strain DNA sequence.
XX Tomato leaf curl virus; Australia strain; plant disease; ds.
XX Tomato leaf curl virus (Australia).
XX W09503404-A.
XX 02-FEB-1995.
XX 22-JUL-1993; 93MO-EP01946.
XX 22-JUL-1993; 93AU-0047014.
XX 22-JUL-1993; 93MO-EP01946.
XX (BIOCEN) BIOCEN SA.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX Baudino S., Rezaian D., Dry IB, Grubor V., Lence P.
XX Mason J., Rezaian MA, Riden JE, Rezaian MA:
XX WPI: 1995-07532/10.
XX Synthetic DNA virus ribozyme(s) - reduce replication, infection
XX and/or assembly of viruses by cleaving target virus sequence,
XX useful for preparing resistant plants, esp tomatoes.
XX Disclosure: Fig 1; 90pp; English.
XX The sequence represents the complementary sense DNA strand of an
XX Australian strain of tomato leaf curl virus. Ribozyme(s)
XX for this sequence may be used in generation of transgenic plants
XX with disease-resistance.
XX Sequence 550 BP; 148 A; 120 C; 134 G; 142 T; 6 other;
XX
XX alignment_scores:
XX Quality: 234.50 Length: 86
XX Ratio: 3.844 Gaps: 1
XX Percent Similarity: 70.930 Percent Identity: 53.488
XX
XX alignment_block:
XX US-09-289-346a-10 x AA084375 ..
XX
XX Align seg 1/1 to: AA084375 from: 1 to: 550
XX
XX 1 ThrleuValTPrGlygluPheGlnValAspGlyAAserAlaArgGlyGI 17
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 201 ACCCTGCAATGGGAGATTTCAGATGATGAGACATCTGCAGAGGGG 250
XX 17 yCysGlnThrSerAsnAspLeuLeuGlnAlaLeuAsnAlaSerL 34
XX 251 ACACATACAGCAATACGCTTACGCGCAGCCCTTACACATGCAAG 300
XX 34 yGlnGlnAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeu 50
XX ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 301 AGTCAGAGCGCTTAAACGCTCTTAGGGAATACCCCTTAAGGATTTAT 350
XX 51 PheGlnPheHisAsnLeuAsnSerAsnLeuAsnAspArglle..... 63
XX ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 351 TTTCAATTTCAATATATATATATATATATATATATATATATATAT 400
XX 64 ..... PheAspLysT 67
XX 401 TCCGTTGAGAGTTATATCTTCCTTTTATCTCTTCCTTTGATCAAG 450
XX 67 hrProGlu 69

```

```

seq_name: /cgnl_8/gcdate/geneseq/geneseq/NA1997.DAT:AAU93317
451 TTCAGAAA 458
:|||||
seq_documentation_block:
ID: AAU93317 standard; DNA: 2744 BP.
AC AAU93317;
XX 27-APR-1998 (first entry)
XX Tomato leaf curl virus from Southern India (stem-loop begin).
XX Geminivirus; TLGV-IND; AC1 gene; transdominant mutation;
XX transgenic plant; disease resistance; ss; cyclic; circular.
XX Tomato leaf curl virus from Southern India.
XX W09739110-A1.
XX 23-OCT-1997.
XX 15-APR-1997; 97MO-US06300.
XX 16-APR-1996; 96US-0015517.
XX (SPIN-) SEMINIS VEGETABLE SEEDS INC.
XX (MISC) WISCONSIN ALUMNI RES POUND.
XX Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT;
XX WPI: 1997-526447/48.
XX Transgenic plants expressing geminivirus AC1 and CI wild-type and
XX CI wild-type and CI wild-type and CI wild-type and CI wild-type
XX e.g tomato mottle virus tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX Disclosure: Page 119-121; 132pp; English.
XX
XX This genomic DNA sequence comprises a full-length sequence
XX of a full-length geminivirus genome. The genome contains an
XX AC1 gene. The AC1 gene encodes a protein that is a transgenic plant
XX containing DNA comprising geminivirus AC1 or CI wild-type or mutant
XX sequences (see AAU93282-93) that negatively interfere in trans with
XX CC geminiviral replication during infection. Such transgenic plants
XX are resistant to viral infection. The AC1/CI genes are especially
XX good from tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic virus.
XX Sequence 2744 BP; 742 A; 539 C; 637 G; 826 T; 0 other;
XX
XX alignment_scores:
XX Quality: 232.00 Length: 65
XX Ratio: 4.296 Gaps: 1
XX Percent Similarity: 83.077 Percent Identity: 69.231
XX
XX alignment_block:
XX US-09-289-346A-10 x AAU93317/rev ..
XX
XX Align seg 1/1 to reverse of: AAU93317 from: 1 to: 2744
XX
XX 4 TrpGlygluPheGlnValAspGlyAAserAlaArgGlyCysGln 20
XX ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 2266 TGGGGTGGAGTTTCAGATGATGAGACATCTGCAGAGGGGCAACAC 2217
XX 20 rSerAsnAspLeuLeuGlnAlaLeuAsnAlaSerLysGlnGln 37
XX ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 2216 AGCTAATGATGCTGCGGACGAGCCCTTAAATGAGATCTACGTGAACAG 2167
XX 37 lAlaGlnIleIleArgGluLysIleProGluLysTyrLeuPheGlnPhe 53

```

```

|||||
2166 CTTTACCAATATTAGAGAAAACCTCCCAAAATTTTATTTTCAATAT 2117
54 H1sAnleuAsnSerAnleuAsnArgIlePheAspLysThrPro 68
|||||
2116 CATTAAATTAAATGTAATTTAGATAGATTTTTC.....NCACG 2078
seq_name: /cgnl_8/gcycdata/geneseq/geneseq/NA1998.DAT:AAV29761

```

```

seq_documentation_block:
ID AAV29761 standard: DNA: 2766 BP.

```

```
AAV29761:
```

```
11-AUG-1998 (first entry)
```

```
DE Tobacco leaf curling virus gene.
```

```
KW Tobacco leaf curling virus gene; TlCV; promoter; ds.
```

```
XX Tobacco leaf curling virus.
```

```
PN JP10070982-A.
```

```
PD 17-MAR-1998.
```

```
PP 30-AUG-1996: 96JP-0230394.
```

```
PK 30-AUG-1996: 96JP-0230394.
```

```
PA (NORQ ) NORINSUTSANSO KYUSHU NOKYO SHIKENYU.
```

```
DR WPI: 1998-233630/21.
```

```
PT Tobacco leaf curling virus gene - useful for inserting into vectors
```

```
PS for expression to, e.g., tomato plants
```

```
PS Claim 1: Figs 1-3: 9pp: Japanese.
```

XX This sequence represents the tobacco leaf curling virus (TlCV) gene of the invention. TlCV gene or its promoter can be inserted into a vector for expression in plants, e.g. tobacco and tomato. This sequence is believed to encode the TlCV proteins shown in AAW34433-445439.

Sequence 2766 BP: 722 A: 576 C: 609 G: 859 T: 0 other:

```
alignment_scores:
```

```

Quality: 225.00 Length: 84
Ratio: 3.780 GAPS: 1
Percent similarity: 72.819 Percent identity: 53.571

```

```
alignment_block:
US-09-289-346A-10 x AAV29761/rev ..
```

```
Align seg 1/1 to reverse of: AAV29761 from: 1 to: 2766
```

```
2 TenvATTPGlyGlyPheGlyValSerArgSerAlaArgGlyGly 18
```

```
2436 CTTGATTTCAGATTTCACAGTCGATGAGATCATCAGTCAGGAGGTTG 2387
```

```
18 sGlnThrSerAsnAspLeuLeuGluAlaLeuAsnAlaSerSerLys 35
```

```
2386 CCAATTCGACACACGCCATATCCGACGACATCACTACGATCAAACT 2337
```

```
35 TugLysAlaGlnGlnIleIleArgGlyLysLysLeuPheLysLys 51
```

```
2336 CATCGCAGCTCAATATATATTAAGGAGAAAGCCCAAGATTGGTTTA 2287
```

```
52 GlnPheHisAsnLeuAsnSerAsnLeuAspArgLys..... 63
```

```
2286 CAAATTCAATATTAAATTAATTAATGATAGATTTTTCCTCCTCAAT 2237
```

```

64 .....PheAspLysThrPro 69
2236 CGAGCTTTTGTTCCTTTCTACTCTTCATTCATTCATGATGCTCTG 2187
69 Lu 69
2186 AA 2185
seq_name: /cgnl_8/gcycdata/geneseq/geneseq/NA1997.DAT:AAV3291

```

```
seq_documentation_block:
ID AAV3291 standard: DNA: 1062 BP.

```

```
AAV3291:
```

```
27-APR-1998 (first entry)
```

```
DE Bean golden mosaic geminivirus CI mutant ORF BGAC221.
```

```
KW Geminivirus: BGWV; CI gene; transdominant mutation;
```

```
XX transgenic plant; disease resistance; ss; cyclic; circular.
```

```
OS Bean golden mosaic virus type II isolate Guatemala.
```

```
PN WO9739110-A1.
```

```
PD 23-OCT-1997.
```

```
PP 15-APR-1997: 97MO-US06300.
```

```
PK 16-APR-1996: 96US-0015517.
```

```
PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
```

```
PT (WISC ) WISCONSIN ALMONI RBS FOUNDD.
```

```
DR Ahlquist PG, Hanson SF, Iann HT, Maxwell DP, Stout JF.
```

```
DR P-PSDB: AAW34333.
```

XX Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant genes - have increased resistance to geminivirus infection

XX e.g., tomato mosaic virus, tomato yellow leaf curl virus or bean golden mosaic geminivirus

PS Claim 13: Page 107-109; 132pp: English.

XX This DNA sequence comprises construct BGAC221 that codes for a transdominant lethal mutant (see AAW34333) of the CI protein (see AAW34338) of bean golden mosaic virus (BGWV). The AAW34333 construct is required for replication. The invention involves production of transgenic plants containing DNA comprising geminivirus CI or AC1 wild-type or mutant sequences that negatively interfere in trans with geminiviral replication during infection. Such transgenic plants are resistant to viral infection. The AC1/CI genes are especially useful for resistance to bean golden mosaic virus (see AAW3282193) and other geminiviruses (see AAW34324-35) that have mutations in the highly conserved DNA-nicking and/or the NTP-binding domains.

Sequence 1062 BP: 339 A: 245 C: 259 T: 0 other:

```
alignment_scores:
```

```

Quality: 223.00 Length: 70
Ratio: 3.780 GAPS: 0
Percent similarity: 84.286 Percent identity: 60.000

```

```
alignment_block:
US-09-289-346A-10 x AAV3291 ..
```

```
Align seg 1/1 to: AAV3291 from: 1 to: 1062
```

```

1 ThrLeuValTrpGlyIuPhgInValAspGlyArSerAlaArgIylG1 17
   |||
328 ACAATCGAATGGGAGCAATTCGACAGTCGACGACATCTGCAGAAAGAG 377
17 YcsgIuPhgInTrSerAspLeuLeuGluAlaLeuAsnAlaSerSerL 34
   |||
378 TCAGACGCTCGCCACGACATCTCATCTGCAGACGATTTAAACGAGATTCMA 427
34 YcsgIuGluAlaLeuGluInIleIleArgIuGlyIleProGluuYTyIuDen 50
   |||
428 TCGATCTCGCTCGCAATTCGACAGTCGACGACATCTGCAGAAAGAG 477
51 PhgGluPhgInPhgInAsnLeuAsnSerAsnLeuAspArgIlePhAspIySTh 67
   |||
478 CTCACACATCCACACATCCCTCTCATCTGCAGACGATCTTCGCAAACT 527
67 rProGluPro 70
   |||
528 GCCGAGAACCA 537

seq_name: /cgnl_8/ycgdata/geneseq/geneseq/NA1997.DAT:AA193292
seq_documentation_block:
ID AA193292 standard: DNA; 1062 BP.
XX
XX AA193292:
XX
XX 27-APR-1998 (first entry)
XX
XX Bean golden mosaic geminivirus CI mutant ORF BGAC228.
XX
XX Geminivirus: BGWV; CI gene; transdominant mutation;
XX transgenic plant; disease resistance; ss: cyclic; circular.
XX
XX Bean golden mosaic virus type II isolate Guatemala.
XX
XX MO9739110-A1.
XX
XX 23-OCT-1997.
XX
XX 15-APR-1997: 97MO-U0506300.
XX
XX 16-APR-1996: 96US-0015517.
XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX (WISC) WISCONSIN ALUMNI RES FOUND.
XX
XX Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT:
XX WPI: 1997-526447/48.
XX P-PSDB: AAM34334.
XX
XX Transgenic plants expressing geminivirus ACI and CI wild-type and
XX mutant genes - have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX
XX Claim 13: Page 111-112; 132pp; English.
XX
XX This DNA sequence comprises construct BGAC228 that codes for a
XX transdominant lethal mutant (see AAM34334) of the CI protein (see
XX AAM34338) of bean golden mosaic virus (BGWV). It was obtained by
XX Kunzi mutagenesis of the wild-type CI gene (see AA193314). CI is
XX required for replication. The invention involves production of
XX transgenic plants containing DNA comprising geminivirus CI or ACI
XX gene sequences that negatively affect the ability of the virus to
XX with geminiviral replication during infection. Such transgenic
XX plants are resistant to viral infection. The ACI/CI genes are
XX especially from BGWV, tomato mottle virus or tomato yellow leaf
XX curl virus (see AA193283-93) and encode polypeptides (see AAM34324-35)
XX that have mutations in the highly conserved DNA-nicking and/or the
XX NTP-binding domains.

```

```

XX
XX Sequence 1062 BP; 328 A; 247 C; 218 G; 259 T; 0 other;
XX
XX Alignment_scores:
XX Quality: 223.00 Length: 70
XX Ratio: 3.780 Gaps: 0
XX Percent Similarity: 84.286 Percent Identity: 60.000
XX
XX Alignment_block:
XX US-09-289-346a-10 x AA193292 ..
XX
XX Align seg 1/1 to: AA193292 from: 1 to: 1062
XX
XX 1 ThrLeuValTrpGlyIuPhgInValAspGlyArSerAlaArgIylG1 17
   |||
328 ACAATCGAATGGGAGCAATTCGACAGTCGACGACATCTGCAGAAAGAG 377
17 YcsgIuPhgInTrSerAspLeuLeuGluAlaLeuAsnAlaSerSerL 34
   |||
378 TCAGACGCTCGCCACGACATCTCATCTGCAGACGATTTAAACGAGATTCMA 427
34 YcsgIuGluAlaLeuGluInIleIleArgIuGlyIleProGluuYTyIuDen 50
   |||
428 TCGATCTCGCTCGCAATTCGACAGTCGACGACATCTGCAGAAAGAG 477
51 PhgGluPhgInPhgInAsnLeuAsnSerAsnLeuAspArgIlePhAspIySTh 67
   |||
478 CTCACACATCCACACATCCCTCTCATCTGCAGACGATCTTCGCAAACT 527
67 rProGluPro 70
   |||
528 GCCGAGAACCA 537

seq_name: /cgnl_8/ycgdata/geneseq/geneseq/NA1997.DAT:AA193293
seq_documentation_block:
ID AA193293 standard: DNA; 1062 BP.
XX
XX AA193293:
XX
XX 27-APR-1998 (first entry)
XX
XX Bean golden mosaic geminivirus CI mutant ORF BGAC262.
XX
XX Geminivirus: BGWV; CI gene; transdominant mutation;
XX transgenic plant; disease resistance; ss: cyclic; circular.
XX
XX Bean golden mosaic virus type II isolate Guatemala.
XX
XX MO9739110-A1.
XX
XX 23-OCT-1997.
XX
XX 15-APR-1997: 97MO-U0506300.
XX
XX 16-APR-1996: 96US-0015517.
XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX (WISC) WISCONSIN ALUMNI RES FOUND.
XX
XX Ahlquist PG, Hanson SF, Luu HT, Maxwell DP, Stout JT:
XX WPI: 1997-526447/48.
XX P-PSDB: AAM34335.
XX
XX Transgenic plants expressing geminivirus ACI and CI wild-type and
XX mutant genes - have increased resistance to geminivirus infection
XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
XX golden mosaic geminivirus
XX
XX Claim 13: Page 115-116; 132pp; English.
XX

```


DF Bean golden mosaic geminivirus CI mutant gene.
 XX Geminivirus; BGMV; CI gene; transdominant mutation;
 XX transgenic plant; disease resistance; ss; cyclic; circular.
 XX Bean golden mosaic virus type II isolate Guatemala.
 OS
 FH Key Location/Qualifiers
 FH CDS 1..1062
 FH /tag= a
 XX MO979110-A1.
 XX
 XX 23-OCT-1997.
 XX
 XX 15-APR-1997: 97WO-US06300.
 XX
 XX 16-APR-1996: 960S-0015517.
 XX (SEM-) SEMINIS VEGETABLE SEEDS INC.
 XX (WISC-) WISCONSIN ALUMNI RES FOUND.
 XX
 XX Ahiquist PG, Hanson SF, Luu HF, Maxwell DP, Stout JT:
 XX WPI: 1997-526447/48.
 XX P-PSDB: AAM34332.
 XX
 XX Transgenic plants expressing geminivirus AC1 and CI wild-type and
 XX mutant genes - have increased resistance to geminivirus infection
 XX e.g. tomato mottle virus, tomato yellow leaf curl virus or bean
 XX golden mosaic geminivirus
 XX
 XX Claim 13: Page 103-105; 132pp; English.
 XX
 XX This DNA sequence comprises construct BGC190 that codes for a
 XX chimeric protein (AA1432). It was obtained by fusion of bean
 XX golden mosaic virus (BGMV)-CI gene with the C-terminal region of the
 XX of the wild-type CI gene (see AA93314). CI is required for
 XX replication. The invention involves production of transgenic
 XX plants containing DNA comprising geminivirus CI or AC1 wild-type or
 XX mutant sequences that negatively interfere in trans with
 XX geminivirus replication during infection. Such transgenic plants
 XX are resistant to geminivirus infection. The AC1 genes are especially
 XX from BGMV, tomato mottle virus, tomato yellow leaf curl virus (see
 XX AA93282-93) and encode polypeptides (see AA94322-35) that have
 XX mutations in the highly conserved DNA-nicking and/or the NTP-binding
 XX domains.
 XX
 XX Sequence 1183 BP; 371 A; 277 C; 249 G; 266 T; 0 other;
 SO
 Alignment_scores:
 Alignment_quality: 223.00 Length: 70
 Alignment_ratio: 3.780 Gaps: 0
 Percent Similarity: 84.286 Percent Identity: 60.000
 alignment_block:
 US-09-289-346a-10 x AA933290 ..
 Align seg 1/1 to: AA933290 from: 1 to: 1183
 1 Thleuvaltrfpglyglupheginvalapclvayseerlaatrgygl 17
 328 ACATGTGATGATGGGACATTCGACATGCGACGACATTCGACAGAGAG 377
 17 YCysGILthSerAspLeuLeuLeuLualalaLeuAlaSerL 34
 378 TCACAGAGTCGACAGACGTCATATGCAAGCATTAAAGCGAGATTCA 427
 34 YGSLuGLuAlaLeuGlnLleIeaRgluLysIleproGluLysTYfieu 50
 428 TTGAATCTGCTTGCAATATTAAGAGAAACGCAAAAGATTATGTC 477

51 PheGlnPheHisAsnLeuAsnSerAsnLeuAspArgIlePheAspLysTh 67
 478 CTTGACATGACACATCCGCTTACTATCGAAGCGATTCGTCGAAGT 527
 67 +ProGluGlu 70
 528 GCGCGAACCA 537
 seq_name: /cgnl_8/gcgdata/geneseq/genesepq/NA2000.DAT:AAA94700
 seq_documentation_block:
 20 AAA94700 standard; DNA; 1651 BP.
 AC AAA94700:
 DT 15-JAN-2001 (first entry)
 DE PMR3 2288 35S-rep gene cassette.
 XX Geminivirus; DNA-A; geminivirus replication inhibition; ac3 gene;
 XX transgenic plant; disease resistance; ss; cyclic; circular.
 XX BGMV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CMV; ds.
 XX
 XX Bean golden mosaic virus.
 XX Cauliflower mosaic virus.
 XX Alfalfa mosaic virus.
 XX Synthetic.
 XX US6118048-A.
 XX 12-SEP-2000.
 XX
 XX 24-APR-1998: 98US-0065999.
 XX
 XX 25-APR-1997: 97US-0044925.
 XX (WISC-) WISCONSIN ALUMNI RES FOUND.
 XX
 XX WPI: 2000-610861/58.
 XX
 XX genetic construct comprising a mutant geminiviral rep gene, useful for
 XX producing a plant resistant to geminiviral infection.
 XX
 XX Example: Column 15-16; 14pp; English.
 XX
 XX The present sequence is a 35S-rep gene cassette comprising the rep gene
 XX of bean golden mosaic virus (BGMV)-GA cloned downstream of the CMV
 XX 35S promoter and an alfalfa mosaic virus (AMV) leader sequence. The
 XX sequence was integrated into pSIL1-KS+ to produce a rep gene expression
 XX vector. DNA-nicking domain mutations may be incorporated into rep gene
 XX to produce a genetic construct that acts as a trans-dominant inhibitor
 XX of geminivirus replication. The inhibitor is able to dramatically reduce
 XX geminivirus replication efficiency in transgenic plants.
 XX Genetic constructs that include sequences containing a portion of the
 XX ac3 gene in addition to the trans-dominant inhibitor exhibit increased
 XX efficiency and broadened specificity of inhibition of geminiviral
 XX replication. Geminiviruses are one of the greatest constraints on
 XX production of important crops, including cassava, beans, cowpeas,
 XX peppers, tomatoes and cotton. The effects of the virus can be overcome
 XX by using the genetic construct.
 XX
 XX Sequence 1651 BP; 517 A; 393 C; 342 G; 399 T; 0 other;
 SO
 Alignment_scores:
 Alignment_quality: 223.00 Length: 70
 Alignment_ratio: 3.780 Gaps: 0
 Percent Similarity: 84.286 Percent Identity: 60.000
 alignment_block:
 US-09-289-346a-10 x AAA94700 ..
 Align seg 1/1 to: AAA94700 from: 1 to: 1651

exhibit increased efficiency and broadened specificity of inhibition of geminiviral replication. Geminiviruses are one of the greatest constraints on production of important crops, including cassava, beans, cowpeas, peppers, tomatoes and cotton. The effects of the virus can be overcome by using the genetic construct.

Sequence 1894 BP; 604 A; 421 C; 388 G; 481 T; 0 other:

alignment_scores:

Quality: 223.00 Length: 70

Ratio: 3.780 Gaps: 0

Percent Similarity: 84.286 Percent Identity: 60.000

alignment_block:

US-09-289-346a-10 x AAA94703 ..

Align seg 1/1 to: AAA94703 from: 1 to: 1894

1 Thleuvaltrpglyluphheglnalaspolyarvgsrslatarglycl 17

796 ACATCGAATGSGGACATTCGACATCGACAGATCTCGACAGAG 845

17 YCYSGLNTHSRASAPLEULELEULALALALALALALALASER 34

846 TCAGAGCTCTCGACAGCATCATATCGAAGCATTAACCGCATTC 895

34 YSGLUJLALALEUGLNLLEATRGILUYSILLEPGLUYSYTYEU 50

896 TTCATCTCGCTCGACCATATTCAGAGCAACGATTAACGATTC 945

51 PhcglNphelHlaenleuanserleuaspapargllapheaply 67

946 CTTCACATCATCACATCCCTCTTAATCTGACAGCATCTTGCA 995

67 PProclupro 70

996 GCCGGAACCA 1005

seq_name: /cgnl_8/gcdata/geneseq/geneseq/NA2000.DAT:AAA94702

seq_documentation_block:

ID AAA94702 standard; DNA: 2072 BP.

AC AAA94702:

XX 15-JAN-2001 (first entry)

XX pTRep23 nucleotide sequence.

XX geminivirus; DNA-T; geminivirus replication inhibition; ac3 gene;

XX transgenic plant; antiviral; gene therapy; ds.

XX Synthetic.

XX US6118048-A.

XX 12-SEP-2000.

XX 24-APR-1998: 98US-0065999.

XX 25-APR-1997: 97US-0044925.

XX (MISC) WISCONSIN ALUMNI RESS FOUND.

XX WPI: 2000-610861/58.

XX Genetic construct comprising a mutant geminiviral rep gene, useful for

XX producing a plant resistant to geminiviral infection -

XX Example: Column 17-20; 14bp; English.

XX The present sequence is pTrep23. It contains the wild type geminivirus

rep gene sequence. Genetic constructs containing DNA-nicking domain mutants in the rep gene may be used as trans-dominant inhibitors of geminiviral replication. When expressed in a plant cell,

these inhibitors are able to dramatically reduce replication of geminiviruses. Genetic constructs that include sequences containing a

geminiviral replication origin and a DNA-nicking domain can be used to

exhibit increased efficiency and broadened specificity of inhibition of

geminiviral replication. Geminiviruses are one of the greatest

constraints on production of important crops, including cassava, beans,

cowpeas, peppers, tomatoes and cotton. The effects of the virus can be

overcome by using the genetic construct.

Sequence 2072 BP; 661 A; 467 C; 421 G; 523 T; 0 other:

alignment_scores:

Quality: 223.00 Length: 70

Ratio: 3.780 Gaps: 0

Percent Similarity: 84.286 Percent Identity: 60.000

alignment_block:

US-09-289-346a-10 x AAA94702 ..

Align seg 1/1 to: AAA94702 from: 1 to: 2072

1 Thleuvaltrpglyluphheglnalaspolyarvgsrslatarglycl 17

796 ACATCGAATGSGGACATTCGACATCGACAGATCTCGACAGAG 845

17 YCYSGLNTHSRASAPLEULELEULALALALALALALALASER 34

846 TCAGAGCTCTCGACAGCATCATATCGAAGCATTAACCGCATTC 895

34 YSGLUJLALALEUGLNLLEATRGILUYSILLEPGLUYSYTYEU 50

896 TTCATCTCGCTCGACCATATTCAGAGCAACGATTAACGATTC 945

51 PhcglNphelHlaenleuanserleuaspapargllapheaply 67

946 CTTCACATCATCACATCCCTCTTAATCTGACAGCATCTTGCA 995

67 PProclupro 70

996 GCCGGAACCA 1005

seq_name: /cgnl_8/gcdata/geneseq/geneseq/NA1996.DAT:AA112904

seq_documentation_block:

ID AA112904 standard; DNA: 1080 BP.

AA112904:

XX 07-NOV-1996 (first entry)

XX Sardinian tomato yellow leaf curl virus mutated C1 gene (K227A).

XX Nucleotide triphosphate binding site; DNA helicase; RNA helicase;

XX viral resistance; geminivirus; tomato yellow leaf curl virus;

XX Sardinian isolate; SYRVCY; transgenic plant; P-loop; C1 gene;

XX All gene; dominant negative phenotype; ss.

XX Sardinian tomato yellow leaf curl virus.

XX Key

XX Location/Qualifiers

XX 11080

XX CDS

XX /tag= a

XX /product= Rep (K227A)

XX /note= "encodes Rep protein in which wild-type Lys

at position 227, i.e. within the NTP-

binding site, is replaced by Ala"

XX MO3608573-A1.

alignment_scores:

Quality: 68.50 Length: 54
Ratio: 1.903 Gaps: 3
Percent Similarity: 66.667 Percent Identity: 35.185

alignment_block:

US-09-289-346a-10 x BG595046/rev ...

Align seq 1/1 to reverse of: BG595046 from: 1 to: 732

```

11 GYAGSerGAlaArgLYGcysGlnHtSerGAsp.....Leu25
|||||.....|
408 GCAAGTCAGCTGCTAGCAAGCTCTAGAGAGTATAGCAATGACCTT 359
|||||.....|
25 uLcngUAlaLeuAsnAlaSerSerLYGcysGlnUAlaLeuG 42
|||||.....|
358 TATTAGAGCCAAATAGCAAGCTCTTACCAATATTCACAGTTAGCA 309
|||||.....|
42 rGcUdysIleProGluLYSTyLeupHneGlnHtAsn.....Leu58 57
|||||.....|
308 AATAAGAGTTT.....CTTCAGCTGTGTACAGTTCACAGTACGCTCAG 265
|||||.....|
58 SerAsnLeuAsp 61
|||||.....|
264 AACATATTCAC 253

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seq_name: gb_est2.BF544043

seq_documentation_block:

LOCUS BF544043 297 bp mRNA 11-DEC-2000
DEFINITION UI-R-E0-cl-e-12-0-UI.r1 UI-R-E0 Rattus norvegicus cDNA clone
UI-R-E0-cl-e-12-0-UI.5', mRNA sequence.
ACCESSION BF544043 GI:11635150
VERSION BF544043.1
KEYWORDS EST.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 297)
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
JOURNAL Genome Res. 6 (9): 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Email: msoares@blue.weeg.uiowa.edu
Fax: 319 335 9565

FEATURES
SOURCE
1..297
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="UI-R-E0-cl-e-12-0-UI"
/clone_1lb="UI-R-E0"
/lab_host="DH10b (Life Technologies)"
/note="Vector: pT730-Pac (Pharmacia) with a modified
polylinker. Site_1: NotI; Site_2: EcoRI; This library
consists of a mixture of individually tagged normalized
libraries constructed from 8, 12 and 18-day embryo. The
tag is a string of 3-5 nucleotides present between the

Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture.."

alignment_scores:

Quality: 68.00 Length: 59
Ratio: 2.125 Gaps: 2
Percent Similarity: 54.237 Percent Identity: 37.288

alignment_block:

US-09-289-346a-10 x BF544043 ...

Align seq 1/1 to: BF544043 from: 1 to: 297

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6 GluPheGlnValAspLYAGSerGAlaArgLYGcysGlnHtSerGAs 22
|||||.....|
69 CAGCTTACGGCTCAGTCGACGACGAGAGTAT.....TGTGACAGCTCA 109
|||||.....|
22 rAspLeuLeuGluAlaLeuAsnAlaSerSerLYGcysGlnUAlaLeu 39
|||||.....|
110 ACGTTCTCTTGGCTTCGCCAGCACGACGAGGAGGAGGAGAACCA.... 155
|||||.....|
39 InUleIleArgLYSTyIleProGluLYSTyLeupHneGlnHtAsn 55
|||||.....|
156 .....AAT 158

```

seq_name: gb_est1.AA72985
seq_documentation_block: 396 bp mRNA 22-JAN-1998
LOCUS AA72985 n34b10.s1 NCI_CGAP_C04 Homo sapiens cDNA clone IMAGE:125797 3',
DEFINITION mRNA sequence.
ACCESSION AA72985.1 GI:2751344
VERSION AA72985.1
KEYWORDS EST.
SOURCE Human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.

REFERENCE 1 (bases 1 to 396)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Contact: Robert Stransberg, Ph.D.
Email: stransb@remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Sequencing Center
This library was constructed by the NCI-CGAP Consortium. Information can be
found through the I.M.A.G.E. Consortium/LINL at:
www.bio.llnl.gov/bpfr/image/image.html
Insert Length: 551 Std Error: 0.00
Seq primer: 40ml3 fwd. ET from Amersham
High quality sequence stop: 380.
Location/Qualifiers
1..396
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/db_xref="taxon:9606"
/clone="IMAGE:125797"
/clone_1lb="NCI-CGAP_C04"
/lab_host="DH10b (Life Technologies) with a modified
polylinker. Site_1: NotI; Site_2: EcoRI; This library
consists of a mixture of individually tagged normalized
libraries constructed from 8, 12 and 18-day embryo. The
tag is a string of 3-5 nucleotides present between the


```

|||||
228 TAGAATCATCTCTCTAAACACTTCCACATCTCATCTTCCCTTTAAAA 277
53 Glaphehis 54
|||||
278 CAGTTTCNC 286
seq_name: gb-est1:A1335201

seq_documentation_block:
LOCUS A1335201 407 bp mRNA EST 13-FEB-1999
DEFINITION gb85h10.x1 NCI_CGAP_K1d5 Homo sapiens cDNA clone IMAGE:191563 3',
mRNA sequence.
ACCESSION A1335201
VERSION A1335201.1 GI:40721228
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Colarthrin; Homnidae; Homo.
REFERENCE
1 (bases 1 to 407)
NCI-CCAP http://www.ncbi.nlm.nih.gov/nciccap
AUTHORS (NCI) Cancer Institute; Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-tr@mail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmett-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Screening: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/IML at:
www-bio.liml.gov/bbtp/image/image.html
Insert length: 908 Std Error: 0.00
Seq primer 500P forward
High quality sequencing stop 405.
location/Qualifiers
1..407
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="1915363"
/clone_lib="NCI_CGAP_K1d5"
/submitter="NCI"
/notes="278 cloned tumors (clear cell type)"
/assay="PCR"
/ass host="pH10H8"
/notes="Organ: Kidney; Vector: pTZ19-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
AAGTCGACGATTCGCGCCGCAATATTTTCTTTTCTTTT 3').
double-stranded cDNA was ligated to EcoRI adaptor
(Pharmacia) and ligated into the Not I
restriction sites of the modified pTZ19 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo. "
```

BASE COUNT 160 a 73 C 62 g 112 T

ORIGIN

alignment_scores:
Quality: 66.50 Length: 57
Ratio: 1.750 Gaps: 4
Percent similarity: 66.667 Percent identity: 33.333

alignment_block:

US-09-289-346a-10 x A1335201
Align seg 1/1 to: A1335201 from: 1 to: 407

15 ArgGlyGlyCysGln.....ThrsrAsnAspLeuLeuGlnGln 28
|||||
127 AGGGAGGTTCCACTTATATACACTTAAATACACTTCTCATATACG 176

```

28 AlaAsnAlaSerLysGlnGlnAlaLeuGlnIleLeuArgGln.... 43
|||||
177 TTATACGACATCACCAGGGCTAAGGATTAAAGATTTCACAGACGACAT 226
|||||
44 .....LysIleProGlnLysGlyTyrLeuPheGlnIlePheHisAsn 55
|||||
227 CCAGGACACACATGAAACCTCCCA...AAGTTCATATTCGAG..... 264
|||||
56 LeuAsnSerAsnLeuAspArg 62
|||||
265 CTAAATGCTTCATTTTAAACCG 285
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Fri Jan 4 09:37:09 2002

us-09-289-346a-10.p2h.rst

Page 10

Align seq 1/1 to: US-08-838-151A-48 from: 1 to: 1062

1 TTTTAAATCTPpD1yGtLupheC1ValAspClYasGerAtAlArGdYlYgl 17
2 TTTTAAATCTPpD1yGtLupheC1ValAspClYasGerAtAlArGdYlYgl 18
3 ACACATCAATTGGAGCATTCGACAGTGACGCGACATCTCCAGACAGC 377
4 TTGTGGGCTTAATGTAATAATpLeuAplleuGCUAlAlaAenAlASerSeRt 34
5 TT 35
6 TGCAGCATCTGCCACACGACTCATATCGATCAAAGCATTTAAACCAGATTTAA 427
7 yGtGUAlAlaAuGSh1e1leIAreGtUtlrStIleProDUlyvryfIden 50
8 TT 51
9 TGAATATCTCTTGACATTTATTCGAGAAGAACGACAAAGATACATC 477
10 PhelGpPhAlHAspIleAsnSerSAsenSAsnApArGlIlePhesPlYrTh 67
11 TT 68
12 CTTCACATCACACAACATCGCTTATCTGACGACGATCTTCGCAAGC 527
13 TTTTAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 528
14 GCGGGAACCA 537

seq_name: /cgn1_7/pdatocare/1/mna/R.COMB.seq-US-08-838-151A-51
seq_documentation_block:
Sequence 51, Application US/08038151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T.
INVENTOR: Luu, Hang T.
APPLICANT: Maxwell, Douglas
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPILER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/PMS-DOS
SOFTWARE: Platinum Release #1.0, Version #1.30
CURRENT RELEASE DATE: 05/08/93B,151A
APPLICATION NUMBER: US/08/938,151A
FILING DATE:
CLASSIFICATION: B00
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEX: 312-616-5460
INFORMATION FOR SEQ ID NO.: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
RECOMBINANT/DNA CLONING VECTOR:
ART OR SYNTHETICALLY DERIVED: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Geminivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala


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1 ThleuValITpGlyglnupheglnValaspGlyArgSerAlaArgGly 17
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
796 ACATATCAATGAGGACATCTCAATCAAGCAGCAGCATCTCCAAAGAG 845
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
17 YCysGlnThrSerAsnAspLeuLeuGlnValAlaLeuAsnAlaSerSer 34
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846 TCAGCAGCTCCGCAACGACATCATCAAGGCAATTAACGCAATTCGA 895
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34 yGlnGlnAlaLeuGlnIlleIleArgGlnGlyAlleProGlnGlyTyrLeu 50
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946 CTTCAACATCAACACATCCGCTTATCACTCGAACGAGATCTCGCAAGT 995
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seq_name: /cgnl_7/ptodata/1/lna/6A_COMB.seq:us-09-065-999-8

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seq_documentation_block:
/ Sequence 8, Application US/09065999
/ Patent No. 6,110,018
/ General Information:
/ APPLICANT: Hanson, Stephen F.
/ TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
/ TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS: Brady
/ STREET: One South Pinckney Street
/ CITY: Madison
/ STATE: WI
/ COUNTRY: US
/ ZIP: 53701-2113
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/065,999
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hanson, Stephen F.
/ REGISTRATION NUMBER: 27,386
/ REFERENCE/DOCKET NUMBER: 960296,94754
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 608-251-5000
/ TELEFAX: 608-251-9166
/ INFORMATION FOR SEQ ID NO: 8:
/ SOURCE: CHARACTERISTICS:-
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-09-065-999-8

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alignment_scores:

Quality:	223.00	Length:	70
Ratio:	3.780	Gaps:	0
Percent Similarity:	84.286	Percent Identity:	60.000

alignment_block:

US-09-289-346a-10 x US-09-065-999-8

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Align seq 1/1 to: US-09-065-999-8 from: 1 to: 1894
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796 ACATATCAATGAGGACATCTCAATCAAGCAGCAGCATCTCCAAAGAG 845
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17 YCysGlnThrSerAsnAspLeuLeuGlnValAlaLeuAsnAlaSerSer 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
846 TCAGCAGCTCCGCAACGACATCATCAAGGCAATTAACGCAATTCGA 895
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34 yGlnGlnAlaLeuGlnIlleIleArgGlnGlyAlleProGlnGlyTyrLeu 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
896 TTGATCTGCGCTTCACATCTTAAAGAGAACACACGAAACATTCACGC 945
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51 PheGlnPheIleAsnLeuAsnSerAsnLeuAspArgIlePheAspArg 67
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
946 CTTCAACATCAACACATCCGCTTATCACTCGAACGAGATCTCGCAAGT 995
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
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996 GCGGAAACCA 1005

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seq_name: /cgnl_7/ptodata/1/lna/6A_COMB.seq:us-09-065-999-7

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seq_documentation_block:
/ Sequence 7, Application US/09065999
/ Patent No. 6,110,018
/ General Information:
/ APPLICANT: Hanson, Stephen F.
/ TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
/ TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS: Brady
/ STREET: One South Pinckney Street
/ CITY: Madison
/ STATE: WI
/ COUNTRY: US
/ ZIP: 53701-2113
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/065,999
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hanson, Stephen F.
/ REGISTRATION NUMBER: 27,386
/ REFERENCE/DOCKET NUMBER: 960296,94754
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 608-251-5000
/ TELEFAX: 608-251-9166
/ INFORMATION FOR SEQ ID NO: 7:
/ SOURCE: CHARACTERISTICS:-
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-09-065-999-7

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alignment_scores:

Quality:	223.00	Length:	70
Ratio:	3.780	Gaps:	0
Percent Similarity:	84.286	Percent Identity:	60.000

alignment_block:

US-09-289-346a-10 x US-09-065-999-7

Align seg 1/1 to: US-09-065-999-7 from: 1 to: 2072

[illegible]

seq_name: /cgn1_7/ptodata/1/ina/5A_COMB.seq:US-08-809-103B-7

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seq_documentation_block:
Sequence 7, Application US/06891013B
Patent No. 0113503
GSMN: 1100003 CN
APPLICANT: GROENBORGH, Bruno
TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT TO TRANSGENIC PLANTS AND SEEDS FOR OBTAINING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: JONGE & THOMPSON
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: SYMBIOSIS/MSDOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: FR 94,11040
FILING DATE: 15-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: NO PCT /FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
RESISTRATION NUMBER: 32,925
REGISTERED ADDRESS: 1000 S. GARDNER AVE., SUITE 100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1145 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1077

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US-08-809-103B-7

alignment_scores:	Quality: 221.00	Length: 69
	Ratio: 3.877	Caps: 0
Percent Similarity:	82.609	Percent Identity: 56.522

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 18 sGlnThrSerAsnAspLeuLeuGluGlnAlaLeuAlaLysSerSetIysG 35
 381 AGCAGCAGGCCAACGACGGCTTACGCAAAAGCCAAATTAACCCAGGACAGTAACT 430
 33 LcdGlnAlaLeuGlnLleLeuArgGlyLysIleProGlyStryLeuPhe 51
 431 CGGAGCTCTGATGATGATTAAGAGCAATTAACGCTCAAGACATCTTCA 480
 52 GlnProHisAsnIleuLysSerAsnLeuAspArgIleLeuPheAspIyThrPr 68
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 66 ogIuPro 70
 531 GGCACT 537

seq_name: /cgn1_7/ptodata/1/lna/5A_COMB.seq:US-08-809-103B-1

Seq.documentation_block:
1. Sequence 1, Application US/088091038
2. Patent No. 6133505
3. GENERAL INFORMATION:
4. APPLICANT: IRONENBORN, Bruno
5. TITLE OF INVENTION: TRANSGENIC DNA VIRUS RESISTANT
6. TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS FOR OBTAINING SAME
7. NUMBER OF SOURCES: 17
8. CORRESPONDENCE ADDRESS:
9. ADDRESSEE: YOUNG & THOMPSON
10. STREET: 745 South 23rd Street
11. CITY: Arlington
12. STATE: Virginia
13. COUNTRY: U.S.A.
14. ZIP: 22202
15. COMPUTER READABLE FORM:
16. MEDIUM TYPE: Floppy disk
17. OPERATING SYSTEM: IBM PC compatible
18. SOFTWARE: Patent Release #1.0, Version #1.30
19. CURRENT APPLICATION NUMBER: US/08/809,1038
20. PRIORITY NUMBER: 17-Sep-1997
21. CLASSIFICATION: B001-1997
22. PRIORITY APPLICATION DATA:
23. APPLICATION NUMBER: FR 94, 11040
24. FILING DATE: 15-SEP-1994
25. PRIORITY APPLICATION DATA:
26. APPLICATION NUMBER: WO PCT/FR95/01192
27. FILING DATE: 15-SEP-1995
28. ATTORNEY/AGENT INFORMATION:
29. REGISTRATION NUMBER: U3, 925
30. REFERENCE/DOCKET NUMBER: US94AL CNR TOM
31. TELECOMMUNICATION INFORMATION:
32. TELEPHONE: (703) 521-2297
33. TELEFAX: (703) 685-0573
34. TELEX: 248425 EMBON

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? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 148 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1077
? US-08-809-103B-1

alignment_scores:
? Quality: 221.00 Length: 69
? Ratio: 3.877 Gaps: 0
? Percent Similarity: 82.609 Percent Identity: 56.522

alignment_block:
? US-09-289-346a-10 x US-08-809-103B-1
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Align seg 1/1 to: US-08-809-103B-1 from: 1 to: 1148

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331 CTTGATGGGGTACTTCCACATCGACGACGACGATCGCTAGGGAGACGACA 380
18 scIlnTrSerAraAspLeuGluGlnAlaLeuAsnAlaSerSerIysG 35
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381 ACAGACGCCACGACGCGCTTACCCAAAGCAATTATACCGACGACGATGACT 430

35 IuGlnAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
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431 GCGAGCGCTTCATGATTAATTAAGAAATACGCGCTTAGAGATTCGTTCTCA 480
52 GlnPheHisAsnLeuAsnSerAraLeuAsnAlaArgIlePheAspLysThr 68
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 530
68 GcLupPro 70
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531 GCGACGCT 537

seq_name: /cgnl_7/ptodeta/1/lna/6a_comb.seq:us-08-809-103B-3
seq_documentation_block:
? Sequence 3, Application US/08809103B
? Patent No. 6133505
? GENERAL INFORMATION:
? INVENTOR: GROWNBORN, BRUNO
? TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
? NUMBER OF SEQUENCES: 17
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: YOUNG & THOMPSON
? STREET: 745 South 23rd Street
? CITY: Arlington
? STATE: Virginia
? COUNTRY: U.S.A.
? ZIP: 22202
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? CURRENT RELEASE: Release #1.0, Version #1.30
? APPLICATION NUMBER: US/08/809,103B
? FILING DATE: 17-MAR-1997
? CLASSIFICATION: B00
? PRIOR APPLICATION DATA: FR 94,11040
? FILING DATE: 19-SEP-1994
? PRIOR APPLICATION DATA:

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? APPLICATION NUMBER: NO PCT/FR95/01192
? FILING DATE: 15-SEP-1995
? ATTORNEY/AGENT INFORMATION:
? NAME/ADDRESS: Andrew J.
? TELEPHONE NUMBER: 312, 925
? REFERENCE/DOCKET NUMBER: US99AL CNR TOM
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 521-3297
? TELEFAX: (703) 685-0573
? TELEX: 248425 EMBRON
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1150 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1077
? US-08-809-103B-3

alignment_scores:
? Quality: 221.00 Length: 69
? Ratio: 3.877 Gaps: 0
? Percent Similarity: 82.609 Percent Identity: 56.522

alignment_block:
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18 scIlnTrSerAraAspLeuGluGlnAlaLeuAsnAlaSerSerIysG 35
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381 ACAGACGCCACGACGCGCTTACCCAAAGCAATTATACCGACGACGATGACT 430
35 IuGlnAlaLeuGlnIleIleArgGluLysIleProGluLysTyrLeuPhe 51
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431 GCGAGCGCTTCATGATTAATTAAGAAATACGCGCTTAGAGATTCGTTCTCA 480
52 GlnPheHisAsnLeuAsnSerAraLeuAsnAlaArgIlePheAspLysThr 68
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 CATTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 530
68 GcLupPro 70
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531 GCGACGCT 537

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seq_documentation_block:
? Sequence 5, Application US/08809103B
? Patent No. 6133505
? GENERAL INFORMATION:
? INVENTOR: GROWNBORN, BRUNO
? TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
? NUMBER OF SEQUENCES: 17
? CORRESPONDENCE ADDRESSES:
? ADDRESSEE: YOUNG & THOMPSON
? STREET: 745 South 23rd Street
? CITY: Arlington
? STATE: Virginia
? COUNTRY: U.S.A.
? ZIP: 22202
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/809,1038
 PRIORITY NUMBER: 800
 CLASSIFICATION: B00
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 94.11040
 FILING DATE: 15-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/FR95/01192
 FILING DATE: 15-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: PATCH, Andrew J.
 REGISTRATION NUMBER: 32,925
 REFERENCE/DOCKET NUMBER: US94AL CNR TOM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 521-2297
 TELEFAX: (703) 685-0573
 TELETYPE: 248233800
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1150 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 Molecule type: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1077
 US-08-809-1038-5

alignment_scores:
 Quality: 221.00 Length: 69
 Ratio: 3.877 Gaps: 0
 Percent Similarity: 82.609 Percent Identity: 56.522

alignment_block:
 US-09-289-346a-10 x US-08-809-1038-5 ..

Align seg 1/1 to: US-08-809-1038-5 from: 1 to: 1150

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18 scldtrSerAsnAspLeuLeuLeuGlnAlaLeuAsnAlaSerSerlysg 35
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381 ACGACACCGCCACCGCCCTTACCGACCAAGCATTAACCGACGATTAAGT 430
35 luegluAlaLeuGlnIleIleIleAspGlnLysIleProGlnLysIlePhe 51
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
431 CGCAGCGCTCTGTGATTAATTAAGCAATTAACCGCTTACGATTAAGTCT 480
52 GlnPheIleAsnLeuAsnSerAsnLeuAspArgIlePheAspLysThrpt 68
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seq_documentation_block:

Sequence 1 Application US/08838151A
 Patent No. 6291743
 GENERAL INFORMATION:
 APPLICANT: SCOUT, John T
 APPLICANT: Liu, Hang T
 APPLICANT: Maxwell, Douglas
 APPLICANT: Antiquist, Paul

```

APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CURRENT ADDRESS: Rockey, Milanow & Katz
ADDRESS: 1000 N. Dearborn
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
Molecule type: DNA (clon)
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE: 800
PRIORITY NUMBER: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS1801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
TELETYPE: 312-616-5400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
Molecule type: DNA (genomic)
Molecule type: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Gemini Virus
INDIVIDUAL ISOLATE: Florida
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1127
PUBLICATION INFORMATION:
AUTHORS: Gilbertson, RL
AUTHORS: Hildeval, SH
AUTHORS: Papilomacas, EJ
AUTHORS: Rojas, MR
AUTHORS: Hou, YM
AUTHORS: Maxwell, DP
TITLE: Pseudorecombination between the infectious
TITLE: dsRF mosaic geminiviruses.
JOURNAL: Jour. General Virol.
VOLUME: 74
PAGES: 23-31
DATE: 1993
US-08-838-151A-1
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alignment_scores:
 Quality: 221.00 Length: 70
 Ratio: 3.746 Gaps: 0
 Percent Similarity: 84.286 Percent Identity: 57.143

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 US-09-289-346a-10 x US-08-838-151A-1 ..

Align seg 1/1 to: US-08-838-151A-1 from: 1 to: 1162

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